

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 05:29:07 ; Search time 4527.51 Seconds

(without alignments)  
18316.216 Million cell updates/sec

Title: US-09-325-095-32

Perfect score: 3412

Sequence: 1 ATGCTTCGAAGACCATCATC.....TAACTAGTTCATTCAAAA 3412

Scoring table: IDENTITY NUC

Gapop 10.0, Gapexc 1.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: em\_estdb:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vit:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rtd:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2387.2	70.0	3866	11 AK051885	AK051885 Mus muscu
2	806	23.6	872	13 BQ228953	BQ228953 AGENCOURT
3	739.4	21.7	750	9 AL706270	AL706270 DKF2P6860
4	722	21.2	1063	12 BM470620	BM470620 AGENCOURT

Result No.	Score	Query Match	Length	DB ID	Description
5	719.4	21.1	834	13 BX437220	BX437220 AGENCOURT
6	678.8	19.9	827	13 BU167122	BU167122 AGENCOURT
7	678.2	19.9	833	13 BX437219	BX437219 AGENCOURT
8	666	19.5	753	10 BG497751	BG497751 602543009
9	641.2	18.8	854	14 CB723732	CB723732 UI-M-PYO-
10	633	18.6	809	14 CB246283	CB246283 UI-M-ROO-
11	612	17.9	753	9 AU128890	AU128890 AGENCOURT
12	609.8	17.9	833	12 BM986382	BM986382 EST531169
13	607.8	17.8	759	14 CB520825	CB520825 UI-M-GHO-
14	607.2	17.8	789	13 BU852815	BU852815 AGENCOURT
15	603.6	17.7	785	14 CD349473	CD349473 UI-M-PYO-
16	602.8	17.7	706	9 AU134684	AU134684 AGENCOURT
17	594.2	17.4	844	10 BG31265	BG31265 602417308
18	566.2	16.6	1051	12 BG974639	BG974639 60284877
19	560.8	16.4	730	13 BU481912	BU481912 603470693
20	560.6	16.4	696	14 CD351100	CD351100 UI-M-PYO-
21	554.6	16.3	627	2 HSM084196	HSM084196 Homo sapi
22	551.6	16.2	864	10 BF242935	BF242935 601877985
23	544.2	15.9	759	12 BG867168	BG867168 60286782
24	540.6	15.8	798	10 BG436153	BG436153 602508555
25	540.2	15.8	836	10 BF691754	BF691754 602248287
26	538.4	15.8	548	9 AU280420	AU280420 AGENCOURT
27	534.8	15.7	767	14 CB964053	CB964053 AGENCOURT
28	532.4	15.0	601	10 BE379970	BE379970 60158472
29	506.4	14.8	784	14 CA511243	CA511243 UI-R-FUO-
30	501.8	14.7	505	2 HSM096925	HSM096925 Homo sapi
31	500	14.7	636	9 AV693521	AV693521 AGENCOURT
32	499.6	14.6	533	10 BE279196	BE279196 601156673
33	492.6	14.4	818	13 BU06943	BU06943 603739688
34	491.2	14.4	685	10 AW914263	AW914263 EST345567
35	489.8	14.4	614	13 BU478467	BU478467 603470610
36	486.2	14.2	663	10 BB657738	BB657738 BB657738
37	485	14.2	613	12 B1249391	B1249391 60295709
38	480.6	14.1	841	14 CA791375	CA791375 AGENCOURT
39	480.4	14.1	918	10 BF784374	BF784374 602110149
40	476.8	14.0	887	14 CA986999	CA986999 AGENCOURT
41	472	13.8	600	12 BG806901	BG806901 2042-70 M
42	466.6	13.7	531	9 AW209721	AW209721 u146d02.Y
43	466.2	13.7	978	13 BQ933837	BQ933837 AGENCOURT
44	461.8	13.5	563	13 BQ570031	BQ570031 g1143B05.
45	449.8	13.2	633	9 A1632172	A1632172 t885g07.x

## ALIGNMENTS

RESULT 1  
AK051885  
LOCUS  
DEFINITION  
Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length  
3-kinase, catalytic, alpha polypeptide, full insert sequence.  
ACCESSION  
AK051885  
VERSION  
AK051885.1 GI:26094824  
KEYWORDS  
HTC; CAP trapper.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
REFERENCE  
1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE  
99279253  
PUBMED  
10349636  
AUTHORS  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL  
Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE  
20499374  
PUBMED  
11042159

- REFERENCE  
AUTHORS  
3  
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komano,H., Akiyama,J., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)
- TITLE  
JOURNAL  
PUBMED  
20530913  
11076861  
4  
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Komano,H., Adachi,D., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamana,K., Saito,T., Okazaki,Y., Gotohori,T., Bono,H., Kaubawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,T., Pesole,G., Quackenbush,J., Schriml,L.M., Staahl,F., Suzuki,R., Tomita,M., Wagner,L., Mashio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hotmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzei,L., Mombere,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Sessa,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyokawa,K., Wang,K.H., Weitz,C., Whitaker,C., Wilmberg,L., Wyshak-Borja,A., Yoshida,K., Hasegawa,Y., Kawaji,I., Kohlschki,S. and Hayashizaki,Y.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)
- TITLE  
JOURNAL  
MEDLINE  
2108560  
11217851  
5  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 386)
- REFERENCE  
AUTHORS  
JOURNAL  
ADACHI,J., AIZAWA,K., AKIMURA,T., ARAKAWA,T., BONO,H., CARNINCI,P., FUKUDA,S., FURUNO,M., HANAGAKI,T., HARA,A., HASHIZUME,M., HAYASHIDA,K., HAYASEN,N., HIRAMOTO,K., HIRAKA,T., HIROYANE,T., HOJI,P., IMOCANI,K., ISHII,Y., ITOH,M., KAGAWA,I., KASUKAWA,T., KATO,H., KAWAI,J., KOJIMA,Y., KONDO,S., KONNO,H., KOUDA,M., KOYA,S., KURIHARA,C., MATSUYAMA,T., MIYAZAKI,A., MURATA,M., NAKAMURA,M., NISHI,K., NOMURA,K., NUMAZAKI,R., OHNO,M., OHGOTO,N., OKAZAKI,Y., SAITO,R., SAITOH,H., SAKI,C., SAKAI,K., SAKAZUME,N., SANO,H., SASEKI,D., SHIBATA,K., SHINAGAWA,A., SHIRAKI,T., SOGABE,Y., TAGAMI,M., TAGAWA,A., TAKAHASHI,F., TAKAKU-AKIHARA,S., TAKEDA,Y., TANAKA,T., TOMARU,U., TOYA,T., YASUNISHI,A., MURAMATSU,M. and HAYASHIZAKI,Y.  
Direct Submission  
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsukuba-shi, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)  
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.go.jp/  
URL:http://fantom.gsc.riken.go.jp/  
Location/Qualifiers
- FEATURES

SOURCE	
1. 3866	/organism="Mus musculus"
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	/clone_id="RIKEN full-length enriched mouse cDNA library"
	/dev_stage="12 days embryo"
misc_feature	
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ORIGIN	
Query Match 70.0%; Score 2387.2; DB 11; Length 3866;	
Best Local Similarity 86.8%; Pred. No. 0;	
Matches 2663; Conservative 0; Mismatches 398; Indels 7; Gaps 3;	
Qy	345 AGAATGTTGTTTCTGTCGCGATCGCAGTGTGCAATTGATGTTAAAGATCTGA 404
Db	33 ACATTTCGTTTGTATTGGCATGCCAGTGTGAAATTGATGTTAAAGATCCAGA 92
Qy	405 AGTACAGACTTCGGAAGAAATATCTTAATGTTTGAAGAACTGTGATCTTACGGA 464
Db	93 AGTCCAGACTTTCGGAAGAACTTGAATGTTTGAAGAACTGTGACCTGCGGGA 152
Qy	465 TCTTAATTCACCATAGTGTAGCAATGTATGTCATCCGCGACATGTAGATTTACC 524
Db	153 TCTCACTCGCTCATGACGAGGAATGATGTCCTCCCAATGTGCAAGTCTTCCC 212
Qy	525 AGACTCCCAAGACATATATATATTAATGATAGAGGCCAATAATAGTGTGATTTG 584
Db	213 AGAATCTCCAAAGACATCTACCAAGATTAAGTAAGCAATATATAGTGTGATTTG 272
Qy	585 GGTAAATGTTTCTGCAAAATATATGACAGAGAAATATCTGAAATCAACATGACTG 644
Db	273 GGTAAATGTTTCTGCAAAAGACAGACAGAAATATCACTGAAATCAATCATGACTG 332
Qy	645 TGTGCCGAACAAATATTTGCTGAGCAATCAGAGAAAACCTGAAATGATGTTGCTATC 704
Db	333 TGTGCCAGACAAATCTTGTCTGAAGCAATCAGAGAAAACCTGGAATGTTGTTGTC 392
Qy	705 ATCTGAACAATTAATCTGTGTGTAGATATCAGGCAAGTACATTTTAAAGTGTG 764
Db	393 CTCTGACAGCTGAATCTGTGTCTTGAATATCAGGCAAGTATTTCTGAAGTGTG 452
Qy	765 TGGATGTGATGAATATCTTCTAGAAAATATCTCTGAGTCAATTAAGTATTAAGAG 824
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Qy	825 CTGTATATATGCTTGGAGAGATGCCCAATTTGAAGATATGCTTAAGAAAGCCTTATTC 884
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Qy	885 TCAATCTCAATGAGACTGTTTACCAATGCCATCTTATTCAGAGCACTTCCACAGCTAC 944
Db	573 TCAATCTCAATGAGACTGTTTACCAATGCCATCTTATTCAGAGCACTTCCACAGCTAC 632
Qy	945 ACCATATATGATGAGAAACATCTACAAATCCCTTGGGTATTAATAGAGCACTCAG 1004
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Qy	1005 AATAAAATTTCTTGTGCAACCTTACGATCTTAATATTTGAGACATTTGACAAAGATTTA 1064
Db	693 AATAAAATTTCTTGTGCAACCTTACGATCTTAATATTTGAGACATTTGACAAAGATTTA 752
Qy	1065 TGTTCGAACAGGTATCTACCATGAGAGAAACCTTATGTGACAAATGTAACACTCAAG 1124
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Qy	3345	TACTATATTAATTTAAATATATGTAAACCGCAACAGCGTTTGATAGACTTAAACTTATGTTCA	3404	
Db	3027	TGCTCTAATTAATGTAAACACTGTACACGCAAGCAGGTTTGATAGAC- TAAACTAGTTTA	3085	
Qy	3405	TTTCAAAA	3412	
Db	3086	TTTCAAAA	3093	
RESULT 2	B0228953	872 bp	mRNA	linear
LOCUS	B0228953			EST 02-MAY-2002
DEFINITION	AGENCOURT.7572613 NIH_MGC_92 Homo sapiens CDNA clone IMAGE:6044713			
ACCESSION	B0228953			
VERSION	B0228953.1	GI:20410353		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
AUTHORS	1 (bases 1 to 872)			
TITLE	NIH-MGC http://mgc.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)			
COMMENT	Unpublished			
	Contact: Robert Strausberg, Ph.D.			
	Email: csagbs-remail.nih.gov			
	Tissue Procurement: ATCC			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
	DNA Sequencing by: Agencourt Bioscience Corporation			
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov			
	Plate: LLM13287 row: m column: 02			
	High quality sequence stop: 648.			
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	/lab_host="DH10B (phage-resistant)"			
	/clone_lib="NIH MGC 92"			
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BASE COUNT	265 a	166 c	186 g	255 t
ORIGIN				
Query Match	23.6%	Score 806;	DB 13;	Length 872;
Best Local Similarity	97.9%;	Pred. No. 5.6e-163;		
Matches 848;	Conservative	0;	Mismatches 15;	Indels 3;
Gaps	3;			
Qy	1190	CTCGGCGTGCAGACTTTGCGCTTCCATTTGCTGTGTAAGGCCGAAGGSGTGTAAAG	1249	
Db	1	CTCGTGCTGCTGACTTTGCCGTCGCAATTTGCTGTGTAAGGCCGAAGGSGTGTAAAG	60	
Qy	1250	AGGAACACTGTCATTTGGCATGGGCAATATTAACCTTTGATTACACAGACTCTAG	1309	
Db	61	AGGAACACTGTCATTTGGCATGGGCAATATTAACCTTTGATTACACAGACTCTAG	120	
Qy	1310	TATCTGAAAAAATGCGCTTTGAATCTTTGGCCAGTACCTCATGATTTAGAAATTTGCTGA	1369	
Db	121	TATCTGAAAAAATGCGCTTTGAATCTTTGGCCAGTACCTCATGATTTAGAAATTTGCTGA	180	
Qy	1370	ACCCATATGGTGTTACTGATCAATCAATTAAGAACTCCATGCTTAAGATTGGAGT	1429	

D	b		181	ACCCATTATGGTGTACTGAGTCAAAATCCAAATAAAGAACCCTCATGCTTAGAGTTGGAGT	246
O	y		1430	TTGACTCGTTCAGCAGTGCTGGTAAGTTCCAGATATGTCAGTGATTTGAAGAGCATGCCA	1489
D	b		241	TTGACTGCTGCACGAGTGCTGTAAGTTCCAGATATGTCAGTGATTTGAAGAGCATGCCA	300
O	y		1490	ATTGTCGTGTATCCCGAAGACAGGATTTTGACTATTCGCCAGCAGGACTGAGTAACAGAC	1549
D	b		301	ATTGTCGTGTATCCCGAAGACAGGATTTTGACTATTCGCCAGCAGGACTGAGTAACAGAC	360
O	y		1550	TAGCTAGAGACAATGAATTAAGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACAC	1609
D	b		361	TAGCTAGAGACAATGAATTAAGGAAAATGACAAAGAACAGCTCAAAGCAATTTCTACAC	420
O	y		1610	GAGATCCTCTCTCTGAAATCACTGACGAGAGAAAGATTTCTATGGAATCACAGACACT	1669
D	b		421	GAGATCCTCTCTCTGAAATCACTGACGAGAGAAAGATTTCTATGGAATCACAGACACT	480
O	y		1670	ATTGTGTAACTATCCCGAAATTCCTACCMAATTCGCTCTGTGTTAAATGCAATTCCTA	1729
D	b		481	ATTGTGTAACTATCCCGAAATTCCTACCMAATTCGCTCTGTGTTAAATGCAATTCCTA	540
O	y		1730	GAGATGAAGTAGCCCAAGATGATTTGCTTGGTAAAGAATGGCCCTCAACCAACTGAC	1789
D	b		541	GAGATGAAGTAGCCCAAGATGATTTGCTTGGTAAAGAATGGCCCTCAACCAACTGAC	600
O	y		1790	AGGCTATGAACTTCTTGAGCTGTATATCCCAAGTCTTATGTTGCGATTTGCTGTTG	1849
D	b		601	AGGCTATGAACTTCTTGAGCTGTATATCCCAAGTCTTATGTTGCGATTTGCTGTTG	660
O	y		1850	GGTCTTGAAAAATATTTAACAGATGACAAACTTCTCAGTATTTAATTCAGCTACTAC	1909
D	b		661	GGTCTTG--AAATATTTAACAGATGACAAACTTCTCAGTATTTAATTCAGCTACTAC	719
O	y		1910	AGGCTCTAAATATGAACAATATTTGGATTAAGTCTTGAGATTTTTACTGAAAGAAAG	1969
D	b		720	AGGCTCTAAATATGAACAATATTTGGATTAAGTCTTGAGATTTTTACTGAA- AAAG	778
O	y		1970	CATTGACTAATCAAGAGATTGGGCACTTTTCTTTT- GGCATTTTAAATCGAGATGCAC	2028
D	b		779	CATTGACTAATTCAAAGAGATTGGGCACTTTTCTTTTGGGCTTTTAAACCTGAATGCC	838
O	y		2029	AATTAACCAATTAGCCNAGAGTTTG 2054	
D	b		839	CATTAACCGTTAACCCAAAGTTTG 864	
<hr/>					
RESULT 3					
LOCUS D1706270					
DEFINITION DKFZP860163 r1 686 (synonym: hicc3) Homo sapiens cDNA clone					
ACCESSION AL706270 mRNA					
VERSION AL706270					
KEYWORDS AL706270.1 GI:19689625					
SOURCE EST.					
ORGANISM Homo sapiens (human)					
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE 1 (bases 1 to 750)					
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann					
TITLE 'S.					
JOURNAL Est (Duesterhoeft, et al.)					
COMMENT Unpublished					
CONTACT: Duesterhoeft A					
MIPS					
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany					
This is the 5' sequence of the clone insert					
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer					
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;					
sequenced by Olagen (Hilden/Germany) within the cDNA sequencing					
consortium of the German Genome Project.					
No sl sequence available.					





QY 1243 GCTAAGAGAACTGCTTCATTGGCATGGGAAATATAACTGTTGATTACAGAC 1302  
 DB 372 GCTAAGAGAACTGCTTCATTGGCATGGGAAATATAACTGTTGATTACAGAC 431  
 QY 1303 ACTAGATCTGGAAGAAAGCTTTGAACTTTGGCAGAGACCTCATGATTTGAGAT 1362  
 DB 432 ACTAGATCTGGAAGAAAGCTTTGAACTTTGGCAGAGACCTCATGATTTGAGAT 491  
 QY 1363 TTGCTGAACCTATTTGTTGTTAGTATCTTTGGCAGAGACCTCATGATTTGAGAT 1422  
 DB 492 TTGCTGAACCTATTTGTTGTTAGTATCTTTGGCAGAGACCTCATGATTTGAGAT 551  
 QY 1423 TTGAGATTGACTGTTAGCAGAGTGTGTAAAGTTCCAGATATGTCATGATTGAGAG 1482  
 DB 552 TTGAGATTGACTGTTAGCAGAGTGTGTAAAGTTCCAGATATGTCATGATTGAGAG 611  
 QY 1483 CATGCAATTGGTCTGATCCCGAAGACAGATTATTAATTCCTCCAGCAGACTGAGT 1542  
 DB 612 CATGCAATTGGTCTGATCCCGAAGACAGATTATTAATTCCTCCAGCAGACTGAGT 671  
 QY 1543 AACAGACTAGCTAGAGACATGAAATTAAGGAAATGACAAAGACAGCTCAAGCAATT 1602  
 DB 672 AACAGACTAGCTAGAGACATGAAATTAAGGAAATGACAAAGACAGCTCAAGCAATT 731  
 QY 1603 TCTACAGAGATCTCTCTCTCTGAAA--TCACTAGACA-GGAGAAAGATTTCTATGG-AG 1658  
 DB 732 TCTACAGAGATCTCTCTCTCTGAAAATCACTGAGCAGAGGAGAAAGATTTCTATGGAG 791  
 QY 1659 TCACAGACACTATT 1672  
 DB 792 TCACAGACACTATT 805

RESULT 5  
 LOCUS BX437220 834 bp mRNA linear EST 15-MAY-2003  
 DEFINITION BX437220 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP00505P10  
 5'-PRIME, mRNA sequence.  
 ACCESSION BX437220  
 VERSION BX437220.1 GI:30781556  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 834)  
 Li, W. B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 1992.f For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0CAP00505P1&cluster=1992.f. Contact :  
 Feng Liang Email : fliang@life.techn.com URL :  
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0CAP00505P1.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
 /clone="CS0CAP00505P10"  
 /issue\_type="THYMUS"  
 /clone\_lib="Homo sapiens THYMUS"  
 /notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed  
 with a NotI-oligo(dT) primer. Five prime end enriched,  
 double-strand cDNA was digested with Not I and cloned into  
 the Not I and EcoRV sites of the pCMVSPORT 6 vector."

FEATURES  
 SOURCE

BASE COUNT 256 a 152 c 184 g 241 t 1 others  
 ORIGIN  
 Query Match 21.1%; Score 719.4; DB 13; Length 834;  
 Best Local Similarity 98.9%; Pred. No. 2.ee-144;  
 Matches 723; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1742 CCCAGATGATTTGCTTGGTAAAGATTTGCGCTCAATCAAACTGAACAGAGCTATGAGAC 1801  
 DB 104 CACAGATGATTTGCTTGGTAAAGATTTGCGCTCAATCAAACTGAACAGAGCTATGAGAC 163  
 QY 1802 TTCTGACTGATTAATTAACCAAGATCTATGAGTTGAGAGTTTGGTCTGCTGGAAA 1861  
 DB 164 TTCTGACTGATTAATTAACCAAGATCTATGAGTTGAGAGTTTGGTCTGCTGGAAA 223  
 QY 1862 AATTTTAAGAGATGAACAACTTTCAGATTTAATTCAGCTAGTACAGTCTTAAT 1921  
 DB 224 AATTTTAAGAGATGAACAACTTTCAGATTTAATTCAGCTAGTACAGTCTTAAT 283  
 QY 1922 ATGACAAATATTTGATTAATCTGCTGAGATTTTAACTGAAGAAAGCAATGACTATC 1981  
 DB 284 ATGACAAATATTTGATTAATCTGCTGAGATTTTAACTGAAGAAAGCAATGACTATC 343  
 QY 1982 AAGGATTTGGCACTTTTCTTTTGGCATTAAATCTGATGACACATTAACAGTTA 2041  
 DB 344 AAGGATTTGGCACTTTTCTTTTGGCATTAAATCTGATGACACATTAACAGTTA 403  
 QY 2042 GCCAGAGTTTGGCTGCTGCTTTTGGAGTCCATTTGCTGATGAGTTGGATTTATTTGAGC 2101  
 DB 404 GCCAGAGTTTGGCTGCTGCTTTTGGAGTCCATTTGCTGATGAGTTGGATTTATTTGAGC 463  
 QY 2102 ACCGTAATAGCAAGTTCAGAGCAATGAAAGCTCAATTAATTAATGATGATTTCTCAAC 2161  
 DB 464 ACCGTAATAGCAAGTTCAGAGCAATGAAAGCTCAATTAATTAATGATGATTTCTCAAC 523  
 QY 2162 AGGAGAGAAAGATGAACCAAAAGGTACAGATGAAGTTTATGTTGAGCAATGAGGC 2221  
 DB 524 AGGAGAGAAAGATGAACCAAAAGGTACAGATGAAGTTTATGTTGAGCAATGAGGC 583  
 QY 2222 GACCAGATTTTCAGAGATGAGTCCCTACAGGCTGCTGCTCTCAAAACCTGCTCATCAAC 2281  
 DB 584 GACCAGATTTTCAGAGATGAGTCCCTACAGGCTGCTGCTCTCAAAACCTGCTCATCAAC 643  
 QY 2282 TAGGAAACCTCAGAGCTTAAAGATGATGATTTGCTTCTGCAAAAAGCCACTGAGT 2341  
 DB 644 TAGGAAACCTCAGAGCTTAAAGATGATGATTTGCTTCTGCAAAAAGCCACTGAGT 703  
 QY 2342 TGAATTGGAGAAACCCAGACATCATGTCAAGTTACTGTTTCAGAACAATGAGATCATCT 2401  
 DB 704 TGAATTGGAGAAACCCAGACATCATGTCAAGTTACTGTTTCAGAACAATGAGATCATCT 763  
 QY 2402 TTTAAATTTGGGATGATTTTACGGCAAGATATGCTAACACTTCAATTTATTCGATTTATGG 2461  
 DB 764 TTTAAATTTGGGATGATTTTACGGCAAGATATGCTAACACTTCAATTTATTCGATTTATGG 823  
 QY 2462 AAAATATCTGG 2472  
 DB 824 AAAATATCTGG 834

RESULT 6  
 LOCUS BU167122 883 bp mRNA linear EST 04-SEP-2002  
 DEFINITION AGENOURT\_7958965 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6163350  
 5', mRNA sequence.  
 ACCESSION BU167122  
 VERSION BU167122.1 GI:22681087  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.



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Db      707  AAAAATTTGGTTATTAACGAGACGTGTCCATTGTTTTCACACAGGATTTCTTAATAG 648
Qy      2888 TGATTAGTAAAGAGCCCAAGATGCACAAGAGAGAAATTTAGAGGTTTCAGAGAGA 2947
Db      647  TGATTAGTAAAGAGCCCAAGATGCACAAGAGAGAAATTTAGAGGTTTCAGAGAGA 588
Qy      2948 TGTGTTACAGGCTTATCTAGCTATTGACACGATGCCAATCTCTTCATAAATCTTTTCT 3007
Db      587  TGTGTTACAGGCTTATCTAGCTATTGACACGATGCCAATCTCTTCATAAATCTTTTCT 528
Qy      3008 CAATGAGCTTGGCTCGGAATGCGAGACATCATCTTTGATGACATTTGATACATTC 3067
Db      527  CAATGAGCTTGGCTCGGAATGCGAGACATCATCTTTGATGACATTTGATACATTC 468
Qy      3068 GAAAGACCTTAGCTTATAGTAACTGAGCAAGAGGCTTTGAGATTTTCATGAACAA 3127
Db      467  GAAAGACCTTAGCTTATAGTAACTGAGCAAGAGGCTTTGAGATTTTCATGAACAA 408
Qy      3128 TGAATGATGCACATCATGTGTGGCTGACACAAATAATGATTTGATTCACACAAATTA 3187
Db      407  TGAATGATGCACATCATGTGTGGCTGACACAAATAATGATTTGATTCACACAAATTA 348
Qy      3188 AACGACATGCACTTGAACCTG-AAAGATACAGAGAAATGAAAGCTCCTGAGACATC 3246
Db      347  AACGACATGCACTTGAACCTGAGAAAGATACAGAGAAATGAAAGCTCCTGAGATTCAC 288
Qy      3247 ACTGCACTGTTAATTAATCTCAGCAGGCAAGACCCGATTGATGAGATTCACAAATCA 3306
Db      287  ACTGCACTGTTAATTAATCTCAGCAGGCAAGACCCGATTGATGAGATTCACAAATCA 228
Qy      3307 TGAACAGCATTTAG-ATTACACGCAAGAACAGAAATTAATATCTATTAATTAATATG 3365
Db      227  TGAACAGCATTTAGATTACACGCAAGAACAGAAATTAATATCTATTAATTAATATG 168
Qy      3366 TAAACGCAACAGGCTTTGATAGCACTTAACTAGTTCATTTCAAAA 3412
Db      167  TAAACGCAACAGGCTTTGATAGCACTTAACTAGTTCATTTCAAAA 121

RESULT 8
LOCUS   BG497751 753 bp mRNA linear EST 27-MAR-2001
DEFINITION
mRNA sequence.
ACCESSION BG497751
VERSION   BG497751.1 GI:13459268
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 753)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapds-remail.nih.gov
          Tissue Procurement: DCTD/DTP
          CDNA Library Preparation: CLONTECH Laboratories, Inc.
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LIML at:
          http://limc1471.nhl.gov
          Plate: LIMC1471 row: a column: 03
          High quality sequence. Stop: 649.
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            1..753
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:4655482"
              /issue_type="adenocarcinoma"

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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_60"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgccggccg); Site 2: SfiI (ggccatcagcgc)
); Double-stranded cDNA was prepared from cell line RNA.
5', and 3' adaptors were used in cloning as follows: 5'
sequence: 5'-ATTCTAGAGCGCGAGCGCGCCGACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
BASE COUNT 241 a 136 c 176 g 200 t
ORIGIN
Query Match 19.5%; Score 666; DB 10; Length 753;
Best Local Similarity 97.0%; Pred. No. 8.3e-133;
Matches 733; Conservative 0; Mismatches 15; Indels 8; Gaps 5;
Qy      2080 GCATGTGGATGATATTGAAGCACCTGAATGAGCAATGAGGCAATGAGAAAGCTATT 2139
Db      1 GCATGTGGATGATATTGAAGCACCTGAATGAGCAATGAGGCAATGAGAAAGCTATT 60
Qy      2140 AACTTAACTGACATTTCTCAAAACGAGAGAGAGATGAAACACAAAAGGTACAGATGAAG 2199
Db      61 AACTTAACTGACATTTCTCAAAACGAGAGAGAGATGAAACACAAAAGGTACAGATGAAG 120
Qy      2200 TTTTGTAGTGAAGAAATGAGAGCGACAGATTTGATGATGAGCCCTTACAGGGCTGCTCT 2259
Db      121 TTTTGTAGTGAAGAAATGAGAGCGACAGATTTGATGATGAGCCCTTACAGGGCTGCTCT 180
Qy      2260 CCTCTAAACCTGCTCATCACTAGAGAAACCTCAGGCTTAAAGATGTCGAAATTAATGCT 2319
Db      181 CCTCTAAACCTGCTCATCACTAGAGAAACCTCAGGCTTAAAGATGTCGAAATTAATGCT 240
Qy      2320 TCTGCAAAAAGGCGACATGTGTGAATTTGGAGAACCCAGACATCATGTGAGATTAAGT 2379
Db      241 TCTGCAAAAAGGCGACATGTGTGAATTTGGAGAACCCAGACATCATGTGAGATTAAGT 300
Qy      2380 TTTTCAGAACATGAGATCATCTTTAAAAATGGGGAGATTTACGGCAAGATATGCTAAC 2439
Db      301 TTTTCAGAACATGAGATCATCTTTAAAAATGGGGAGATTTACGGCAAGATATGCTAAC 360
Qy      2440 CTTCAAAATTTATGTAATGAGAAATATCTGCAAAATCAAGGCTTGTGATCTTCAATG 2499
Db      361 CTTCAAAATTTATGTAATGAGAAATATCTGCAAAATCAAGGCTTGTGATCTTCAATG 420
Qy      2500 TTACTTATGTTGTCTGTCATTCGTTGACTGTGTGGAGCTTATGAGGTGTGCGAAT 2559
Db      421 TTACTTATGTTGTCTGTCATTCGTTGACTGTGTGGAGCTTATGAGGTGTGCGAAT 480
Qy      2560 TCTCACACTTATATGCAAAATTCAGTGCMAAGGGGCTTGAAGAGTGCATGCGAGTTCAAC 2619
Db      481 TCTCACACTTATATGCAAAATTCAGTGCMAAGGGGCTTGAAGAGTGCATGCGAGTTCAAC 540
Qy      2620 AGCACAACACTATCATCATGCTGCTCAAAAGACAAAGAAATATATGATGACGCC 2679
Db      541 AGCACAACACTATCATCATGCTGCTCAAAAGACAAAGAAATATATGATGACGCC 600
Qy      2680 ATTGACCTGTTTACAGGTTGATGCTGATGATGATGATGATGATGATGATGATGATG 2737
Db      601 ATTGACCTGTTTACAGGTTGATGCTGATGATGATGATGATGATGATGATGATGATG 660
Qy      2738 TTGAGATGCTGCAATAG-TAAATCATAT-GGTAAAGAGATGACACACTGTTTCATAT 2795
Db      661 TTGAGATGCTGCAATAGTAAATCATATGAGTGAAGAGATGACCAATG-TTCATAT 719
Qy      2796 AGATTTTGACACTTTTGGATCAACAAGAGAAAA 2831
Db      720 AGATTTTG---ACATTTGGATCAACAAGAGAAAA 752

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http://image.llnl.gov  
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)  
 Seq primer: PYX-5.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /strain="C57BL/6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6834931"  
 /issue\_type="whole brain"  
 /dev\_stage="embryo 12.5dpc"  
 /lab\_host="DH10B (T1 phase resistant)"  
 /clone\_lib="NIH BMAP F00"  
 /note="Organ: Brain; Vector: PYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into PYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TGAGAGGCC. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., Program coordinator."

BASE COUNT 248 a 173 c 179 g 206 t 3 others  
 ORIGIN

Query Match 18.6% Score 633; DB 14; Length 809;  
 Best Local Similarity 87.1% Pred. No. 1.1e-125;  
 Matches 704; Conservative 0; Mismatches 103; Indels 1; Gaps 1;

177 TCAACTCTTCAGATGATCTTCTTACATTTTGTGTAAGTTACCCAGAGAGAGAAG 236  
 1 TCAGCTTCGCAACAGAACTTTTACATTTTGTGTAAGTCTACCCAGAGAGAGAAG 60  
 237 GGAAGAAATTTTGTATGAAACAGACGATTTGTGATCTTGGCTTTTTCACCACTTTT 296  
 61 GGAAGAAATTTTGTATGAAACAGACGATTTGTGATCTTGGCTTTTTCACCACTTTT 120  
 297 AAAAGTAATGAAACAGACGATTTGTGATCTTGGCTTTTTCACCACTTTT 356  
 121 AAAAGTAATGAAACAGACGATTTGTGATCTTGGCTTTTTCACCACTTTT 180  
 357 TGCATCGGATGCGAGTGTGCGAATTTGATATGTTAAAGATCTGAGTACAGACTT 416  
 181 TGTATTGGCATGCGAGTGTGCGAATTTGATATGTTAAAGATCTGAGTACAGACTT 240  
 417 CCGAAGAAATTTTGTATGTTTGTAAAGAACTGTGATCTTAAAGATCTTAAATTCAC 476  
 241 TCGAAGAAATTTTGTATGTTTGTAAAGAACTGTGATCTTAAAGATCTTAAATTCAC 300  
 477 TCAATGAGAGCAATGATGTCATCGGCCATGTAAGTCTTACACAGAGCTGCCAA 536  
 301 TCAATGAGAGCAATGATGTCATCGGCCATGTAAGTCTTACACAGAGCTGCCAA 360  
 537 GCACATATATTAATTTGATAGAGCCCAATATATGTTGATTTGGTAATAGTTTC 596  
 361 GCACATATATTAATTTGATAGAGCCCAATATATGTTGATTTGGTAATAGTTTC 420  
 597 TCCAAATATGAGCAAGAGATTAATCTTGAATAATCAACCATGATCTGTGCGAGACA 656  
 421 TCCAAATATGAGCAAGAGATTAATCTTGAATAATCAACCATGATCTGTGCGAGACA 480  
 657 AGTAATGCTGAAGCAATCAGAGAAATTAATGAGTATGTTGATATCATCTGAACTT 716  
 481 AGTAATGCTGAAGCAATCAGAGAAATTAATGAGTATGTTGATATCATCTGAACTT 540

QY 717 AAAACTCTGTGTTTGAATATACGCGCAAGTACATTTTAAAGTGTGATGTGATGA 776  
 DB 541 GAAACTCTGTGTTTGAATATACGCGCAAGTATATCTTGAAGTGTGATGTGATGA 600  
 QY 777 ATACTCTCTGAAATATATCTCTGATGATGATGATGATGATGATGATGATGATGAT 836  
 DB 601 ATACTCTCTGAAATATATCTCTGATGATGATGATGATGATGATGATGATGATGAT 660  
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 QY 897 GGAAGTATTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGAT 956  
 DB 720 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 779  
 QY 957 TGGAGAAACATCTTCAAAATCCCTTTGG 984  
 DB 780 TGGAGAAACATCTTCAAAATCCCTTTGG 807

RESULT 11  
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 DEFINITION AUI29890 NT2RP2 Homo sapiens cDNA clone NT2RP2006455 5', mRNA  
 sequence.  
 ACCESSION AUI29890  
 VERSION AUI29890.1 GI:10990244  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y.,  
 Yamamoto.J., Nakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and  
 Isogai.T.

REFERENCE  
 AUTHORS  
 TITLE HRI human cDNA project  
 JOURNAL Unpublished  
 COMMENT Contact: Takao Isogai  
 Genomics Laboratory  
 Helix Research Institute  
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 Tel: 81-438-52-3975  
 Fax: 81-438-52-3986  
 Email: genomics@hri.co.jp  
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix  
 Research Institute; cDNA library construction; Department of  
 Virology, Institute of Medical Science, University of Tokyo, and  
 Helix Research Institute.  
 Location/Qualifiers  
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 cells after 2-weeks retinoic acid (RA) induction"

BASE COUNT 232 a 133 c 160 g 219 t 9 others  
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Query Match 17.9% Score 612; DB 9; Length 753;  
 Best Local Similarity 97.4% Pred. No. 3.7e-121;  
 Matches 662; Conservative 0; Mismatches 14; Indels 4; Gaps 4;

QY 762 GTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 821  
 DB 1 GTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60  
 QY 822 AACCTGTATATGCTTGGAGATGCCCAATTTGAAGATGATGCTTAAAGAAAGCCTTTA 881

Db 61 AACCTGATATATGCTGGAGATGCCCAATTTGATTTATGCTAAAGAACCTTTA 120  
 QY 882 TTCTCACTGCAATGAGACTGTTTACATGCCATCTTATTCAGACGATTTCCACAGC 941  
 Db 121 TTCTCACTGCAATGAGACTGTTTACATGCCATCTTATTCAGACGATTTCCACAGC 180  
 QY 942 TACACCATATATGATGAGAAACATCTACAAAATCCCTTGGGTTATTAATAGAGACT 1001  
 Db 181 TACACCATATATGATGAGAAACATCTACAAAATCCCTTGGGTTATTAATAGAGACT 240  
 QY 1002 CAGATTAATAATCTTGTGCAACCTACAGTAATCTTAATATTCAGACATTCAGAAAT 1061  
 Db 241 CAGATTAATAATCTTGTGCAACCTACAGTAATCTTAATATTCAGACATTCAGAAAT 300  
 QY 1062 TTATGTTGCAACAGATATCTACATGAGAGAACCTTATGTGCAATGTGAACACTCA 1121  
 Db 301 CTATGTTGCAACAGATATCTACATGAGAGAACCTTATGTGCAATGTGAACACTCA 360  
 QY 1122 AAGAGTACTCTGTTCCAAATCCAGGTGGAATGAATGGCTGAATATATATACATTC 1181  
 Db 361 AAGAGTACTCTGTTCCAAATCCAGGTGGAATGAATGGCTGAATATATATACATTC 420  
 QY 1182 TGATCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1241  
 Db 421 TGATCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
 QY 1242 TGCTAAAGAGAACACTGCTCATTTGGCATGGGAAATATTAACCTGTTGATTAACAGA 1301  
 Db 481 TGCTAAAGAGAACACTGCTCATTTGGCATGGGAAATATTAACCTGTTGATTAACAGA 540  
 QY 1302 CACTCTAGTATCTGGAATAATGGCTTGAATCTTGGCCAGTACCTCATGAGATT-AGAG 1360  
 Db 541 CACTCTAGTATCTGGAATAATGGCTTGAATCTTGGCCAGTACCTCATGAGATT-AGAG 600  
 QY 1361 ATTTGCTGAACCTT-ATTTGCTGATCTGATCAAAATCCAAA-TAAGAACTCCATGCTT 1418  
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 QY 1419 AGAG-TTGGAGTTGACTGG 1437  
 Db 661 AAGATTGAGATTGACTGG-680

RESULT 12  
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 LOCUS  
 DEFINITION  
 BM986382 833 bp mRNA linear EST 25-MAR-2002  
 norvegicus cDNA clone RGIAC69 5' end similar to P13 kinase p110  
 subunit alpha, mRNA sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 EST  
 Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 833)  
 Walek,R.L., Cho,J., Lee,Y., Karamycheva,S., Parvizli,B., Pertea,G.,  
 Sultana,R., Tsai,J., White,J., Quackenbush,J. and Lee,N.H.  
 Generation of ESTs from a rat multiple tissue survey  
 Unpublished  
 Other ESTs: EST445877 EST345567  
 COMMENT  
 Contact: Lee, NH  
 The Institute for Genomic Research  
 9712, Medical Center Drive, Rockville, MD 20850, USA  
 Tel: (301)-838-3529  
 Fax: (301)-838-0208  
 Email: nhlee@tigr.org  
 This clone is available through the ATCC, contact the ATCC  
 tel#703-365-2700 for further information  
 Seq primer: M13 reverse.

FEATURES  
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 Location/Qualifiers  
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 /clone\_lib="Rat gene index, normalized rat, norvegicus"  
 /note="Vector: pT73Pac; Site 1: EcoRI, Site 2: NotI;  
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 libraries, and Bento Soares normalized libraries of ovary,  
 brain, kidney, liver, placenta, lung, embryo, skeletal  
 muscle, spleen, heart"  
 BASE COUNT  
 ORIGIN  
 225 a 196 c 224 g 188 t  
 Query Match 17.9%; Score 609.8; DB 12; Length 833;  
 Best Local Similarity 87.3%; Pred. No. 1.1e-120;  
 Matches 668; Conservative 0; Mismatches 97; Indels 0; Gaps 0;  
 QY 2044 CAGAGGTTGGCCTGCTTTTGGAGTCTTATGTCGATGAGATGATTTGAAGCAC 2103  
 Db 69 CAGAGGTTGGCCTGCTGCTTTGGAGTCTTATGTCGATGAGATGATTTGAAGCAC 128  
 QY 2104 CTGAATAGCAAGTCGAGGCAATGGAAGCTCATTAATTAATGACATTTCTCAACAG 2163  
 Db 129 CTGAATAGCAAGTCGAGGCAATGGAAGCTCATTAATTAATGACATTTCTCAACAG 188  
 QY 2164 GAGAGGAAGATGAAACACAAAAGTACAGATGAAGTTTGTAGTGAAGAAATGAGCGCA 2223  
 Db 189 GAGAGGAAGATGAAACACAAAAGTACAGATGAAGTTTGTAGTGAAGAAATGAGCGCA 248  
 QY 2224 CCAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2283  
 Db 249 CCAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 308  
 QY 2284 GGAACCTGAGGCTTAAGAGTGTGCAATATGTCTTTCGAAAAAGGCACTGTGGTTG 2343  
 Db 309 GGAACCTGAGGCTTAAGAGTGTGCAATATGTCTTTCGAAAAAGGCACTGTGGTTG 368  
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 Db 369 AATTGGGAAGACCCAGACATCATGTGAGATTACTGTTTCAGAACATGATCATCTTT 428  
 QY 2404 AAAAATGGGATGATTTAGGCAAGATAGTCAACCTTCAAAATTTGGTTATGAA 2463  
 Db 429 AAAAATGGGATGATTTAGGCAAGATAGTCAACCTTCAAAATTTGGTTATGAA 488  
 QY 2464 AATATCTGCAAAATCAAGGCTTGTGATCTTGAATGTTACTTATGTTGCTGTCAATC 2523  
 Db 489 AATATCTGCAAAATCAAGGCTTGTGATCTTGAATGTTACTTATGTTGCTGTCAATC 548  
 QY 2524 GGTGACTGTGTGGACTTATTTAGGTGTGTGCGAAATTTCTCACTATTTATGCAATTGAG 2583  
 Db 549 GGTGACTGTGTGGACTTATTTAGGTGTGTGCGAAATTTCTCACTATTTATGCAATTGAG 608  
 QY 2584 TCGAAAGGGGCTTGAAGGTCACCTGCAAGGCTTCAAGGCAAGCACTAATGATGATGATGAT 2643  
 Db 609 TCGAAAGGGGCTTGAAGGTCACCTGCAAGGCTTCAAGGCAAGCACTAATGATGATGATGAT 668  
 QY 2644 AAGAGCAAGAAAGAGAGAAATATATGATGAGCACTGATGATGATGATGATGATGATGAT 2703  
 Db 669 AAGAGCAAGAAAGAGAGAAATATATGATGAGCACTGATGATGATGATGATGATGATGAT 728  
 QY 2704 GCTGATCTGTGTAGCTTACTTCAATTTGGAAATTTGAGATGTCACATATGTAACATC 2763  
 Db 729 GCTGATCTGTGTAGCTTACTTCAATTTGGAAATTTGAGATGTCACATATGTAACATC 788  
 QY 2764 ATGGTAAAGAGATGAGCAACCTGTTCAATATAGATTTTGGACAC 2808  
 Db 789 ATGGTAAAGAGATGAGCAACCTGTTCAATATAGATTTTGGACAC 833

RESULT 13  
 CBS20825 759 bp mRNA linear EST 28-MAR-2003  
 LOCUS U1-M-GH0-cel-n-01-0-UI.r1 NIH\_BMAP\_GH0 Mus musculus cDNA clone  
 DEFINITION IMAGE: 6641250 5', mRNA sequence.  
 ACCESSION CBS20825.1 GI:29354180  
 VERSION CBS20825.1  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
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 1 (bases 1 to 759)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strauberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: Dr. Jim Lin, University of Iowa  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at  
 http://genome.uiowa.edu/distribution/mouse1.html  
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)  
 Seq primer: PYX-5.  
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 /note="Organ: Brain; Vector: PYX-Asc; Site 1: EcoR I; Site 2: Not I. The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into PYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGACTGAAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."  
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 1 (bases 1 to 789)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strauberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: CLONTECH  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LICM2867 row 1 column 12  
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/Note="Organ: testis; Vector: pDNR-LIB (Clontech); Site: 1;
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sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGGGCGGCACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

BASE COUNT      297 a      128 c      149 g      214 t      1 others
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Best Local Similarity 99.2%; Pred. No. 4e-120; 3; Indels 2; Gaps 2;
Matches 631; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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QY 2839 TATTAACGAGAACGTGGCCATTGTTTGGACACAGATTCTTTAATAGTATTAGTAA 2898
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LOCUS        UI-M-Fyo-ctf-g-12-0-UI.r1 NIH_BMAP_Fyo Mus musculus cDNA clone
DEFINITION: IMAGE: 6854605 5', mRNA sequence.
ACCESSION   CD349473
VERSION     CD349473.1 GI:31140988
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)

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ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 785)
AUTHORS      NIH-MGC http://mgs.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: rgs@bbs-riemail.nih.gov
              Tissue Procurement: Dr. Jim Lin, University of Iowa
              cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
              DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
              Distribution: Distribution information can be found at
              http://genome.uiowa.edu/distribution/mousefl.html
              This clone was contributed by the Brain Molecular Anatomy Project
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                  Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
                  1996. Denatured RNA was size fractionated on a 1% agarose
                  gel. First strand cDNA synthesis was primed with oligo-dT
                  primer containing a Not I site. Double strand cDNA was
                  size selected according to mRNA size fraction, ligated
                  with Ecor I adaptor, digested with NotI and then cloned
                  directionally into pyx-Asc vector. The library tag
                  sequence located between the Not I site and the polyA tail
                  is ACCGAGACAGC. This library was created for the University
                  Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the
                  Developing Mouse Nervous System", supported by National
                  Institute of Mental Health (NIMH), Hemm Chin, Ph.D.,
                  program coordinator."
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QY 481 AGTAGAGCAATATGATCTATCCGCACATGATCTTCAACAGAGCTGCCAAAGCAC 540
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DB 2821 AAGAGAAAAAATTTGGTTATAAAGAAAGGTCGATTTGTTTGGACAGGATTTT 2880
QY 2881 TTAATAGTATGTTAATAGAGCCCAAGATGACAAAGACAGAGATTTGAGAGTTT 2940
DB 2881 TTAATAGTATGTTAATAGAGCCCAAGATGACAAAGACAGAGATTTGAGAGTTT 2940
QY 2941 CAGAGATGTGTTACAAAGGCTTATCTAGTATTCAGACATGCAATCTCTTCAAT 3000
DB 2941 CAGAGATGTGTTACAAAGGCTTATCTAGTATTCAGACATGCAATCTCTTCAAT 3000
QY 3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCAAGCTCAATCTTTTGAATGATGCA 3060
DB 3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCAAGCTCAATCTTTTGAATGATGCA 3060
QY 3061 TACATTCGAAAGACCTAGCCTTAGATPAAACGAGAGACCTTTGGAGTATTTATG 3120
DB 3061 TACATTCGAAAGACCTAGCCTTAGATPAAACGAGAGACCTTTGGAGTATTTATG 3120
QY 3121 AAACAATGATGATGACATCATGCTGAGCAACAAATGATGATCTTCCAC 3180
DB 3121 AAACAATGATGATGACATCATGCTGAGCAACAAATGATGATCTTCCAC 3180
QY 3181 ACAATTAAACGATGATGATGCA 3207
DB 3181 ACAATTAAACGATGATGATGCA 3207

RESULT 2
US-09-764-877-3796/c
; Sequence 3796, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antihodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; PRIORITY FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 3796
; LENGTH: 4074
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TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1934)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-877-3796

Query Match
Best Local Similarity 98.6%; Pred. No. 8e-105;
Matches 477; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 2931 TGAGAGTTTCAGAGATGTTTACAAAGCTTATCTAGTATTTGACAGATGCAATCT 2990
DB 3417 TTAATAGTTTCAGAGATGTTTACAAAGCTTATCTAGTATTTGACAGATGCAATCT 3358
QY 2991 CTTCAATTAATCTTTTCCAAATGATGCTGCTGGAATGCGCAAGACTAATCTTTTGA 3050
DB 3357 CTTCAATTAATCTTTTCCAAATGATGCTGCTGGAATGCGCAAGACTAATCTTTTGA 3298
QY 3051 TGACATTCATACATTCGAAAGACCTAGCCTTAGATTAATCTGACAGCAAGAGCTTTGA 3110
DB 3297 TGACATTCATACATTCGAAAGACCTAGCCTTAGATTAATCTGACAGCAAGAGCTTTGA 3238
QY 3111 GATTTTCATGAAACAAATGATGATGATGATGATGATGATGATGATGATGATG 3170
DB 3237 GATTTTCATGAAACAAATGATGATGATGATGATGATGATGATGATGATGATGATG 3178
QY 3171 GATCTTCCACACATTTAAACAGATGATTTGAATCTG-AAAGATTAATCTGAGAAATGAAG 3229
DB 3177 GATCTTCCACACATTTAAACAGATGATTTGAATCTGAAAGATTAATCTGAGAAATGAAG 3118
QY 3230 CTCACCTGAGACCTACCTACCTGCTGTTAATCTGACAGCAAGAGCCGATTTGAT 3289
DB 3117 CTCACCTGATTCACACCTGCTGCTGTTAATCTGACAGCAAGAGCCGATTTGAT 3058
QY 3290 AGGAATTCGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 3348
DB 3057 AGGAATTCGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATG 2998
QY 3349 ATATTAATTTAAATGATTAAGCGCAAGAGGTTTATGATGATGATGATGATGATG 3408
DB 2997 ATATTAATTTAAATGATTAAGCGCAAGAGGTTTATGATGATGATGATGATGATG 2938
QY 3409 AAAA 3412
DB 2937 AAAA 2934

RESULT 3
US-09-814-353-19587
; Sequence 19587, Application US/09814353
; Patent No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIORITY FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
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PRIOR APPLICATION NUMBER: US 60/257,672  
PRIOR FILING DATE: 2000-12-21  
NUMBER OF SEQ ID NOS: 22037  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 19587  
LENGTH: 3777  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 3772\_3773, 3774, 3775, 3776, 3777  
OTHER INFORMATION: n = A,T,C or G  
US-09-814-353-19587

Query Match 12.9% Score 441; DB 12; Length 3777;  
Best Local Similarity 50.2%; Pred. No. 5,1e-102;  
Matches 1567; Conservative 0; Mismatches 1450; Indels 106; Gaps 15;  
QY 58 ATCTAGTGAATGTTTACTACCAATGGAATGATGACTTATAGATGCTCCGTGAG 117  
DB 426 ATACTGTGATTCCTTTTCCGACGTGGATTTATATCCAGTTGAGGTACTCGGGA 485  
QY 118 GCTACATTAGTACTATTAAGCATGAACTATTTAAGACGAGAAATACCTCTCAT 177  
DB 486 GCTACCAATTTCTATATTAGCAGATGTTAGAACCAATTCACCAATTCATGTC 545  
QY 178 CAACCTCTCAAGATGAACTCTTACATTTTCGTAAGTGTACCCCAAGACGAAAG 237  
DB 546 AACCTCTTATGATATGATGCTCTATATGTTTGATGTGAAATCAGACTGCTGTAT 605  
QY 238 GAAGAATTTTGTGAGAAACGAAAGCTTGTGATCTTCGCTTTTCAACATTTTGA 297  
DB 606 GAGAGCTTGAAATGAAACGAAAGCTGTGATGACACCTTTTCTCCAGTTCTC 665  
QY 298 AAAGTATGACCAAGTGGCAACCGTGAAGAAAGATCTCAATCCAGAAATGTTT 357  
DB 666 AAATTAGACAGAAAGTTGTGACCCAGGGGAAAA--ATPAGCTCAAAATTTGAGTC 722  
QY 358 GCTATCGGCATGCCAGTGGCAATTTGATGTTGAAGAGTCTGAAAGTACAGACTTC 417  
DB 723 CTATAGGAAAGGTCTGATGAAATTTGATTCCTTGAAGATCTGAAAGTAAATGAA 782  
QY 418 CGAAGAAATTTCTTAATGTTTGAAGAGCTGTGATCTTAAAGATCTTAATTCCT 477  
DB 783 CGAAGAAATGCGCAATTCAGCGA-----GGAAGAAATCTGTCA 824  
QY 478 CATGTAGAGCAATGTATGTCTATCCGACATGTAGATCTTCAACGAGCTGCCAAG 537  
DB 825 CTGTGGGATTTGTCTGTGATGACTGTGCTAAACCAATATCCACGAGCATGAACA 884  
QY 538 CACATATATTAATTTGATGAGGCAATTAATAGTGTGATTTGGTAAATGTTCT 597  
DB 885 TCCATCCCTGAAACCTTAGAATTAATTTATGGGGAAGCTCATCTGATGCTGTAT 944  
QY 598 CCAATATATGACAGCAAGAACTATCTGAAATCAACATGACTGTGTGCCAGAAACA 657  
DB 945 TTGAAAACTGCCGAGAGTGTATTAAGTGTCTCAAGTGTCTTAATATGAATCTATCAA 1004  
QY 658 GTAATGTGTGAGCAATCAGAAAAAACTAGAAATGTGTTGCTATCTGAAACATTA 717  
DB 1005 GTAATGTAATGGCAATC---CAAAACGTTGACTATTCATGGGAAGGAATGAAGTT 1061  
QY 718 AAACCTGTGTTTGAATATCAGGCGCAATCAATTTTAAAGTGTGTGATGATGA 777  
DB 1062 AGCCCTATGATATG-----TGTGCAAGTCAAGGGAAGATGA 1103  
QY 778 TACTTCCAGAAAAATATCTCTGAGTCAATATAGTATTAAGAGCTGTATATGCTT 837  
DB 1104 TATGTTTTTGTGATCAATCCATATTCAGTTTCCAGTATATCCGAACTGTGTATGAC 1163  
QY 838 GGGAGATGCCCAATTTGAGAT-----GATGGCTAAAGAAAGCTTATTTCAACTGC 892  
DB 1164 AGAGCCCTGCCCCATTTTATCTTGTGGAATGTGCAAGATCAAGAAATGTATGAACA 1223

QY 893 CAATGACGTGTTTACATGCCATCTTATTCAGAGCAATTTCCACAGCTACACATATA 952  
DB 1224 GAATATATTCATAGAGCTGCGCATTAATGAAATTTCACTATCTTCTCTTCCATTA 1283  
QY 953 TGAATGAGAAACATCTCAAAAATCCCTTTGGGTTATTAATAGACACTAGATTAATA 1012  
DB 1284 CCACCAAGAAACACCAATTAATTTCAAGTTTGGGAAATTAACAACCTTTCCAAAT 1343  
QY 1013 TTCTTGTGCAACCTGTAATCTAAATTTGAGACATTTGCAAGATTATTTGTTGA 1072  
DB 1344 GTCTGTGTTAAGGAA--ATTAATTAACAGAGAACTGTAAAGTTTCACTGACGG 1401  
QY 1073 CAGGTATCTACATGAGAGAAACCTTATGTA---CAATGTGAACCTCAAGAGTAC 1129  
DB 1402 CTGCTCTTTTCAATGATGACTGAGCTCCTGTGTAACCAATCTGATGAGATACAG 1461  
QY 1130 CTGTTCCAAATCCAGGTGAATGATGCTGTAATTAATATATACATTTCTGATCTT 1189  
DB 1462 GGAATAATGATCATATTGGAATGAACACATGGAATTTGATTAATTTGTGACTTAC 1521  
QY 1190 CTGCTGCTGCACTTTGCTTCAATTT-----GCTGTAAAGGCGGAAGGCTG 1244  
DB 1522 CAGAAATGCTCATTAATGTTTGTCTGTTATGCAAGTTTGAATTAAGTAAGAAACGAGA 1581  
QY 1245 TAAAGAGAACACTGTCCAT-----TGGCATGGGAAATATTAACCTTGTG 1291  
DB 1582 AATCAAGAAACATTAATCCCTTAATATGAGCAATCAGAAAGCTGGAAGATGC 1641  
QY 1292 ATTAACAGACACTCTAGTATCTGAAAAATGCTTTGAATCTTTGGCCAGTACTCATG 1351  
DB 1642 ATTATCTGTAGGCTGGGTAAATACATGCTTTTGAATTAAGCAATTTAGAAGCTG 1701  
QY 1352 GATTAGAGATTTGCTGAACCTATTTGTTTGTGATGATCAATCCAAATTAAGAAATC 1411  
DB 1702 GAGACATATTAATACAGCTGCTCTTCAATTTCTGATGAACTCGAAGAAATGTTGATC 1761  
QY 1412 CATGCTTAAAGTTGAGATTGATGCTGTTGACAGATGTTGAAGTTCCAGATATGCTAG 1471  
DB 1762 CAATGGAACTGTTCAACAAATTCATATCTGAAATGCAAGCTTTGATGATTAAT 1821  
QY 1472 TGATTAAGACATGCCCAATTTGCTGTATCTCCGAGAGAGCAATTTAGCTATTTCCAG 1531  
DB 1822 TTCAGAGAAATTAACCACTTAATATACCTCTCTCGATTAAGATTAATGAAGG 1881  
QY 1532 CAGACCTGAATACAGACTGATGAGACAAATGAATTAAGGAAATGACAAAGAACAGC 1591  
DB 1882 CAGCTGATTTGCAAGAGTGAATGATGCTATATGTCMAATGAGGTGAAAAAAGTTTC 1941  
QY 1592 -----TCAAGCAATTTCTACAGAGATCTCTCTGAAATCACTGAGCAGAGA 1642  
DB 1942 TTCTGTATTTGAAGAAATCTTGAACAGGATCTCTGTCTCACTGTGTGAAATGAA 2001  
QY 1643 AAGATTTTCTATGAGTCAAGAC---ACTATTTGTACTATCTCCGAAATTTCAACCA 1699  
DB 2002 TGATCTTATTTGCACTTTCGCAAGACGCGAGAGATTTTCCCAATCTACCTGCAA 2061  
QY 1700 AATTGCTTCTGTCTGTTAATTTGAATTTGAATGAATGAAGCCAGATGTATTTGCTGG 1759  
DB 2062 AATTACGTGTCAATCAATGAATTAACCTTAGAGATGTTGCTCAGCTTCAGGCGTGC 2121  
QY 1760 TAAAGATTTGGCTCCCAATCAAACTGAAACAGGCTATGAACTTCTGAGCTGTAAATTC 1819  
DB 2122 TTCAAGATTTGGCTTAAACTGCCCCCGGAGAGCCCTAGAGCTTGTGATTTCAACTATC 2181  
QY 1820 CAGATCTATGTTTGAAGTTTGTCTGTTGCTTGGAAAAATTAACAGATGACA 1879  
DB 2182 CAGACAGTACGTTCGAGATATGCTGTAGCTGCTG---CGACAGATGAGTGAAG 2238  
QY 1880 AACTTTCTAGTATTAATTTAGCTAGTACAGGCTCTAAATTAATGAACAAATTTTGATA 1939  
DB 2239 AACTTTCTCAATATCTTTTCAAACTGTGTGAAGTGTAAATGTAGGCTTTTCTTGATTT 2298

QY 1940 ACTTGCTTGAGATTTTCTAGTGAAGAAAGATTGACATTAATCAAGATTGGGCACTTT 1999  
 Db 2299 GTGCCCTCTAGATTTCTATTAAGAAAGCACTGTGTAATCGAGATAGGGGAGTTTC 2358  
 QY 2000 TCTTTGGCATTTAAATCTGAGATGCAATTAATAACGATTAGCCAGAGTTGGCCGC 2059  
 Db 2259 TATTTGGCATTTAGGTCAGAGATGCAATTTCTGCTGTCTCAGTACAAATTTGGTGTCA 2418  
 QY 2060 TTTTGAATCCTATTGTGTCATGTGGGATGTATTTGAAACACCTGAATAGCAATCG 2119  
 Db 2419 TCCTTGAAGCATACTGCCGGGAGTGTGGGCAATGAAAGTCTTTCTAAGCAGGTG 2478  
 QY 2120 AGGCAATGAAAAGCTCTTACTTAATTAATTAATTAATTAATTAATTAATTAATTA 2179  
 Db 2479 AAGCACTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2538  
 QY 2180 CACAAAGGTACAGATGAAGTTTATGATGCAAAATGAGCCGACGATTTCAATGATG 2239  
 Db 2539 ACAAGGCCAAAGGAAAGGAGGCCATGCAATCTGTTTAAACAGAGTGTACCGGAG 2598  
 QY 2240 CCTTACAGAGGCTGCTGTCTCTCTTAAACCTGCTCACTCACTAGAAACCTGAGCTTA 2299  
 Db 2599 CCTCTGACCTGACAGTCAACCCCTGAACCATGTTTATCTCTCAGAACTCTATGTTG 2658  
 QY 2300 AAGAGTGCATTAATGTCTTCTGCAAAAGGCCACTGTGTTGAATTTGGAGAACCCAG 2359  
 Db 2659 AAAAGTCAATTAATCATGATTCGAAATGAAGCTTTGTGGCTGATATCAATTAAGG 2718  
 QY 2360 ACATCATGTCAAGTACTGTTTGAAGAAATGAGATCATCTTTAAATTTGGGATGAT 2419  
 Db 2719 TATTTGTGAGATTCAGT-----TGAAGTATTTTAAATTTGGTATATTT 2766  
 QY 2420 TACGCAAGATATCTTAACACTTCAATTAATTTGATTAATTAATTAATTAATTAATTA 2479  
 Db 2767 TAGACACAGATATTTGACACTCCAAATTTGGCTGTGATGATTTACTCTGGAAGAG 2826  
 QY 2480 AAGCTCTTATCTTGAATGTTTACCTTAATGTTGTTCTGCAATGTTGACTGTGTGGAC 2539  
 Db 2827 CTGATTTGGAATCTTCGATGTGTGCTTATGCTGTATGAGCAAGGAGATGGCTGGCC 2886  
 QY 2540 TTATTTGAGTGTGCGAAATTTCTACATTAATTAATTAATTAATTAATTAATTAATTA 2586  
 Db 2887 TCATTGAAGTTGTAGACCTCTGAACAAATTTGTGATTCAGCTGAACAGTAGCATG 2946  
 QY 2597 TGAAGGTGCACTGCACTTCAACAGCACACACTACATCACTGCTGCAAGAGCAAGACA 2656  
 Db 2947 TGGTGTCTGACAGACCTTCAACAAAGATGCCCTTCTGAACTGCTTTAAAGATTAACA 3006  
 QY 2657 AAGGAGAAATATATGATGACGCCATTGACCTGTTTACAGCTTCAATGTGTGATCTGT 2716  
 Db 3007 CTGGGAGATGACCTGACCGAGCCATTGAGGAATTTACATGCTGTGCTGGCTACTGTG 3066  
 QY 2717 TAGTACTTCAATTTTGGGAATTTGAGATGCTCAATAGTATCATGTGTGAAAGAGC 2776  
 Db 3067 TAGCTTTTATGCTTGGGATTTGGTACAGACATAGTCAACATCATGTGTCAAAAAA 3126  
 QY 2777 ATGCAACAAGTTCATATAGATTTTGGACCTTTTGGATTCACAAAGAAAAAATTTG 2836  
 Db 3127 CTGGCCAGCTCTTCAATTAATGATTTTGGACATTAATTTTGGAAATTTCAAAATCTA 3186  
 QY 2837 GTTATAACAGAGAGCTGTGCAATTTTGGACAGATTTTGAATAGTGTGTA 2896  
 Db 3187 GCATTAAGAGAGAGAGTGTGCTTTTATTTTACCTATGATTTTATCATGTCAATTAAC 3246  
 QY 2897 AAGGAGCCCAAGATGACAAAGACAGAGATTTTGAAGGTTTCAAGAGATGTGTACA 2956  
 Db 3247 AAGG-----AAAAACAGAAATACAGAAAATTTGCGCTTCCGCAATGTGTGAGG 3300  
 QY 2957 AGGCTTATAGCTATTCAGAGATGCAATCTTCAATTAATTTTCTCAATGATGTC 3016  
 Db 3301 ATGATATCTGATTTTACAGAGGATGGAATCTTCTCAATCACTCTTTTGGCGTGTATG 3360  
 QY 3017 TTGGCTCTGGAATGCCAGAACTACAAATCTTTTGTATGATGATTCATTCATTCGAAGACC 3076

Db 3361 TGACTGAGGAGCTTCCGAACTCAATCACTCAAGATATATAGTATCTTAAGACTCTC 3420  
 QY 3077 TAGCTTAGATTAATAACAGACAGAGAGCTTTGGAGTATTTCAAGAAACAATGATGATG 3136  
 Db 3421 TTGCATTAAGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3480  
 QY 3137 CAC 3139  
 Db 3481 CGC 3483  
 RESULT 4  
 US-09-352-2439  
 ; Sequence 2439, Application US/09960352  
 ; Patent No. US20020137139A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Warren, Wesley C.  
 ; APPLICANT: Tao, Nengbing  
 ; APPLICANT: Byatt, John C.  
 ; APPLICANT: Mathalagan, Nagappan  
 ; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
 ; FILE REFERENCE: 16511.006/37-21 (10298)C  
 ; CURRENT FILING DATE: 2001-09-24  
 ; NUMBER OF SEQ ID NOS: 15112  
 ; SEQ ID NO 2439  
 ; LENGTH: 412  
 ; TYPE: DNA  
 ; ORGANISM: Bos taurus  
 ; OTHER INFORMATION: Clone ID: 11-LIB3058-019-Q1-K1-C11  
 US-09-352-2439  
 Query Match 11.2%; Score 380.6; DB 10; Length 412;  
 Best Local Similarity 95.4%; Pred. No. 4.1e-87;  
 Matches 392; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
 QY 1355 TAGAAGATTGCTGAACCCCTATTGTGTGTACTGATCAATTCGAATTAAGAAATCTCAT 1414  
 Db 2 TAGAAGATTGCTGAACCCCTATTGTGTGTGTACTGATCAATTCGAATTAAGAAATCTCAT 61  
 QY 1415 GCTTAGATTGAGATTGATCTGCTGATGAGAGTGTGTAAGTTCCAGATATGTCACTGA 1474  
 Db 62 GTTAAAGATTGAGATTGATCTGCTGATGAGAGTGTGTAAGTTCCAGATATGTCACTGA 121  
 QY 1475 TTGAAGAGATGCCAATTTGCTGTATCCGAGAGACAGATTTAGCTATTTCCACGAG 1534  
 Db 122 TTGAAGAGATGCCAATTTGCTGTATCCGAGAGACAGATTTAGCTATTTCCACGAG 181  
 QY 1535 GATGAGTAAACAGACTAGCTAGAGACATGAATTAAGGAAAAATGCAAGAAACAGCTCA 1594  
 Db 182 GACTGAGTAAACAGACTAGCTAGAGACATGAATTAAGGAAAAATGCAAGAAACAGCTCC 241  
 QY 1595 AAGCAATTTCTACAGAGATCTCTCTGAAATCACTGAGAGAGGAAAGATTTCTCAT 1654  
 Db 242 GAGCAATTTCTACAGAGATCTCTCTGAAATCACTGAGAGAGGAAAGATTTCTCAT 301  
 QY 1655 GGAGTCAACAGACTATTTGTAATCTATCCGAAATTTTACCAATTTGCTGTCTG 1714  
 Db 302 GGAGTCAACAGACTATTTGTAATCTATCCGAAATTTTACCAATTTGCTGTCTG 361  
 QY 1715 TTTAAATGGAATTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1765  
 Db 362 TTTAAATGGAATTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 412  
 RESULT 5  
 US-10-162-160-2  
 ; Sequence 2, Application US/10162160  
 ; Publication No. US20030099627A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Van Hasedroeck, Bart

APPLICANT: Waterfield, Michael D.  
 TITLE OF INVENTION: No. US2003009627A1el Lipid Kinase  
 FILE REFERENCE: 2332-1-002  
 CURRENT APPLICATION NUMBER: US/10/162,160  
 PRIOR FILING DATE: 2002-06-03  
 PRIOR APPLICATION NUMBER: US/09/194,640  
 PRIOR FILING DATE: 1998-12-01  
 PRIOR APPLICATION NUMBER: 9611460.8  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 2  
 LENGTH: 3387  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-162-160-2

Query Match 9.7%; Score 329.8; DB 14; Length 3387;  
 Best Local Similarity 53.2%; Pred. No. 1.7e-73;  
 Matches 800; Conservative 0; Mismatches 682; Indels 21; Gaps 4;

1682 TCCCGGAATTTCTACCCAAATTTGCTGTCTGTTAAATGGAATTTCTAGATGAGTAG 1741  
 1625 TCCCGAGGCCCTAGCCCGGCTGCTGTCTGTCACCAAGTGAACAAGCATGAGTGTGG 1684  
 1742 CCCAGATGTATTGCTGTGTAAGATTGGCTCCCAATCAAACTGAACAGGCTATGGAC 1801  
 1685 CCCAGATGCTCTACCTGTGTCTGCTCCGCGAGCTGCCGCTCCAGCGCCCTGGAGC 1744  
 1802 TTCGAGCTGTAAATTAACCAATCTATGTTCCAGATTGTTGCTGTTGGCTTGGAAA 1861  
 1745 TGCTAGACTTACGCTTCCCAATGGCCAGTAGGCTCTCTCCCAATCAAGTCGTCGCGA 1804  
 1662 AATATTTAAGAGATGACAAACCTTCTCAGTATTTAATTCAGTGTAGTACAGGCTCCAAAT 1921  
 1805 AA---CTGACGAGAGATGAGCTGTTCAGTACCTGCTGACAGTGTGAGGTTCTCAAGT 1861  
 1922 ATGAACAATATTGGATTAATCTTGTGTGAGATTTTTAAGTGAAGAAAGCATTTGACTATC 1981  
 1862 ACGAGTCTTACCTGGAAGTGGAGTGAACCAATTCCTGCTGGAACCGGCGCTGGCAAC 1921  
 1982 AAAGATTTGGGACCTTTTCTTTTGGCATTTAAATCTGAATGACAAATTAACAGTTA 2041  
 1922 GCAAGATCTGGACACTTCTTTTCTGGCACTCCGCTCCGAGATGACCTGCGCTGGTGG 1981  
 2042 GCCAGAGTTTGGGCTGCTTTTGGAGTCTATTTGTGCGAGTGTGGAGTGTATTTGAAGC 2101  
 1982 CCTGCGCTTGGGCTTCACTCCGAGGCTTACTGAGGGGCAAGACCACACATGAAGG 2041  
 2102 ACCTGAATAGGCAAGTCGAGGCAATGAAAAGCTTAACTTAAGTGAATTTCTCAAC 2161  
 2042 TGCTGTGAACAGGAGGAGACACTGAGCAAACTGAAGCCCTGATGACTCTCGCAAGC 2101  
 2162 AGAAGAGAGAGATGAACACAAAAGTACAGATGAAGTTTATGTTAGCAAAATGAGGC 2221  
 2102 TGAAGCTCTCAAGAAAGCCCAAGCCCAAGCAAGAGAGTATGACTTTGCAATGCGGC 2161  
 2222 GACCAATTTTATGATGAGTCCCTACAGGCTTGTCTCTCTTAAACCTTCTCATCAAC 2281  
 2162 AGAAGGCTTACCTTGAAGGCTCTTCCACCTGCAAGTCTCCCTGACCCCAAGACCTTGC 2221  
 2282 TAGAAAACCTCAGGCTTAAAGAGTGTGAATTAATGCTTCTTGCAGAAAAGGCACTGTGT 2341  
 2222 TGGCTGAAGTCTGCTGTGAAGAGTGCACCTTCAATGAGATCCAAAGATGAAGCCCTGTGGA 2281  
 2342 TGAATTTGGAGAACCCAGACATCATGTCAAGTTACTGTTCAGAAACATGAGATCATCT 2401  
 2282 TCATGTACAGCAACGAGAGGAGGCAAGGCGCGC-----AGCTGGGCAATCATCT 2332  
 2402 TTAATAATGGGAGATTTTACGGCAAGTATGCTAACTTAATTTTGTATTTANG 2461  
 2333 TTAAGAAAGGGGATGACTCTCGGCAAGACATGTGACCTTCCAGATGATCAGCTCATGG 2392

2462 AAAATATCTGGCAAAATCAAGTCTTGATCTTTGAAATGTTACTTATGTTGCTGTCA 2521  
 2393 ACGTCTGCTGAAGACAGAGAGGGGCTGGACCTTGAGATGAGACCCCTTATGCTGCTCCCA 2452  
 2522 TCGGTGACTGTGTGGGACTTATTTGAGGTGTGGAAATTTCTCACATTTATGCAATTC 2581  
 2453 CCGGGAGCCGACAGGCTTATTTGAGGTGTGACTCCCTTGAACACCATGACCAATTC 2512  
 2582 A---GTGCAAAAGCGGCTTAAAGTGTGACTGTGCAAGTTTCAACAGCACACATCATAGT 2638  
 2513 AACTCAACAAAGAGAAATATGAGAGCCACAGCCGCTTCAACAAAGATGCCCTGTCACT 2512  
 2639 GGCTCAAGACAAAGAAAGAAATATATGATGAGAGCATTTGACTTGTTCACGTT 2698  
 2573 GGCTGAATGCCAAGAAACCCGGGGAGGCGCTGTGATCAGACCATTTAGAGAGTTCACTCT 2632  
 2699 CATGTGCTGATATCTGTGTAGTACTTCACTTTTGGAAATTTGAGATGTCACATATGTA 2758  
 2633 CTTGTGCTGCTATTTGTGTGGCCACATATGTGCTGGGCAATTTGGCATGCGACACGACA 2692  
 2759 ACATCATGTGTGAAGACGATGCAACTGTTTCAATATAGATTTTGGACACTTTTGGATC 2818  
 2693 ACATCATGATCCGAGAGAGTGGGCACTGTTCCACATTTGATTTGGCACTTTCTGGGGA 2752  
 2819 ACAAGAAAGAAATTTGTTATTAACGAGACGTGTCCATTTGTTTGAACAGATTT 2878  
 2753 ATTTCAGAACCAAGTTTGAATCAACCGGAGGCTGCCATTCATCTCACCTACGACT 2812  
 2879 TCTTTAATAGTATTAGTAAGAGGCCCAAGATGCAAGCAAGAAATTTGAGAGGT 2938  
 2813 TTGTCATGTGATTCAGACAGG-----GAAAGCTAATTAATGAGAAATTTGACGCT 2866  
 2939 TTGAGAGATGTGTTCAGAGGCTTATCTATCTATTCGACAGCATGCCAATCTCTTCAATA 2998  
 2867 TCCGGGGCTACTGTGAAGAGGCTCTACACATCTCTGGGGCCGACGGGCTTCTTCTCC 2926  
 2999 ATCTTTTCTAATGATGCTTGGCTCTGGAATGCCAAGACTCAATCTTTGATGACATTG 3058  
 2927 ACCTCTTGGCTGATCGGGGCGGAGGCTGCTGCTGAGCTGCACTGCTCCAAAGACATTC 2986  
 3059 CATCATTCGAAAGACCTTACCTTGTATTAATCTGACAGAGGCTTTGGAGATTTTCA 3118  
 2987 AGTATTCGAAGACTCTCTGCACTGGGAAACAGAGGGAGGCACTGAACACATTC 3046  
 3119 TGAACAATATGATGATGACATCATGATGCTGAGCAACAAATATGATTTGATCTTCC 3178  
 3047 GAGTGAAGTTTAACGAAGCCCTCGTGAAGCTGGAACCAAGTGAACCTGCTGCGCC 3106  
 3179 ACA 3181  
 3107 ACA 3109

RESULT 6  
 US-10-337-192-1  
 : Sequence 1, Application US/10337192  
 : Publication No. US2003019521A1  
 : GENERAL INFORMATION:  
 : APPLICANT: SABHU, Chanchal et al.  
 : TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA  
 : FILE REFERENCE: 27866/39033  
 : CURRENT APPLICATION NUMBER: US/10/337,192  
 : CURRENT FILING DATE: 2003-01-06  
 : PRIOR APPLICATION NUMBER: 60/199,655  
 : PRIOR FILING DATE: 2000-04-25  
 : PRIOR APPLICATION NUMBER: 60/238,057  
 : PRIOR FILING DATE: 2000-10-25  
 : NUMBER OF SEQ ID NOS: 6  
 : SOFTWARE: Patentin version 3.0  
 : SEQ ID NO 1  
 : LENGTH: 5220  
 : TYPE: DNA  
 : ORGANISM: Human p110delta complete cDNA



QY	1682	CCCCGGAATTCCTACCCAAATTCGCTCTGCTCTGTTAAATGGAATTTCTAGATGAAGTAC	1741
Db	1820	TCCGGAGGCGCTACGCCGCTGCTGCTGCTACCAACTGGAAACAAGCATBAGATGTGG	1879
QY	1742	CCGAGATGTAATGCTTGTTAAAGATTGGCCCTCCAAATCAAACTGAAACAGCTATGGAAC	1801
Db	1880	CCGAGATGCTTACTGCTGTGCTCTGTCGGAGAGTCCCGTCTGAGCGCCTTGGAGC	1939
QY	1802	TTCTGAGCTGTAATTAACCCAGATCTCTATGTTGAGGTTTGTGTTGCGTGGCTTGGAA	1861
Db	1940	TGCTAGACTTCAGCTTCCCGATTGGCAGTAGGCTCCTTGCATCAAGTCGCTGGGA	1999
QY	1862	AATTTTAAAGATGAGCAAACTTTCAGATTTTAAATCAGTACTAGTACAGTCTTAAAT	1921
Db	2000	AA---CTGACGGAGATGATGCTGTTCCAGTACTCTGTCAGCTGATGAGGTGCTCAAGT	2056
QY	1922	ATGAACAATAATTGATTAATCTGCTTGGAATTTTAACTGAAAGAAACATTTGACTATC	1981
Db	2057	ACGAGTCTTACTGTGACTGCGAGCTGACCAAAATTCCTGCTGGAACGGGCCCTGGCCAAAC	2116
QY	1982	AAAGGATTTGGGACCTTTTCTTTTGGCATTTTAAATCTGAGATGACAAATTAACAGTTA	2041
Db	2117	GCAAGATGCGGCACCTTCTTTCTTGGCACTCCGCTCCGAGATGACGTCGCGTGGTGG	2176
QY	2042	GCCAGAGTTTGGGCTGCTTTTGGAGTCTTATGTCGTCATGTGGATGTATTTGAAAC	2101
Db	2177	CCCTGCGCTTCTGCGCTCATCTCTGAAGGCTTACTGAGGGGAGACCCACCATGAAAG	2236
QY	2102	ACCTGAATTAGGCAAGTCGAGGCAATGGAAGAAAGCTCATTAATTAAGTACATTCACAAC	2161
Db	2237	TGCTGATGAAASCAGGGGGGAACACTGAGCAAACTGMAAGCCCTGATATGACTTGTCAAGC	2296
QY	2162	AGGAGAGAAAGATGAAACACAAAAGGTACAGATGAAGTTTATGTTAGCAAAATGAGGC	2221
Db	2297	TGAGCTTCAAGAAACCCCAAGCCCAAGACCAAGAGATGATGACATTGTGATGCGGC	2356
QY	2222	GACCAATTTTCATGATGATGTCCTTAAGAGGCTTGTCTCTCTTAAACCTGCTCATCAAC	2281
Db	2357	AGGAGGCTTACTAGAGGCGCTCTCCACCTGCAAGTCCCCACTGAGCCCAAGCAGCCCTGC	2416
QY	2282	TAGGAAACCTCAGGCTTAAAGAGTGTGGAATTAATGTCTTTCGAAAAAGGCACTGTGGT	2341
Db	2417	TGCGTGAAGTCTGCGTGGAGAGTGCACACTTTCATGAGACTCCMAATGMAAGCCTTGTGGA	2476
QY	2342	TGAATTGGGAACCCAGACATCATGTCTAGAGTTACTGTTTCAGAACAAATGATCATCT	2401
Db	2477	TCAATGTACAGCAAGAGAGGCAAGCGGCGGC-----AGCGTGGGACTCATCT	2527
QY	2402	TTAAAAATGGGAGATGATTTACGGCAAAATATGCTTAACACTTCAAAATTAATTCATATG	2461
Db	2528	TTAAGAAACGGGAGATGACCTCCGGCAGAGCAATGTCTGACCTTCGACATATATCAGCTC	2587
QY	2462	AAAAATATCTGSCAAATATCAAGGTCTTGATCTTTCGAATGTTTACCTTATGTTGTGTCA	2521
Db	2588	ACGTCTCTGTGAGACAGAGAGGGCTTGAACCTGAGAGATGACCCCTTAATGGCTGCTCCCA	2647
QY	2522	TGCGTGACTGTGTGGACTTAATTGAGGTGTGCGAAATTCACACACTAATTAATGCAAAATTC	2581
Db	2648	CCGGGAGACCCACAGGCTCATTAAGGTGATCTCCGTTGACACATCATGCGCCAAATCC	2707
QY	2582	A---GTCCAAAGGCGCTTGAAAGTGCATCTGCAGTTTCAACAGCCACACACTACTACAGT	2638
Db	2708	AACCTCAACAAGAGCAATGGCAGCCACAGCGGCTTCAACMAAGATGCCCTGTCTCAACT	2767

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RESULT 7
US-10-027-591-1
; Sequence 1, Application US/10027591
; Publication No. US200201610141
; GENERAL INFORMATION:
; APPLICANT: SADBHU, Chanchal et al.
; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
; FILE REFERENCE: 27866/36170C
; CURRENT APPLICATION NUMBER: US/10/027,591
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/841,341
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/199,655
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/238,057
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Human p110delta complete cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(3327)
US-10-027-591-1

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Query Match 9.7%; Score 329.8; DB 13; Length 5220;  
Best Local Similarity 53.2%; Pctd. No. 2.2e-73;  
Matches 800; Conservative 0; Mismatches 682; Indels 21; Gaps 4;  
1682 TCCCGCAATTCACCAATTCCTCTGCTCTTAATGGAATTCAGAGATAGAGTAG 1741



Db 242 ATTGCAAAATCCATGAAACAGCATTTAGATTTACAGCAAGAAAGAAATTAATCTATAT 301  
QY 3353 AATTTAAATATATGTAACGAAACAGGGTTGTATAGACTTAAATAGTTCATTTCAAA 3412  
Db 302 AATTTAAATATATGTAACGAAACAGGGTTGTATAGACTTAAATAGTTCATTTCAAA 361

RESULT 9  
US-10-101-235A-3  
; Sequence 3, Application US/10101235A  
; Publication No. US20030182669A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockman, Howard A.  
; APPLICANT: Naga Prasad, Sathyamangla V.  
; APPLICANT: Laporte, Stephane A.  
; APPLICANT: Barak, Larry S.  
; APPLICANT: Caron, Marc G.  
; TITLE OF INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCR  
; FILE REFERENCE: 033072-064  
; CURRENT APPLICATION NUMBER: US/10/101,235A  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatsSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 3342  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-101-235A-3

Query Match 8.7%; Score 295.6; DB 12; Length 3342;  
Best Local Similarity 52.6%; Pred. No. 9.9e-65;  
Matches 855; Conservative 0; Mismatches 724; Indels 45; Gaps 8;

QY 1586 AACAGCTCAAGCAATTTCTACAGAGATCTCTCTGAAATCAGTACAGAGAGAAG 1645  
Db 1655 AGCAATGGAGGCGATATAGCCATGATCACTTAACCTCTACAGAGAGACAAG 1714  
QY 1646 ATTTCTATGAGTCAAGACACTATTTGTAACTATCCCGAATTTCTACCCAAATTCG 1705  
Db 1715 AATTGCTCTGCAATTTTATGATGAAAGCCTTAAGACCCAAAGCATATCTTAAGTAT 1774  
QY 1706 TTCGTCTGTTAAATGGAATTTAGAGATGAAGTACCCAGATGTATGCTTG----- 1758  
Db 1775 TTAGTTCAGTGAATGGGACAGCAAGAAATGTGGCCAAACATATCAATGTTGGCCA 1834  
QY 1759 -----GTAAAGATTTGGCCTCCATCAACCTGAAACAGGCTATGGAATCTTGACT 1810  
Db 1835 GAAGGAAGTCTGGGATCAAGTGTGATGTGGATTAAACATGACGCTCTGACT 1894  
QY 1811 GTAATTACCAAGATCTATGATGAGGTTTGTGTTGGTCTTGGAATAATATTTAA 1870  
Db 1895 GCAATCTCTAGATGAAGAAATGTAAGACCATTTGACATTCAGAACTGAGAGC---TTGG 1951  
QY 1871 CAGATGCAAACTTTCTAGTATTTAAATCAGTAGTACAGGTCCTAAATATGAAACAT 1930  
Db 1952 AGAGCATGATGTTCTGCATTAACCTCTACAAATGTGTCAGGCTGTGAAATTTGACAT 2011  
QY 1931 ATTGGAATACCTGCTGTGAGATTTTACTGAAAGAAAGCATTTGACTATCAAGAGATTG 1990  
Db 2012 ACCATGATAGCGCCCTTGCCAGATTTCTGTGAAGCGTGTGTTAAGAAACAAAGAAATG 2071  
QY 1991 GGCATTTTCTTTTGGCATTTAAATCTGAGAT---GCACATTAAGAAAGATTGACCA 2047  
Db 2072 GTCACTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2131  
QY 2048 GGTTCGCTGCTGTTTGGAGTCTTATGTCGTGATGTGGAGTGTATTTGAAGCACTGA 2107  
Db 2132 GGTTCGCTGCTGTTTGGAGTCTTATGTCGTGATGTGGAGTGTATTTGAAGCACTGA 2191  
QY 2108 ATAGGCAAGTGAAGCAATGAAAGATGATTAATCTTAATGATGATTTCTCAAGAGAGA 2167  
Db 2192 TTACCAACAAAGTCAAGTAAATGAGATGTTAAGAAAGTCACTTGTATTTAAATGCG 2251

QY 2168 GGAAGATGAACACAAAGATACAGATGAAGTTTATGTTAGCAAAATGAGCGACAG 2227  
Db 2252 TCTCTCTGTAAGAAATGATGAGTCACTTCCCAATTTTACAACTTAAGCAAAAGCTTG 2311  
QY 2228 ATTTCAATG-----GATGCCCTACAGGGCTGTGCTCTCTTAACCCCTGCTCATC 2278  
Db 2312 AAAACCTGAGAAATTTCTCACTCCCGAAAGCTTTAGAGTTTCATATGATTCCTGAGCTGA 2371  
QY 2279 AACTAGAAACCTCAGGCTTTAAAGAGTGTGAATTTATGTTCTTGTGCAAAAGGCGACTGT 2338  
Db 2372 AACGAGAGCGCTGCGAATTTGAAATGTAAGTATGAGCTCTCCAGAAAGAAACCACTAT 2431  
QY 2339 GGTGAATTTGGAGAAACCAAGATCATGTCAAGTTACTGTTTCAGAAACATGAGATCA 2398  
Db 2432 GGCTGAGTTTAAATGTGCGATCTTA---CAGCCCTATCAAAATGAACAAATGGAATTA 2488  
QY 2399 TCTTTAAATGGGAGTGAATTTAGCGCAAGATATGTAACACTTCAATATATGATTA 2458  
Db 2489 TCTTTAAACATGTGATGATCTGCGCAAGACATGCTTTATTTACAGATTTACGAATTA 2548  
QY 2459 TGGAAATATCTGCAAAATCAAGTCTTGATCTTGAATGTTACCTTATGTTGTCTGT 2518  
Db 2549 TGGAGTCTATTTGGAGACTGAATCTTTGATCTATGCTCTCCCATATGTTGATTA 2608  
QY 2519 CAATCGTGACTGTGTGGACTTATGAGTGTGGAAATTTCTCACTATTTATGCAAA 2578  
Db 2609 CAATCGTGAACAAATAGGAATGATCGAATTTGAAAGCGCCAGCAATTTGCCAAA 2668  
QY 2579 TTCAATGCAAGGCGCTGAAAGTGCACACTGACATTTCAACAGCCACACACTATCACT 2638  
Db 2669 TTAG---CAACACAGTGGGCAACGCGACATTTAAAGTGAAGTCTCAATCACT 2725  
QY 2639 GGCTCAAGACAGAAAC---AAGAGAAATATATATGATGAGCGATTTGACTTTTACAC 2695  
Db 2726 GGCTCAAGAAATATCCCTACTGAAGAAAGTTTACGAGAGAGAGAGATTTGTT 2785  
QY 2696 GTTCATGTGTGATATCTGTATGATCTTCACTTCAATTTTGGAAATGAGATGTCACATA 2755  
Db 2786 ATTCCTGTGAGCTATGTTGTGTGCAACCTTTGTTTGGAAATGAGCGACAGACATG 2845  
QY 2756 GTAACTATGTGTGAAGAGAGATGACACTGTTTCAATATGATTTTGGACACTTTTGG 2815  
Db 2846 ACAATATATGATCACCGAGACAGAAACCTATTTATATGATTTGCGGCAATTTCTG 2905  
QY 2816 ATCAAGAAAGAAATTTGTTTAAACGAGAGAGTGTGCAATTTGTTGACACAGG 2875  
Db 2906 GGAATTAACAAAGTTTCTGCGCATTTATTAAGAGAGTGCATTTTGTCTAAACCTTG 2965  
QY 2936 GGTTCAGAGATGTTTACAGGCTTATTTACTATTGACAGATGCCATCTCTTCA 2995  
Db 3020 AATTTCAAGCATCTGTGTTAAGCTTATCTACCCCTTCTGTCACACAAACCTCTGA 3079  
QY 2996 TAAATCTTTCTCAATGATGCTTGCTGTGAATGCGAGAACTACATCTTTGATGACA 3055  
Db 3080 TCAATCTGTTCTCATGATGCTGATGACAGAAATGCCCCGTTTAAAGAAAGAGACA 3139  
QY 3056 TTGCATACATTTGAAAGACCTTAGCTTATGATTAATCTGACAGAGAGCTTTGAGATTT 3115  
Db 3140 TTGAATATATCCGGAGATGCCCTCAAGTGGGAAATATGAGGATGCTTAAAGATTT 3199  
QY 3116 TCATGAACAAATGAATGATGACATCATATGTTGCTGTCGACACAAAAATGATTTGATCT 3175  
Db 3200 TTTCTGATCGATCGAAGTTTGAAGACAAAGATGAGCTGTGCAAGTTTAATTTGTTTC 3259  
QY 3176 TTCA 3179  
Db 3260 TAQA 3263

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RESULT 10
US-10-092-219-1
; Sequence 1, Application US/10092219
; Publication No. US20020115114A1
; GENERAL INFORMATION:
; APPLICANT: Domain, Jan
; TITLE OF INVENTION: No. US20020115114A1el Lipid Kinase
; FILE REFERENCE: 1064HG/50947
; CURRENT APPLICATION NUMBER: US/10/092,219
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: PCT/GB98/00244
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 09/355,160
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 9701652.1
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5061
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(5058)
; OTHER INFORMATION:
US-10-092-219-1

Query Match      6.5%; Score 223; DB 13; Length 5061;
Best Local Similarity 49.3%; Pred. No. 5.5e-46;
Matches 806; Conservative 0; Mismatches 790; Indels 39; Gaps 7;

Db      Oy      1566  ATTAAGGAAATGCAAGAAACGCTCAAGCAATTTCTACAGAGATCCCTCTCGA 1625
      Oy      2598  ACTAGAGATGATATATAAGGAAACTCTTGATATCTTCAATAAGCTATCACTGG 2657
      Oy      1626  AATCACTGAGCAGAGAAAGATTTTCTATGAGTCACAGACACTTTGTAACTATCC 1685
      Db      2658  ACTTCTTAAAGAAATTAAGCTTTTATGGAAGAAAGTTATTTCTTCAAAACACC 2717
      Oy      1686  CGAAATCTCAACCAATGCTCTGTCTGTCTTAATGAAATCTAGAGATGAAGGCCA 1745
      Db      2718  AAATGCTCTCTAAATATTAGCAAGCGCCCAACTGAAATGGGCTAACTCTGCCA 2777
      Oy      1746  GATGATGCTTGGTGAAGAAAGATGGCTTCAATCAACCTGAACGGCTATGAACTCT 1805
      Db      2778  AACTTACTCATGCTTTCACAGTGGCTGCAATGTACCACTAATTGATTGGAACCTCT 2837
      Oy      1806  GGACTGTATTAACCAAGATCCATGTTGAGAGTTTGTGCTGCGTCTTGAAGAAATA 1865
      Db      2838  TGATTCAAAAATTTGCTGATCAAGAGTAAGATCCCTAGCTGT--GACCTGATGAGGC 2894
      Oy      1866  TTTAAGATGACAAACCTTCTCAGTATTTAATTCAGTATGACAGTCTCTAAATATGA 1925
      Db      2895  CATTAGTATGATGATGATCAAGATCTTCTTCCACAGTTTGAACGTTTGAATATGA 2954
      Oy      1926  ACAATATTTGATTAACCTGCTGTGAGATTTTACTGAAGAAAGATTGACTTAACAAG 1985
      Db      2955  AATTACTTGAATATGATTAATGATGCAATTCCTTTTTCAGGGGATGGGAAATATCCA 3014
      Oy      1986  GATTGGGACCTTTTCTTTGGCATTAAATCTGAGATGACATTAACAGTAAAGCCA 2045
      Db      3015  GATGACACACAAATTTATATGCTTCTCAAGATCCCTGCTGATGATGACAGTTTATGAC 3074
      Oy      2046  GAGGTTTGCCCTGCTTTGGAGTCTTATGTCGTCATGTGGATGTATTTGAAGCACTT 2105
      Db      3075  CCGATAGCAACATGTTTTGG-----GTGCTCTCTGTCAGTGAAGGAAAGACACTT 3126
      Oy      2106  GAATGAGCAAGTCAGGCAATGGAAGAGCTCATTAACCTTAACGATTTCTCAACAGGA 2165
      Db      3127  AGAGAAAGAACTTTCAAAACGACGAACCTTGTACAGCTTTTGAAGGAGATGACAGAAAA 3186
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      Oy      2166  GAGGAAGATGAAACAAAGGTACAGATGAAGTTTATGTTGACCAATGAGCGACC 2225
      Db      3187  GTAAGCAGGCTAGTGATCAGCCAGACAGATGTTCTCCAAAGAGT-ATGGAACAGAT 3245
      Oy      2226  AGATTGATGATGCCCTACAGGCTTGCTGTCTCTCTAAACCCCTGCTATCAACTAGG 2285
      Db      3246  ACAGTCTTTTTCAGAAAATTAATGCCCTCTCCCTCAAGCCAAAGCTTAGTGGCAAA 3305
      Oy      2286  AAACCTCAGGCTTAAAGATGCAATTAATGCTCTGCAAAAAGGCACTGTGTGAA 2345
      Db      3306  AGAATTAATATTAATGAGTGTTCTCTTCAAGTTCAATAGTGTCCCTTAAAGACAC 3365
      Oy      2346  TTGGGAGAACCCAGACATCATGTCAGATTACTGTTTCAAGACATAGATCATCTTAA 2405
      Db      3366  AATGTAAATGCTGACCCCTCTGGAG-----AAGAATTAATGTGATGTTAA 3413
      Oy      2406  AAATGGGATGATTTAGGCAAGATATGCTAACACTTCAATATATGCTTATGAAAA 2465
      Db      3414  GGTGTTGAAGATCTTGCGCAAGATATGTTAGCTTTACAGATGATTAAGATTAAGATTA 3473
      Oy      2466  TATCTGCAAAATCAAGTCTTGATCTTCGAATGTTACCTTATGTTGTCTGTCAATCGG 2525
      Db      3474  GATCTGCTTAAAGAAAGACTAGATCTGAGATGATGATTTTCAAAATGTCTTCAACGCG 3533
      Oy      2526  TGACTGTGGGACTTATTTAGTGCTGTCGAATTTCTACACTATTTATGCAATTCAGTG 2585
      Db      3534  CAGAGATCGAGCGATGTGTGAGCTGTTCTGCTGCTCGATACCTTCAGAAATCCAGT 3593
      Oy      2586  CAAAGCGGCTTGAAGAGTCCATGCTCAACAGCCACACACTACATAGTGGCTCAA 2645
      Db      3594  GGAATATGTTGTGACAGATCTTTAAAGATTAACCACTTGCAAGATGCTTAAAG--AA 3650
      Oy      2646  AGACAAAGACAAAGGAAATATATGATGACAGCCATGACCTGTTTACAGCTTATGTGC 2705
      Db      3651  ATACATCCCTCTGAAAGAAATATGAAGGCTTCAGAGAACTTATCTATTCCTGTGC 3710
      Oy      2706  TGATATCTGTGTAGCTACCTTCAATTTGGAAATTTGAGATGCTACATATGATCAT 2765
      Db      3711  TGATGCTGTGTGACCACTATGTTTATGATCTGTGATGACACATATGATATATAT 3770
      Oy      2766  GGTAAAGACATGACAACTGTTTCAATATGATTTTGGACACTTTTGGATGACAGAA 2825
      Db      3771  GCTTGAAGACCGGACACATGTTTCACTTGTGAAAGTTTGTGGACATGACA 3830
      Oy      2826  GAAATAATTTGTTATTAACAGAACGTGTGCCATTTGTTTGCACAGATTTCTTAAT 2885
      Db      3831  GATGTTGGCAGCTTCAAAAGGATTCGGGCTCTTTGTGTGACCTGATATGACATA 3890
      Oy      2886  AGTATAGTAAAGAGCCCAAGATGCACAAAGACAAAGAAATTTGAGAGTTTCAGGA 2945
      Db      3891  TGTCAATTAATGGGGGTGA-----AAAGCCACCATTCGTTTCAAGTTGTGTGA 3941
      Oy      2946  GATGTGTACAAGCTTATCTAGTATTTGACAGCAATGCCAATCTCTCATTAATCTTT 3005
      Db      3942  CCTGTGCTGTGAGGCTTCAAACTTGATTAAGAACCAAAACCTTTTCTTAACTCTCT 4001
      Oy      3006  CTCATGATGCTTGGCTCTGGAATGCCAGAACTCAATCTTTTATGATGACATTTGATCAT 3065
      Db      4002  TTCATGATGATTTCTTCAAGGTTTACCAAGAACTTACAGATTTGAATATAGCT 4061
      Oy      3066  TCGAAGACCTTACCTTATGATTAACCTGACAAAGAGCTTTGGATGATTTTCAATAACA 3125
      Db      4062  TAGAGATGACATTCACCCCAAACTACAGAGCGAAGCT--ACAATTTTCTTACTAG 4118
      Oy      3126  AATGAATGATGACATATGTTGCTGACAAACAAATGATTTGATGATTTTCCACACAT 3185
      Db      4119  GCTTATGAAATCAAGTTTGGAAAGCAATTCGACAAAGTTTAACTTCTTCAATCAACCT 4178
      Oy      3186  TAAACAGATGATTT 3200
      Db      4179  TGCTGAGCTTGCTTT 4193
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RESULT 11
US-10-027-632-213996
; Sequence 213996, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213996
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-213996

Query Match
Best Local Similarity 5.1%; Score 173.8; DB 12; Length 1248;
Matches 228; Conservative 0; Mismatches 72; Indels 1; Gaps 1;

QY 1890 GTATTTAATTCAGCTAGTACAGGTCCTAAATATGAACAATATTGGATTAACCTGCTGT 1949
DB 653 GTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 712
QY 1950 GAGATTTTCTAGTGAAGAACATTTGA-CTAATCAAGAGATGGGCACTTTTCTTTGGC 2008
DB 713 CAAAGATTATTTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 772
QY 2009 ATTAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2068
DB 773 CTTTAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 832
QY 2069 CTTATTCGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2128
DB 833 CTTATTCGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 892
QY 2129 AAAAGCTATTAACTTAAGTCACTTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2188
DB 893 AAAAGCTATTAACTTAAGTCACTTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 952
QY 2189 T 2189
DB 953 T 953

RESULT 12
US-10-027-632-213996
; Sequence 213996, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
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; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213996
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-213996

Query Match
Best Local Similarity 5.1%; Score 173.8; DB 13; Length 1248;
Matches 228; Conservative 0; Mismatches 72; Indels 1; Gaps 1;

QY 1890 GTATTTAATTCAGCTAGTACAGGTCCTAAATATGAACAATATTGGATTAACCTGCTGT 1949
DB 653 GTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 712
QY 1950 GAGATTTTCTAGTGAAGAACATTTGA-CTAATCAAGAGATGGGCACTTTTCTTTGGC 2008
DB 713 CAAAGATTATTTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 772
QY 2009 ATTAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2068
DB 773 CTTTAAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 832
QY 2069 CTTATTCGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2128
DB 833 CTTATTCGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 892
QY 2129 AAAAGCTATTAACTTAAGTCACTTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2188
DB 893 AAAAGCTATTAACTTAAGTCACTTCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 952
QY 2189 T 2189
DB 953 T 953

RESULT 13
US-09-814-353-21472
; Sequence 21472, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; FILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-006B
; CURRENT FILING DATE: 2001-03-21
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
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PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: US 60/257,672  
PRIOR FILING DATE: 2000-12-21  
NUMBER OF SEQ ID NOS: 22037  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 21472  
LENGTH: 1020  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 1018, 1019, 1020  
OTHER INFORMATION: n = A,T,C or G  
US-09-814-353-21472

Query Match  
Best Local Similarity 5.1%; Score 173.4; DB 12; Length 1020;  
Matches 208; Conservative 0; Mismatches 16; Indels 5; Gaps 2;

2933 AGAGGTTTCAGAGATGTTTACAGAGCTTATCTAGCTATTCGACAGCATCCATCTCT 2992  
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666 ATAGGTTTCAGAGATGTTTACAGAGCTTATCTAGCTATTCGACAGCATCCATCTCT 725  
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2993 TCATTAATCTTTCT-CATGATGCTTGGCTCTGGAATGCCAATCTTCTTGTAT 3051  
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726 TCATTAATCTTTCTCCAGAGATGCTGGGTTCTGGAATGCCAATCTTCTTGTAT 785  
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3052 GACATTCGATCATTCGAAAGACCTTACCTTATGAACTGAGCAAGAGCTTGGAG 3111  
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786 GACATTCGATCATTCGAAAGACCTTACCTTATGAACTGAGCAAGAGCTTGGAG 841  
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3112 TATTCATGAACAATAATGATGATCATCATGCTGCTGCAACACA 3160  
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842 TATTCATGAACAATAATGATGATCATCATGCTGCTGCAACACA 890  
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RESULT 14  
US-10-101-235A-5  
Sequence 5, Application US/10101235A  
Publication No. US20030182669A1  
GENERAL INFORMATION:  
APPLICANT: Rockman, Howard A.  
APPLICANT: Naga Prasad, Sathyanagla V.  
APPLICANT: Laporte, Stephanie A.  
APPLICANT: Barak, Larry S.  
APPLICANT: Caron, Marc G.  
TITLE OF INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCRs  
FILE REFERENCE: 033072-064  
CURRENT APPLICATION NUMBER: US/10/101.235A  
CURRENT FILING DATE: 2002-03-19  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 3237  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-101-235A-5

Query Match  
Best Local Similarity 5.0%; Score 172.2; DB 12; Length 3237;  
Matches 607; Conservative 0; Mismatches 543; Indels 39; Gaps 7;

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1555 AGCAATGGAGGCGATCATACCACTGATCACTTAACCTCTCACAGAGAGAGAGAAG 1714  
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1646 ATTTTATGAGTCACAGACATATGTAACATATCCCGAAATTTACCAAAATTC 1705  
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1715 AATGCTCTGGCATTTTGAATACGAAGCCTTAAGACCCAAAGCATATCTTAAGCAT 1774  
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1706 TTCTGCTGTTAAATGAATTTCTAGAGATGAAGCCAGATGATGCTTG----- 1758  
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1775 TTAGTTCAAGTAATGGGAGACAGCAAGAAATTTGGCCAAAACATACCAATTTGTTGGCA 1834  
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1759 -----GTAAAGATTGGCCCTCCATCAAACTGAAAGGCTATGAACTTCTGACT 1810  
|||||  
1835 GAAGGGAAGCTGGGATCAAAAGTCTTTGATGTTGGGTTAAACAATGCACCTCTGACT 1894  
|||||  
1811 GTAAATACCAAGATCTATGCTTGCAGGTTTGTCTGTCTGCTGCTGGAATAATTTAA 1870  
|||||  
1895 GCAACTTCTCAGATGAAGAAATGAAGCCATTCAGTTCGAAACTGGAGAGC---TTGG 1951  
|||||  
1871 CAGATGCAAACTTCTCAGATTTAATTAGCTAGTACAGTCTCTAAATATGAACAAT 1930  
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1952 AGAGCATGATGTTCTGATTTACCTTTCAAAATGCTCCAGGCTGCAAAATTTGAACAT 2011  
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1931 ATTTGATTAACCTTCTGATGATTTTCTGGAAGAAAGCATTTGACTTAACAAAGATTG 1990  
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2012 ACATGATACCGCCCTTGCAGATTTCTGCTGAAGGCTGTTTAAAGAAACAAAGAAATTG 2071  
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1991 GGCACCTTTTCTTTGGGCAATTTAAATCTGAGT--GCACAATTAACGTTAGCCAGA 2047  
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2072 GTCACTTTTGTGTTTGTCTTGTGAGATGAGATAGCCAGTCCAGACACTATCAGAGA 2131  
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2048 GATTGGCCCTTTTGGATTCCTATGTCGATGTCGAGTGGAGATGATTTGAAGCACCTGA 2107  
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2132 GATTGCTGATTTCTGAAAGCTTATCTGAGGCTGTGGCAAGCCATCTGCACACT 2191  
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2108 ATAGGCAAGTCGAGGCAATGAAAGCTCAATTAATTAATCTGACATTTCTCAACAGAGA 2167  
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2192 TTACCAACAAGTCAGATGATGAGATGTTACAAAAGTACACCTTTGATTTAAATCGC 2251  
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2168 GGAAGATGAACAACAAGATGATGAGATGTTTATGTTAGCAAAATGAGCCAGCAG 2227  
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2252 TCTCTGCTGAAAGATGATGAGTCCAGTTCAGATTTTACAACTTAAACAAAGCTTG 2311  
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2228 ATTTGATGAT-----GCCCTACAGGCTTGTGCTGCTTAAACCTGCTCATC 2278  
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2312 AAACTGCAAAATTTCAACTCCCGAAGCTTTAGATTTCAATGATGCTGAGCTGA 2371  
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2279 AACTGAAACCTCAGGCTTAAAGATGTCGAATTAATGCTTGCAAAAGGCCACTGT 2338  
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2372 AAGCAGAGGCGCTGGCAATTTGAAATGTAAGTATGCGCTCCAGAAAACCACTAT 2431  
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2339 GGTGAAATGGAGAACCCAGACATCATGTCAGATTTACTGTTTCAGAACATGAGATCA 2398  
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2432 GCGTTGAGTTTAAATGTCGATCTTA---CAGCCCTATCAAAATGAAATTTGAATTA 2488  
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2399 TCTTAAATGGGAGATTTACGCGAAGATATGCAACATTAATTAATGCTATTA 2458  
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2489 TCTTAAACATGGATGATCTGCGCAAGACATGCTTATTTACAGATTTCTAGAAATCA 2548  
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2459 TGGAAATATCTGCAAAATCAAGTCTTATGCTTGCATGTTACCTTATGTTGCTGT 2518  
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2549 TGAAGTATTTTGGAGACATGAATCTTTGATCTATGCTCCGCCATATGTTGATTT 2608  
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2519 CAATCGTGAATGTCGACTTATTTGAGGTCGCAAAATTTCTCACATTTATGCAAA 2578  
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2609 CAATCGTGAACAAATTTGAGATGATCGAATTTGAAAGAGCCACACCAATTTGCCAAA 2668  
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2579 TTCACTGCAAAAGGCGTTGAAAGTGCATCGAGTTCAACAGCACAACCTCATGAGT 2638  
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2669 TTGAG---CAAGGACAGTGGGCAACAGGAGCATTTAAAGATGAGTCTGATACT 2725  
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2639 GGCCTCAAGACAAGAAC---AAAGAGAAATATATGATGAGCATTTGACCTGTTTACAC 2695  
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2726 GGCCTCAAGAAAATATCCCTACATGAGAAAAGTTTACAGCAGCAGTGAAGATTTGTT 2785  
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2696 GTTCATGTCGTGATCTGTGATGCTTCAATTTTGGAAATTTGAGA 2744  
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2786 ATTCTGTGACGCTACTGTGTGCAACCTTTGTTTGAATAGGCGA 2834  
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RESULT 15  
US-09-917-800A-477  
Sequence 477, Application US/09917800A

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: Patent No. US20020119462A1
: GENERAL INFORMATION:
: APPLICANT: Mendrick, Donna
: APPLICANT: Porter, Mark
: APPLICANT: Johnson, Kory
: APPLICANT: Castle, Arthur
: APPLICANT: Elashoff, Michael
: APPLICANT: Gene Logic, Inc.
: TITLE OF INVENTION: Molecular Toxicology Modeling
: FILE REFERENCE: 44921-5038-US
: CURRENT APPLICATION NUMBER: US/09/917,800A
: PRIOR APPLICATION NUMBER: US 60/222,040
: PRIOR FILING DATE: 2000-07-31
: PRIOR APPLICATION NUMBER: US 60/222,880
: PRIOR FILING DATE: 2000-11-02
: PRIOR APPLICATION NUMBER: US 60/290,029
: PRIOR FILING DATE: 2001-05-11
: PRIOR APPLICATION NUMBER: US 60/290,645
: PRIOR FILING DATE: 2001-05-15
: PRIOR APPLICATION NUMBER: US 60/292,336
: PRIOR FILING DATE: 2001-05-22
: PRIOR APPLICATION NUMBER: US 60/295,798
: PRIOR FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: US 60/297,457
: PRIOR FILING DATE: 2001-06-13
: PRIOR APPLICATION NUMBER: US 60/298,884
: PRIOR FILING DATE: 2001-06-19
: PRIOR APPLICATION NUMBER: US 60/303,459
: PRIOR FILING DATE: 2001-07-09
: NUMBER OF SEQ ID NOS: 1740
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 477
: LENGTH: 5990
: TYPE: DNA
: ORGANISM: Rattus norvegicus
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB009636
: US-09-917-800A-477

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Query Match      4.9%; Score 168.2; DB 10; Length 5990;
Best Local Similarity 52.5%; Pred. No. 7.2e-32;
Matches 447; Conservative 0; Mismatches 390; Indels 15; Gaps 3;

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QY 2401 TTTAAATGGGAGTGAATTAAGGCAAGATATGCTTAACACTTCAATTATTCGTATTATG 2460
DB 3048 TTTAAGGCCGCGCGAGATCTTCGCGAGAGATATGCTTGTCTGCAATTATTCAGTGTATG 3107
QY 2461 GAAAAATCTCGGCAAAATCAAGTCTTGATCTTGAATGTTACCTTAATGTTGTGTCTCA 2520
DB 3108 GACAACTTTGGCTTCAGAGGCGCTCGATATGCAAAATGATCATTTATGATGTCTAGCC 3167
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DB 3168 ACAGGAAAGGCTCAGAGATTCATAGAGATGTGCTGATGCTTAACGCTTGCCAGATTC 3227
QY 2581 CAGTCAAAAGGCGGCTTGAAGAGTGCACCTGCACTTCAACAGCCACACACTACATCATG 2640
DB 3228 CATCTGACCTCTGGGCTGATAGACCCCTGAAAGAAAACACATCA--AGAACTGGTTC 3284
QY 2641 CTCAAGACAAAGCAAAAGGAAATATATGATGACAGCATTTGACTGTTTACAGTTCA 2700
DB 3285 AGTCAGACAAACCACTTAAGGAAATATGAAAGAGCTTGAGAACTTTTCTTACTCT 3344
QY 2701 TGTCTGTGATATCTGTATGATCACTTCTTTTGGAAATGAGATGCTCACAAATAGTAAC 2760
DB 3345 TGTCTGTGCTGTGTGTGTGATCACTTGTGGAGTCTGTGTGACGACATTAATGACAAAT 3404
QY 2761 ATCATGTGAAAGAGATGACAACTGTTTCATATAGATTTTGACACTTTTGTGATCAC 2820

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DB 3405 ATCATGCTGCAAAAGTCAGGCCACATGTTTCATATTTGACCTTGGAAAATCTTGGGTCAC 3464
QY 2821 AAGAGAAAAAATTTGGTTTAAACGAGAACGTGTGCATTTGTTTGAACAGGATTC 2880
DB 3465 GCACAAACATTTGGCGGTATTAAGAGGACCGAGCGCTTTCATTTTACTTCAGAGATG 3524
QY 2881 TTAATAGTATTAAGTAAGAGGCCCAAGAAATGCAAAAGCAAGAGAAATTTGAGAGTTT 2940
DB 3525 GAGTACTTTATTTACGAGGGTG-----GGAAAAACACAGCAATTTTCAAGACTTC 3575
QY 2941 CAGAGATGTGTTACAAAGGCTTATCTAGCTATTTGACAGCATGCAATCTCTTCATAAT 3000
DB 3576 GTGGAACCTGTGCGAGAGCCTTACACATTTGTAGAGAACACAGCCAACTGCTCTGAGC 3635
QY 3001 CTTTTCATATGATGCTGTGCTCTGGAATGCCAGAACTACAACTTTTGTATGATGCA 3060
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QY 3061 TACATTCGAAAGACCCCTAGCCTTATAGATTAAGTGAAGAGGCTTTGGAGTATTTGATG 3120
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QY 3121 AAACAAATGATATATGACATCATGTGTGTGACAAACAAAATGATGATCTTTCAC 3180
DB 3756 ACAGAGATTAAGCA--GAGTCTGAGATGCTTCCAGATTAACTGAATTAACCTGATCCAC 3812
QY 3181 ACAATTTAAAG 3192
DB 3813 ACCGTTGACAG 3824

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 05:38:38 ; Search time 155.161 Seconds  
(without alignments)  
9706.030 Million cell updates/sec

Title: US-09-325-095-32

Perfect score: 3412

Sequence: 1 ATGCTCCAGACCATCATC.....TAACTAGTTCATTTCAAA 3412

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	3412	100.0	3412	2	US-08-780-872-32
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4	3236.8	94.9	3240	1	US-08-162-081B-34
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6	3236.8	94.9	3240	3	US-09-085-957-34
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8	3008.6	88.2	3207	2	US-08-780-872-35
9	3008.6	88.2	3207	3	US-09-085-957-35
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13	329.8	9.7	5220	2	US-08-777-405A-1
14	329.8	9.7	5220	2	US-08-977-871A-1
15	329.8	9.7	5220	2	US-09-225-951-1
16	329.8	9.7	5220	4	US-09-841-341-1
17	295.6	8.7	5162	2	US-08-916-917-13
18	295.6	8.7	5162	3	US-09-225-170-13
19	291.8	8.6	4134	2	US-08-817-090B-1
20	291.8	8.6	4137	2	US-08-817-090B-3
21	278.8	8.2	3808	2	US-08-916-917-3
22	278.8	8.2	3808	2	US-08-972-629-3
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24	278.8	8.2	3808	2	US-08-972-630-3
25	278.8	8.2	3808	2	US-08-672-211-3
26	278.8	8.2	3808	2	US-09-225-170-3
27	226.2	6.6	5285	2	US-08-609-049A-29

28	226.2	6.6	5285	3	US-09-170-996-29	Sequence 29, Appl
29	223	6.5	5061	4	US-09-355-160D-1	Sequence 1, Appl
30	130	3.8	3504	3	US-08-857-076-47	Sequence 47, Appl
31	111.8	3.3	6831	2	US-08-609-049A-27	Sequence 27, Appl
32	111.8	3.3	6831	3	US-09-170-996-27	Sequence 27, Appl
33	107	3.1	393	1	US-08-162-081B-40	Sequence 40, Appl
34	107	3.1	393	2	US-08-780-872-40	Sequence 40, Appl
35	107	3.1	393	3	US-09-085-957-40	Sequence 40, Appl
36	90.2	2.6	357	4	US-09-765-298A-13	Sequence 13, Appl
37	70.2	2.1	204	4	US-09-016-434-245	Sequence 245, Appl
38	67	2.0	3252	3	US-09-119-442-1	Sequence 1, Appl
39	67	2.0	3252	3	US-09-677-064-1	Sequence 1, Appl
40	64.4	1.9	232	4	US-09-016-434-525	Sequence 525, Appl
41	63.4	1.9	3063	4	US-09-620-312D-474	Sequence 474, Appl
42	53.2	1.6	277	4	US-09-313-294A-6757	Sequence 6757, Ap
43	44.8	1.3	381	1	US-08-162-081B-38	Sequence 38, Appl
44	44.8	1.3	381	2	US-08-780-872-38	Sequence 38, Appl
45	44.8	1.3	381	3	US-09-085-957-38	Sequence 38, Appl

## ALIGNMENTS

RESULT 1  
US-08-162-081B-32  
Sequence 32, Application US/08162081B  
Patent No. 582492  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph; Otsu, Masayuki; Panayiotou, George; Volinia,  
APPLICANT: Stefano; Gout, Ivan Tarasovitch  
TITLE OR INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Felte & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08162, 081B  
FILING DATE: February 7, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 688-3884  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3412 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single or double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..3204  
OTHER INFORMATION: /standard\_name= "CDS"  
US-08-162-081B-32

Query Match 100.0%; Score 3412; DB 1; Length 3412;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGCGTCCAGACCATCATAGGTGAACCTGGGGGCAATCCACTGATGCCCCCAAGAAC 60  
QY 61 CTAGTGAATGTTTACTACCAATGGAATGATAGTACTTAAATGCTCCGTGAGGCT 120  
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QY 121 ACATTAGTACTTAAAGCATGAACTATTAAAGCAAGAAATACCTCTCCATCAA 180  
DB 121 ACATTAGTACTTAAAGCATGAACTATTAAAGCAAGAAATACCTCTCCATCAA 180  
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DB 241 GAATTTTGTGATGAAACAAGACACTTGTGATCTTGGCTTTTCAACCACTTTTAAA 300  
QY 301 GTATATGAACCACTAGGCAACCGTGAAGAAAGATCCCAATGCAAGAAATGGTTGCT 360  
DB 301 GTATATGAACCACTAGGCAACCGTGAAGAAAGATCCCAATGCAAGAAATGGTTGCT 360  
QY 361 ATGGGATGCGCAATGTCGCAATTTGATGCTTAAAGATCCCAAGAGAGAAAGGAA 420  
DB 361 ATGGGATGCGCAATGTCGCAATTTGATGCTTAAAGATCCCAAGAGAGAAAGGAA 420  
QY 421 AGAAATATTTCTTAATGTTTGAAGAAAGCTGTGATCTTAAAGATCTTAACTCACTCAT 480  
DB 421 AGAAATATTTCTTAATGTTTGAAGAAAGCTGTGATCTTAAAGATCTTAACTCACTCAT 480  
QY 481 AGTAGAGCAATGTATGTCTATCCGCAACATGATGAATCTTCAACAGAGCTGCCAAGAC 540  
DB 481 AGTAGAGCAATGTATGTCTATCCGCAACATGATGAATCTTCAACAGAGCTGCCAAGAC 540  
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DB 541 ATATATATATATATGATAGAGCCCAATATAGTGTGATTTGGTAAATGTTTCTCA 600  
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QY 2761 ATCATGCTGAAAGACGATGACAACTGTTTCAATATGATTTTGGACATTTTGGATTCAC 2820  
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Db 2941 CAGAGATGTGTTACAAAGGCTTATCTAGCTATTTGACAGCATGCCAATCTTTCATTAAT 3000  
QY 3001 CTTTTCTCAATGATGCTGTGCTCTGGAATGCCGAACCTAATCTTTTGTGACATTGCA 3060  
Db 3001 CTTTTCTCAATGATGCTGTGCTCTGGAATGCCGAACCTAATCTTTTGTGACATTGCA 3060  
QY 3061 TACATTCGAAAGACCTAGCCTTAGATTAACCTGAGCAGAGGCTTTTGGATATTTTCAG 3120  
Db 3061 TACATTCGAAAGACCTAGCCTTAGATTAACCTGAGCAGAGGCTTTTGGATATTTTCAG 3120  
QY 3121 AAAACAATGATGATGACATCATGTGCTGACAAACAAAATGATTTGATCTTCCAC 3180  
Db 3121 AAAACAATGATGATGACATCATGTGCTGACAAACAAAATGATTTGATCTTCCAC 3180  
QY 3181 ACAATTTAAACGATGATTTGAACTGAAGATTAACCTGAGAAATGAAAGCTCACTCTGGA 3240  
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Db 3301 AATCCATGAACGACATTAGATTTTACGCAAGAACAGAAATTAATATCTATATATTTAA 3360  
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RESULT 2  
US-08-780-872-32  
; Sequence 32, Application US/08780872  
; Patent No. 5846824  
; GENERAL INFORMATION:  
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
; APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter  
; APPLICANT: Joseph, Osmu, Masayuki; Panayotou, George; Volinia,  
; APPLICANT: Stefano; Gout, Ivan Tarasovich  
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felte & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/780, 872  
; FILING DATE: 09-JAN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/162,081  
; FILING DATE: February 7, 1994  
; APPLICATION NUMBER: PCT/GB93/00761  
; FILING DATE: 13 April 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pasqualini, Patricia A.  
; REGISTRATION NUMBER: 34,894  
; REFERENCE/DOCKET NUMBER: LUD 5256  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 32:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3412 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single or double  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..3204  
; OTHER INFORMATION: /standard\_name= "CDS"  
US-08-780-872-32

Query Match 100.0%; Score 3412; DB 2; Length 3412;  
Best local Similarity 100.0%; Pred. No. 0;  
Matches 3412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTCCAAAGCATCATCAGTGAACCTGTGGGCGATCCACTTGAATGCCCAAGATC 60  
Db 1 ATGCTCCAAAGCATCATCAGTGAACCTGTGGGCGATCCACTTGAATGCCCAAGATC 60

OY	61	CTAGTGGAAATGTTTCTCTCCAAATGGAAATGATAGCACTTTAAGAAATGCTCCGTAAGCT	120
Db	61	CTAGTGGAAATGTTTCTCTCCAAATGGAAATGATAGCACTTTAAGAAATGCTCCGTAAGCT	120
OY	121	ACATTAGTAACCTTAAGCATGAACATATTAAAGAAAGAGAAATAACCTCTCCATCAA	180
Db	121	ACATTAGTAACCTTAAGCATGAACATATTAAAGAAAGAGAAATAACCTCTCCATCAA	180
OY	181	CTTCTTCAAGATGAATCTTCTTACATTTTTCGTAAGTGTACCAGAAAGCAAGGAA	240
Db	181	CTTCTTCAAGATGAATCTTCTTACATTTTTCGTAAGTGTACCAGAAAGCAAGGAA	240
OY	241	GAATTTTTSATGAACAAGACGACTTTGTGATCTTCGGCTTTTTCACCACTTTTAA	300
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OY	301	GTAATTGAACAACGATAGCAACCTGTAGAAAAAGATCTCTCAATCGAATAATGGTTT	360
Db	301	GTAATTGAACAACGATAGCAACCTGTAGAAAAAGATCTCTCAATCGAATAATGGTTT	360
OY	361	ATCGGCATGCCAGTGTGGGAATTTGATATGTTTAAAGATCCGTAAGTACAGAGCTCC	420
Db	361	ATCGGCATGCCAGTGTGGGAATTTGATATGTTTAAAGATCCGTAAGTACAGAGCTCC	420
OY	421	AGAAATATCTTAAATGTTTGTAAAGACCTGTGATCTTAGGATCTTAATTCACCTCAT	480
Db	421	AGAAATATCTTAAATGTTTGTAAAGACCTGTGATCTTAGGATCTTAATTCACCTCAT	480
OY	481	AGTAGAGCAATGTATGTCTATTCGGCACATGTAGAACTTTCACAGAGCTGCCAAAGC	540
Db	481	AGTAGAGCAATGTATGTCTATTCGGCACATGTAGAACTTTCACAGAGCTGCCAAAGC	540
OY	541	ATATTAATTAATTTGATAGAGAGCCAAATTAATAGTGTGATTTGGGTAAATGTTCTCCA	600
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OY	601	AATAATGACAAAGCAGAGATATCTCTGAAAATCAACATGACTGTGTGCCAAACAGTA	660
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OY	661	ATTGCTGAAGCAATAGGAAAAAACTGAAAGTATGTTGATCATCTGGAACATTTAAA	720
Db	661	ATTGCTGAAGCAATAGGAAAAAACTGAAAGTATGTTGATCATCTGGAACATTTAAA	720
OY	721	CTCTGTGTTTTAGAAATATCAGGGCAGTACATTTTAAAGTGTGTGATGTGATGAATAC	780
Db	721	CTCTGTGTTTTAGAAATATCAGGGCAGTACATTTTAAAGTGTGTGATGTGATGAATAC	780
OY	781	TTCTCTAGAAAAATATCTCTGTAGTACATTAAGTATATAAGAGCTGTATATGCTTGG	840
Db	781	TTCTCTAGAAAAATATCTCTGTAGTACATTAAGTATATAAGAGCTGTATATGCTTGG	840
OY	841	AGGATGCCCAATTTTAAGATGATGCTGTAAAGAAAGCCTTTATTTCTCACTGCCATGGAC	900
Db	841	AGGATGCCCAATTTTAAGATGATGCTGTAAAGAAAGCCTTTATTTCTCACTGCCATGGAC	900
OY	901	TGTTTTACAATGCAATCTTATTTCCAGACGACTTTCCACAGCTACACATATATGAATGA	960
Db	901	TGTTTTACAATGCAATCTTATTTCCAGACGACTTTCCACAGCTACACATATATGAATGA	960
OY	961	GAAACATCTACAAATATCCCTTTGGGTTTAAATAGAGACTCAGAAATAAATCTTTGT	1020
Db	961	GAAACATCTACAAATATCCCTTTGGGTTTAAATAGAGACTCAGAAATAAATCTTTGT	1020
OY	1021	GCAACCTACGTGAATCTTAATAATTTGAGACATTTGACAAAGATTTTATGTTGCAACGATATC	1080
Db	1021	GCAACCTACGTGAATCTTAATAATTTGAGACATTTGACAAAGATTTTATGTTGCAACGATATC	1080
OY	1081	TACCATGAGAGAAACCTTATATGTACAAATGTGAACACTCAAAAGATCTTTGTTCCAA	1140
Db	1081	TACCATGAGAGAAACCTTATATGTACAAATGTGAACACTCAAAAGATCTTTGTTCCAA	1140

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Db	1201	CGACTTTCCTCTTCCATTGCTGCTGTTTAAAGCGCAAGGGTGTCTAAAGAGAACACTGT	1260
QY	1261	CCATTGGCATGGGAAATATATAACTGTGTTATATACAGACACTCTATGATCTGAAAA	1320
Db	1261	CCATTGGCATGGGAAATATATAACTGTGTTATATACAGACACTCTATGATCTGAAAA	1320
QY	1321	ATGGCTTTGAATCTTTGGCCAGTACCTCATGGAATTAGAAAGTTTGTGTAACCCATTTGGT	1380
Db	1321	ATGGCTTTGAATCTTTGGCCAGTACCTCATGGAATTAGAAAGTTTGTGTAACCCATTTGGT	1380
QY	1381	GTTACTGATCAAAATCCCAATATAAAGAACTGCATGCTATAGATTGAGATTGACTGTTC	1440
Db	1381	GTTACTGATCAAAATCCCAATATAAAGAACTGCATGCTATAGATTGAGATTGACTGTTC	1440
QY	1441	AGCAGTGTGTAAAGTTCCAGATATGTCAGTGATTGAAGACATGCCAATTTGTGTGTA	1500
Db	1441	AGCAGTGTGTAAAGTTCCAGATATGTCAGTGATTGAAGACATGCCAATTTGTGTGTA	1500
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Db	1501	TCCCGAGAGACAGGATTTAGCTATTTCCACCCAGACACTGAGTAAACACTATGCTAGAGAC	1560
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Db	1861	AAATATTTAACAGATGACAAACTTTCTCAGTATTTTAAATTCAGCTATGACAGTCTTAAA	1920
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Db	1921	TATGAAACAATTTTGGATACTTCCTGTGTGATTTTAACTGAAGAAAGCATTAACATAT	1980
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Db	1981	CAAAAGATTGGGCACTTTTCTTTTGGCAATTAAATCTGAGATGCAAAATTAACAGTT	2040
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Db	2041	AGCCAGAGTGTGGCTGTCTTTTGGAGTCTATTTGTGTGATGTGGGATGTATTTGAAG	2100
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Db 3181 ACAATTAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3240  
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RESULT 3  
US-09-957-32  
Sequence 32, Application US/09085957  
Patent No. 6274327  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph, Oesu, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefano; Gout, Ivan Tarasovich  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
TITLE OF INVENTION: THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/085,957  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/780,872  
FILING DATE: 09-JAN-1997  
APPLICATION NUMBER: 08/162,081  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ. ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3412 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single or double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..3204  
OTHER INFORMATION: /standard\_name= "CDS"  
US-09-085-957-32  
Query Match 100.0%; Score 3412; DB 3; Length 3412;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	241	GAAATTTTGTATGAAACAAAGCACTTGTGATCTTCGGCTTTTCAACCATTTTAA	300
Db	241	GAAATTTTGTATGAAACAAAGCACTTGTGATCTTCGGCTTTTCAACCATTTTAA	300
QY	301	GTAATGGAACAGTAGGCAACCGTGAAGAAAGCCCATTCGAGAAATTGTTTTGCT	360
Db	301	GTAATGGAACAGTAGGCAACCGTGAAGAAAGCCCATTCGAGAAATTGTTTTGCT	360
QY	361	ATCGGCATGCAGTGTGCGAATTTGATATGGTTAAAGATCCGTGAAGTACAGAGCTTCGA	420
Db	361	ATCGGCATGCAGTGTGCGAATTTGATATGGTTAAAGATCCGTGAAGTACAGAGCTTCGA	420
QY	421	AGAAATATTTCTTAATGTTTGTAAAGACCTGTGATCTTAAAGGATCTTAATTCCTCAT	480
Db	421	AGAAATATTTCTTAATGTTTGTAAAGACCTGTGATCTTAAAGGATCTTAATTCCTCAT	480
QY	481	AGTAGAGCAATGATATGCTATTCGCCCAATGTAGAACTCTTCAACAGACCTCCAAAGAC	540
Db	481	AGTAGAGCAATGATATGCTATTCGCCCAATGTAGAACTCTTCAACAGACCTCCAAAGAC	540
QY	541	ATATATTAATAATTTGGATAGAGGCCAATAATAGTGTGATTTGGGTAAATAGTTCTTCCA	600
Db	541	ATATATTAATAATTTGGATAGAGGCCAATAATAGTGTGATTTGGGTAAATAGTTCTTCCA	600
QY	601	AATAATGACAAAGCAGAGTATATCTGTGAAATCAAACATGACTGTGTGCCAAACAGTA	660
Db	601	AATAATGACAAAGCAGAGTATATCTGTGAAATCAAACATGACTGTGTGCCAAACAGTA	660
QY	661	ATTGCTGAAGCAATAGGAAAAAACTAGAAATATGTGTGCTATCATCTGAACAAATTAA	720
Db	661	ATTGCTGAAGCAATAGGAAAAAACTAGAAATATGTGTGCTATCATCTGAACAAATTAA	720
QY	721	CTCTGTGTTTAGAATATCAGGGCAAGTACATTTTAAAGTGTGTGATGATGAATAC	780
Db	721	CTCTGTGTTTAGAATATCAGGGCAAGTACATTTTAAAGTGTGTGATGATGAATAC	780
QY	781	TTCTTAGAAAAATATCTCTGAGTCAGTATAGATATAGAACCTGTATATATGCTTGGG	840
Db	781	TTCTTAGAAAAATATCTCTGAGTCAGTATAGATATAGAACCTGTATATATGCTTGGG	840
QY	841	AGGATGCCCAATTTGAAGATGATGCTTAAGAAAGCCTTATTTCTCAACTGCCAATGGAC	900
Db	841	AGGATGCCCAATTTGAAGATGATGCTTAAGAAAGCCTTATTTCTCAACTGCCAATGGAC	900
QY	901	TGTTTTCAAATGCGCATTTATTCAGAGCATTTCACAGCTACACCATATATGATGGA	960
Db	901	TGTTTTCAAATGCGCATTTATTCAGAGCATTTCACAGCTACACCATATATGATGGA	960
QY	961	GAAACATCTACAAAAATCCCTTTGGGTATTAATAGAGCACTCAGATATAAAATCTTTGT	1020
Db	961	GAAACATCTACAAAAATCCCTTTGGGTATTAATAGAGCACTCAGATATAAAATCTTTGT	1020
QY	1021	GCAACCTTACGTGATCTTAATATTCAGAGCAATTTCCACAGCTACACCATATATGATG	1080
Db	1021	GCAACCTTACGTGATCTTAATATATTCAGAGCAATTTCCACAGCTACACCATATATGATG	1080
QY	1081	TACCAATGGAAGAACCCCTTATGTACATGTGAACCTCAAGAGTACTTTGTTCCAT	1140
Db	1081	TACCAATGGAAGAACCCCTTATGTACATGTGAACCTCAAGAGTACTTTGTTCCAT	1140
QY	1141	CCCAAGTGAATGATGGCTGAATTTATATATATATATATATATATATATATATATATAT	1200
Db	1141	CCCAAGTGAATGATGGCTGAATTTATATATATATATATATATATATATATATATATAT	1200
QY	1201	CGACTTTCCTTTCATTTGCTCTGTAAAGGCGCAAGGCTGTAAAGAGAACACTGT	1260

Db	1201	CGACTTTGGCTTTC	CCATTGCTCTGTTAAAGGCCAAAGGCTGTAAAGGAACA	CTGT	1260
Qy	1261	CCATTGCGATGGGAAAT	ATPAACCTGTGTTGATTACACAGACACTCTAGATCTGGAAAA		1320
Db	1261	CCATTGGCAGTGGGAAAT	ATAAACCTGTGTTGATTACACAGACACTCTAGATCTGGAAAA		1320
Qy	1321	ATGGCTTTGAAATCT	TTTGGCCAGTACCCCACTGATGATTAAGAAATTTGGAAACCCATTTGGT		1380
Db	1321	ATGGCTTTGAAATCT	TTTGGCCAGTACCCCACTGATGATTAAGAAATTTGGAAACCCATTTGGT		1380
Qy	1381	GTTTACTGGATCAAA	TCCAAATAAAGAACTCCATGCTTAGAGTTGAGTTGACTGTTC		1440
Db	1381	GTTTACTGGATCAAA	TCCAAATAAAGAACTCCATGCTTAGAGTTGAGTTGACTGTTC		1440
Qy	1441	AGCAGTGTGTAAGTT	CCAGATATGTCAGTGATTGAAGACATGCCAATTTGTCGTGA		1500
Db	1441	AGCAGTGTGTAAGTT	CCAGATATGTCAGTGATTGAAGACATGCCAATTTGTCGTGA		1500
Qy	1501	TCCCGAAGACGAGAT	TTTACTGTAATCCACAGCGAGGACTGAGTAAACAATAAGCTAGAGAC		1560
Db	1501	TCCCGAAGACGAGAT	TTTACTGTAATCCACAGCGAGGACTGAGTAAACAATAAGCTAGAGAC		1560
Qy	1561	AATGAATTTAAGGAAAT	GACAAAGAACAGCTCAAGCAATTTCTACACGAGATCCTCTC		1620
Db	1561	AATGAATTTAAGGAAAT	GACAAAGAACAGCTCAAGCAATTTCTACACGAGATCCTCTC		1620
Qy	1621	TCTGAAATCACTGAG	CAGAGAAAGATTTTCTATGAGTCAACAGACCTATTTGTAACT		1680
Db	1621	TCTGAAATCACTGAG	CAGAGAAAGATTTTCTATGAGTCAACAGACCTATTTGTAACT		1680
Qy	1681	ATCCCCGAAATTTCA	CCCAATTCCTCTCTGCTTAAATGGAATTTCTAGAGTAAGATA		1740
Db	1681	ATCCCCGAAATTTCA	CCCAATTCCTCTCTGCTTAAATGGAATTTCTAGAGTAAGATA		1740
Qy	1741	GCCCAAGATGTAAT	TCTGTGTAATAAAGATTGGCCTCTCCATCAAACTGTGAAGGAA		1800
Db	1741	GCCCAAGATGTAAT	TCTGTGTAATAAAGATTGGCCTCTCCATCAAACTGTGAAGGAA		1800
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Db	1801	CTTCTGGACTGTAA	TTTACCAGATCTTAATGAGTTCGATGAGGTTTGTCTGGTCTTGGAA		1860
Qy	1861	AAATATTTTAACAG	ATGACAAACTTCTCCAGTATTAATTCAGCTAATGACAGTCTTAA		1920
Db	1861	AAATATTTTAACAG	ATGACAAACTTCTCCAGTATTAATTCAGCTAATGACAGTCTTAA		1920
Qy	1921	TATGAAACAATTT	TGGATTAACCTGCTGTGAGATTTTTCAGAAAGAACATTAAT		1980
Db	1921	TATGAAACAATTT	TGGATTAACCTGCTGTGAGATTTTTCAGAAAGAACATTAAT		1980
Qy	1981	CAAAAGATTTGGGCA	CTTTTCTTTTGGCATTTAAATCTGAGATGCAAAATAAACGTT		2040
Db	1981	CAAAAGATTTGGGCA	CTTTTCTTTTGGCATTTAAATCTGAGATGCAAAATAAACGTT		2040
Qy	2041	AGCCAGAGGTTTGG	CCCTGCTTTTGGAGCTCATTTGTGTGTGATGTGGAGTATATTGAAG		2100
Db	2041	AGCCAGAGGTTTGG	CCCTGCTTTTGGAGCTCATTTGTGTGTGATGTGGAGTATATTGAAG		2100
Qy	2101	CACCTGAATAGGCA	AGTCGAGCAATGGAAGGCTCAATTAACCTAACCATCTCTCAA		2160
Db	2101	CACCTGAATAGGCA	AGTCGAGCAATGGAAGGCTCAATTAACCTAACCATCTCTCAA		2160
Qy	2161	CAGAGAGGAAGAT	GTAACAACAAGGTACAGATGGAATTTTATGTTGAGCAAAATGAGG		2220
Db	2161	CAGAGAGGAAGAT	GTAACAACAAGGTACAGATGGAATTTTATGTTGAGCAAAATGAGG		2220
Qy	2221	CGACCAAGATTTCA	TGATATGCCCTTACAGAGGCTTGTCTCTCTTAAACCTGTCTCATCAA		2280
Db	2221	CGACCAAGATTTCA	TGATATGCCCTTACAGAGGCTTGTCTCTCTTAAACCTGTCTCATCAA		2280
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 Db 2521 ATCGGTGACTGTGTGGGACTTATTTAGAGTGTGTGCGAAATTTCTCACTATTTATGCAAAAT 2580  
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 Db 2581 CAGTGCAGGCGGCTTGAAGGTGCACTGCAAGTTCAACAGCCACACATCAATCAATG 2640  
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 Db 2701 TGTGCTGATATCTGTAGTACCTTCAATTTGGGAATTTGAGATCGTCACAATAGTAAC 2760  
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 Db 2761 ATCATGCTGAAAGACGATGACAACTGTTTCAATATAGATTTTGGACATTTTGGATCAC 2820  
 QY 2821 AAGAGAAAAAATTTGGTTTAAACGGAACGTGTGCAATTTGTTGAACAGAGATTTT 2880  
 Db 2821 AAGAGAAAAAATTTGGTTTAAACGGAACGTGTGCAATTTGTTGAACAGAGATTTT 2880  
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 Db 2941 CAGAGATGTGTTACAAAGCTTATCTAGCTATTTGACAGAGATGCAATCTTTTATTAAT 3000  
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RESULT 4  
 US-08-162-081B-34  
 ; Sequence 34, Application US/08162081B  
 ; Patent No. 5824492  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
 ; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
 ; APPLICANT: Joseph; Otsu, Masaaki; Panayotou, George; Volinia,  
 ; APPLICANT: Stefano; Goul, Ivan Tarasovich  
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
 ; TITLE OF INVENTION: THEIR PREPARATION AND USE  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSES: Felife & Lynch  
 ; STREET: 805 Third Avenue  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10022  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: wordperfect  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/162,081B  
 ; FILING DATE: February 7, 1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/GB93/00761  
 ; FILING DATE: 13 April 1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Pasqualini, Patricia A.  
 ; REGISTRATION NUMBER: 34,894  
 ; REFERENCE/DOCKET NUMBER: LUD 5256  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 688-9200  
 ; TELEFAX: (212) 838-3884  
 ; INFORMATION FOR SEQ ID NO: 34:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3240 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-162-081B-34  
 Query Match 94.9%; Score 3236.8; DB 1; Length 3240;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3238; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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 QY 301 GTAATTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 360

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Db	2521	ATCGGTGACCTGTGGGACCTATTGAGGTGGTGGAAATTCTCAGCATATATGCAAA	2580
Qy	2581	CAGTGCAGAAAGCGGCTTGAAAGGTGCACTGCAGTTTCAACAGCCACACACTACATCAGTGG	2640
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Qy	2641	CTCAAGAACAAGAACAAAGGAAATATATGATGACGCAATTGACCTGTTTACACGTTCA	2700
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Qy	2701	TGTCCTGGATCTGTGTAGTACTACCTTCATTTTGGGAATTTGGAGATTCGCACAAATGTAAC	2760
Db	2701	TGTCCTGGATCTGTGTAGTACTACCTTCATTTTGGGAATTTGGAGATTCGCACAAATGTAAC	2760
Qy	2761	ATCATGTGTAAGAAGACGATGACCAACTGTTTCATATAGATTTTGGACACTTTTGGATCAC	2820
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Db	3061	TACATTTGAAAGAGCCCTAGCCTTGATTAACCTGAGCAAGAGGCTTTGGAGATATTTGATG	3120
Qy	3121	AAACAAATGATGATGACATCATCTGTGGCTGACCAACAAAATGATTTGGATCTTCCAC	3180
Db	3121	AAACAAATGATGATGACATCATCTGTGGCTGACCAACAAAATGATTTGGATCTTCCAC	3180
Qy	3181	ACAATTAAACAGCATGCACTTGAACCTGAAAGATTAACCTGAGAAAATGAAAGCTCACTTGG	3240
Db	3181	ACAATTAAACAGCATGCACTTGAACCTGAAAGATTAACCTGAGAAAATGAAAGCTCACTTGG	3240

RESULT 5

US-08-780-872-34

Sequence 34, Application US/08780872

Patent No. 5846824

GENERAL INFORMATION:

APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu

APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter

APPLICANT: Joseph, Otsu, Maesuyuki; Panayotov, George; Volinia,

APPLICANT: Stefano; Gout, Ivan Tarasovitch

TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,

TITLE OF INVENTION: THEIR PREPARATION AND USE

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pelfe & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

```

1      SOFTWARE: Wordperfect
2      CURRENT APPLICATION DATA:
3      APPLICATION NUMBER: US/08/780,872
4      FILING DATE: 09-JAN-1997
5      CLASSIFICATION: 435
6      PRIOR APPLICATION DATA:
7      APPLICATION NUMBER: 08/162,081
8      FILING DATE: February 7, 1994
9      APPLICATION NUMBER: PCT/GB93/00766
10     FILING DATE: 13 April 1993
11     ATTORNEY/AGENT INFORMATION:
12     NAME: Pasqualini, Patricia A.
13     REGISTRATION NUMBER: 34,894
14     REFERENCE/DOCKET NUMBER: LUD 5256
15     TELECOMMUNICATION INFORMATION:
16     TELEPHONE: (212) 688-9200
17     TELEFAX: (212) 838-3884
18     INFORMATION FOR SEQ ID NO: 34:
19     SEQUENCE CHARACTERISTICS:
20     LENGTH: 3240 base pairs
21     TYPE: nucleic acid
22     STRANDEDNESS: single
23     TOPOLOGY: linear
24     US-08-780-872-34

```

Query Match	94.9%	Score 3236.8;	DB 2;	Length 3240;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 3238;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	ATGCGCTCCAAAGCAACATCATCTACAGTGAACCTGGAGGGCAATCCACTTGAATGCGCCCAAGATC	60
Db	1	ATGCGCTCCAAAGCAACATCATCTACAGTGAACCTGGAGGGCAATCCACTTGAATGCGCCCAAGATC	60
QY	121	ACATTTAGTAACTATTAAGATGAACCTATTTAAAGACAGAAATAATCCCTTCGCATCAA	180
Db	121	ACATTTAGTAACTATTAAGATGAACCTATTTAAAGACAGAAATAATCCCTTCGCATCAA	180
QY	181	CTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTAAACCAAGAAAGCAAGAGGAA	240
Db	181	CTTCTTCAAGATGAATCTTCTTACATTTTCGTAAGTGTAAACCAAGAAAGCAAGAGGAA	240
QY	241	GAAATTTTGTATGAACCAAGACGACTTGTGATCTTGCGCTTTTTCACCATTTTAAAA	300
Db	241	GAAATTTTGTATGAACCAAGACGACTTGTGATCTTGCGCTTTTTCACCATTTTAAAA	300
QY	301	GTAATTTGAACCGATGAGCAACCGTGAAGAAAAAGATCCCTCAATCGAGAAATTTGGTTGCT	360
Db	301	GTAATTTGAACCGATGAGCAACCGTGAAGAAAAAGATCCCTCAATCGAGAAATTTGGTTGCT	360
QY	361	ATGCGCATCCACAGTGTGCGAATTTGTATGTGTTAAAGATCCCTGAAGTACAGACATTTCCGA	420
Db	361	ATGCGCATCCACAGTGTGCGAATTTGTATGTGTTAAAGATCCCTGAAGTACAGACATTTCCGA	420
QY	421	AGAAATATTTCTTAATGTTTGTAAAGACGTGTGATCTTTAGGATCTTTAATTCACCTCAT	480
Db	421	AGAAATATTTCTTAATGTTTGTAAAGACGTGTGATCTTTAGGATCTTTAATTCACCTCAT	480
QY	481	AGTAGAGCAATATATGTCTATCCGCGACAGATGATAGATTTTACCAAGACTCCCAAGCAC	540
Db	481	AGTAGAGCAATATATGTCTATCCGCGACAGATGATAGATTTTACCAAGACTCCCAAGCAC	540
QY	541	ATATATTAATTAATTTGGATAGAGGCCAAATAATAGTGTGATTTGGTAAATAGTTTCTCA	600
Db	541	ATATATTAATTAATTTGGATAGAGGCCAAATAATAGTGTGATTTGGTAAATAGTTTCTCA	600
QY	601	AATATATGACAGACAGATATCTTTGAAAAATCAACCATGACTGTGTGCCAAGAACAGTA	660
Db	601	AATATATGACAGACAGATATCTTTGAAAAATCAACCATGACTGTGTGCCAAGAACAGTA	660

QY	661	TTTGTGTAAGCAATACAGGAAAAAAACCTAGAGTACGTGTCATCATCTGAAACAAATTA	720
Db	661	ATTGTGTAAGCAATACAGGAAAAAAACCTAGAGTACGTGTCATCTGAAACAAATTA	720
QY	721	CTCTGTGTTTAAATATCAGGGCAAGTACATTTTAAAGAGTGTGATGATGATAC	780
Db	721	CTCTGTGTTTAAATATCAGGGCAAGTACATTTTAAAGAGTGTGATGATGATAC	780
QY	781	TTCTTAGAAAAATATCCTTGAGTCAGTATATATTAAGAAAGCTGTATATGCTTGGG	840
Db	781	TTCTTAGAAAAATATCCTTGAGTCAGTATATATTAAGAAAGCTGTATATGCTTGGG	840
QY	841	AGAGTATGCCAATTTGAAGATATGAGCTTAAAGAAAGCTTTATCTGCACTGCGCAATGAC	900
Db	841	AGAGTATGCCAATTTGAAGATATGAGCTTAAAGAAAGCTTTATCTGCACTGCGCAATGAC	900
QY	901	TGTTTTCATATGCGCATCTTATTTCCAGAGCAATTTCCACAGCTACACCATATATGAATGA	960
Db	901	TGTTTTCATATGCGCATCTTATTTCCAGAGCAATTTCCACAGCTACACCATATATGAATGA	960
QY	961	GAACATCTACAAAATCCCTTTGGGTTTAAATAGAGCACTCAGATATAAAAATCTTTGT	1020
Db	961	GAACATCTACAAAATCCCTTTGGGTTTAAATAGAGCACTCAGATATAAAAATCTTTGT	1020
QY	1021	GCAACCTTACGTGAATCTTAATATTTGAGACATTCACAGATTTATATGTTTCCAACTATC	1080
Db	1021	GCAACCTTATGTGAATGTAAATATTCGAGACATTCGACAAATTTATGTTTCCAACTATC	1080
QY	1081	TACCATGAGAGGAAACCCCTTATGTGACATGTGAACACTCAAAAGGTACTGTTTCCAA	1140
Db	1081	TACCATGAGAGGAAACCCCTTATGTGACATGTGAACACTCAAAAGGTACTGTTTCCAA	1140
QY	1141	CCAGAGTGAAATGAATGGCTGATATATATATATATCATCTCTGATCTTCTCGTGTGCT	1200
Db	1141	CCAGAGTGAAATGAATGGCTGATATATATATATATATCATCTCTGATCTTCTCGTGTGCT	1200
QY	1201	GCACTTTGCCCTTTCATTTGCTCTGTCTTAAAGGCCGAAAGGCTGCTTAAAGAGAACACTGT	1260
Db	1201	GCACTTTGCCCTTTCATTTGCTCTGTCTTAAAGGCCGAAAGGCTGCTTAAAGAGAACACTGT	1260
QY	1261	CCATTGGCATGGGAAATATATAACTCTGTGTTTACACAGACACTCTATGATCTTGGA	1320
Db	1261	CCATTGGCATGGGAAATATATAACTCTGTGTTTACACAGACACTCTATGATCTTGGA	1320
QY	1321	ATGGCTTTGAAATCTTTGGCCAGTACCTATGATATAGAAGATTTGGCTGAACCTATTTGCT	1380
Db	1321	ATGGCTTTGAAATCTTTGGCCAGTACCTATGATATAGAAGATTTGGCTGAACCTATTTGCT	1380
QY	1381	GTTACTGATCAAAATCCAAATTAAGAAAACTCCATCTTATGAGTTGAGTTGACTGCTTC	1440
Db	1381	GTTACTGATCAAAATCCAAATTAAGAAAACTCCATCTTATGAGTTGAGTTGACTGCTTC	1440
QY	1441	AGCAGTGTGTAAGTTCGCCAGATATGTACAGTATGTGAAGGACAGCCAAATTTGGCTGTA	1500
Db	1441	AGCAGTGTGTAAGTTCGCCAGATATGTACAGTATGTGAAGGACAGCCAAATTTGGCTGTA	1500
QY	1501	TCCCGAGAGAGAGATTTAGCTATTTCCACGAGCACTGAGTAAACAGACTAGTAGAGAC	1560
Db	1501	TCCCGAGAGAGAGATTTAGCTATTTCCACGAGCACTGAGTAAACAGACTAGTAGAGAC	1560
QY	1561	AATGAATTAAGGAAAAATGACAAAGACAGCTCAAGCAATTTCTACAGAGATCTCTC	1620
Db	1561	AATGAATTAAGGAAAAATGACAAAGACAGCTCAAGCAATTTCTACAGAGATCTCTC	1620
QY	1621	TCTGAAATCACTGAGCAGAGAGAAATTTTCTATGAGTCAACAGACATATTTGTAACT	1680
Db	1621	TCTGAAATCACTGAGCAGAGAGAAATTTTCTATGAGTCAACAGACATATTTGTAACT	1680
QY	1681	ATCCCGGAAATCTTACCCCAAAATGCTTCTGTCTGTTAAATGGAATTTCTAGAGATGAAGTA	1740
Db	1681	ATCCCGGAAATCTTACCCCAAAATGCTTCTGTCTGTTAAATGGAATTTCTAGAGATGAAGTA	1740
QY	1741	GCCCAAGATGATTTGCTGTGTAAGAAATTTGGCTCCAAATCAAACTGAAACAGGCTATGGA	1800

Db	1741	GCCGAGATGTRTTCCTTGCGTAAAGATTTGGCTTCGATCAAACTGGAACAGGCTATGGAA	1800
Qy	1801	CTTCGTGACGTAAATTAACCCAGATCCTATGAGTTCGAGTTCGTGTCGTGCTTGGAA	1860
Db	1801	CTTCGTGACGTAAATTAACCCAGATCCTATGAGTTCGAGTTCGTGTCGTGCTTGGAA	1860
Qy	1861	AAATATTTTAACAGATGACAAACTTTCTCAGTATTTAATCAGCTAGTACAGGTCCTAA	1920
Db	1861	AAATATTTTAACAGATGACAAACTTTCTCAGTATTTAATCAGCTAGTACAGGTCCTAA	1920
Qy	1921	TATGACCAATTTTGGATTAACCTGCTGTGAGATTTTCTAGAAAGAAAGCATTCATAT	1980
Db	1921	TATGACCAATTTTGGATTAACCTGCTGTGAGATTTTCTAGAAAGAAAGCATTCATAT	1980
Qy	1981	CAAGGATTTGGGCACTTTTCTTTTGGCATTTAAATCTGAGATGCAAAATAAACGTT	2040
Db	1981	CAAGGATTTGGGCACTTTTCTTTTGGCATTTAAATCTGAGATGCAAAATAAACGTT	2040
Qy	2041	AGCCAGAGATTTGGCCCTGCTTTGGAGTCCTATTTGCTGTCAGTGGGATGATTTGAAG	2100
Db	2041	AGCCAGAGATTTGGCCCTGCTTTGGAGTCCTATTTGCTGTCAGTGGGATGATTTGAAG	2100
Qy	2101	CACCTGAAATGGGCAAGTCGAGGCCAATGGAAAGCTCATTAACCTTAACGTACATTCGAA	2160
Db	2101	CACCTGAAATGGGCAAGTCGAGGCCAATGGAAAGCTCATTAACCTTAACGTACATTCGAA	2160
Qy	2161	CAGGAGAGGAAGATGTAACAACAAGATACAGATGAAGTTTTAGTTGAGCAAAATGAGG	2220
Db	2161	CAGGAGAGGAAGATGTAACAACAAGATACAGATGAAGTTTTAGTTGAGCAAAATGAGG	2220
Qy	2221	CGACCAAGATTTCATGATGCCCCCTACAGAGGCTGTGCTCTCCTCTAAACCTGCTCATCA	2280
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Qy	2281	CTAGGAAACCTCAGGCTTTAAAGAGTCGAAATTAATGCTCTCTGCAAAAAGGCCAGTGG	2340
Db	2281	CTAGGAAACCTCAGGCTTTAAAGAGTCGAAATTAATGCTCTCTGCAAAAAGGCCAGTGG	2340
Qy	2341	TTGAAATTTGGGAGAACCCAGACATCATGTCAAGAGTACGTGTTTCAGAACATGAGATCATC	2400
Db	2341	TTGAAATTTGGGAGAACCCAGACATCATGTCAAGAGTACGTGTTTCAGAACATGAGATCATC	2400
Qy	2401	TTTAAAAATGGGAGATTTTACGGCAGAGATATGCTTAACACTTCAAAATTAATTCGTATATG	2460
Db	2401	TTTAAAAATGGGAGATTTTACGGCAGAGATATGCTTAACACTTCAAAATTAATTCGTATATG	2460
Qy	2461	GAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAAAGTATTAAGTTATGTTGCTGTCA	2520
Db	2461	GAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGAAAGTATTAAGTTATGTTGCTGTCA	2520
Qy	2521	ATCGGTACGTGTGGGACATTAATGAGGTGGTGGAATTTCTCACATTAATATGCAATTT	2580
Db	2521	ATCGGTACGTGTGGGACATTAATGAGGTGGTGGAATTTCTCACATTAATATGCAATTT	2580
Qy	2581	CAGTGCAAAAGCGGCTTGAAGAGTGCACTGCACTTCAACAGCCAACACTACATCAGTGG	2640
Db	2581	CAGTGCAAAAGCGGCTTGAAGAGTGCACTGCACTTCAACAGCCAACACTACATCAGTGG	2640
Qy	2641	CTCAAAAGCAAGAACAAAGAGAAATATATGATGACGCCATTGACCTGTTACAGCTTCA	2700
Db	2641	CTCAAAAGCAAGAACAAAGAGAAATATATGATGACGCCATTGACCTGTTACAGCTTCA	2700
Qy	2701	TGTCGTGGATATCTGTGTAGCTACCTCATTTTGGGAATTTGAGATGCTCACATATAGTAC	2760
Db	2701	TGTCGTGGATATCTGTGTAGCTACCTCATTTTGGGAATTTGAGATGCTCACATATAGTAC	2760
Qy	2761	ATCATGTGTAAGAAGCAGATGACAACCTGTTTCATATAGATTTTGGACACTTTTGGATCAC	2820
Db	2761	ATCATGTGTAAGAAGCAGATGACAACCTGTTTCATATAGATTTTGGACACTTTTGGATCAC	2820
Qy	2821	AAGAAAGAAAAATTTGGTATTAACGAGAACGTGTGCCATTTGTTTGGACACAGGATTTTC	2880
Db	2821	AAGAAAGAAAAATTTGGTATTAACGAGAACGTGTGCCATTTGTTTGGACACAGGATTTTC	2880

Db 2821 AAGAGAAAAAATTGGTTATTAACGAAAGTGTCATTGTTTGACACAGGATTC 2880  
 QY 2881 TTAATGATGATTGAAGAGGCCAAGAAATGACCAAGAGAAATTTGAGAGTT 2940  
 Db 2881 TTAATGATGATTGAAGAGGCCAAGAAATGACCAAGAGAAATTTGAGAGTT 2940  
 QY 2941 CAGAGATGTTTACAAAGGCTTATCTAGCTATTCGACAGCATGCCATCTTCATMAAT 3000  
 Db 2941 CAGAGATGTTTACAAAGGCTTATCTAGCTATTCGACAGCATGCCATCTTCATMAAT 3000  
 QY 3001 CTTTCATGATGATGCTGGCTGTGAATGCCGAATACATCTTTGATGACATGCA 3060  
 Db 3001 CTTTCATGATGATGCTGGCTGTGAATGCCGAATACATCTTTGATGACATGCA 3060  
 QY 3061 TACATTCGAAAGACCCAGCCTTAGATTAATGAGCAAGAGCTTTGAGATTTTCATG 3120  
 Db 3061 TACATTCGAAAGACCCAGCCTTAGATTAATGAGCAAGAGCTTTGAGATTTTCATG 3120  
 QY 3121 AAACCAATGAATGATGACATCATGTGCTGACCAAAATGATGATCTTCAC 3180  
 Db 3121 AAACCAATGAATGATGACATCATGTGCTGACCAAAATGATGATCTTCAC 3180  
 QY 3181 ACAATTAAACAGATGATGAACTGAAAGATACTGAGAAATGAAAGCTCACTTCGA 3240  
 Db 3181 ACAATTAAACAGATGATGAACTGAAAGATACTGAGAAATGAAAGCTCACTTCGA 3240

## RESULT 6

US-09-085-957-34

; Sequence 34, Application US/09085957  
 ; Patent No. 6274327

## GENERAL INFORMATION:

; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
 ; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
 ; APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,  
 ; APPLICANT: Stefano, Gout, Ivan Tarasovitch  
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Felle & Lynch  
 ; STREET: 805 Third Avenue  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10022

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/085,957

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/780,872

FILING DATE: 09-JAN-1997

APPLICATION NUMBER: 08/162,081

FILING DATE: February 7, 1994

APPLICATION NUMBER: PCT/GB93/00761

FILING DATE: 13 April 1993

ATTORNEY/AGENT INFORMATION:

NAME: Pasqualini, Patricia A.

REGISTRATION NUMBER: 34,894

REFERENCE/DOCKET NUMBER: LUD 5256

TELECOMMUNICATION INFORMATION:

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TELEFAX: (212) 838-3864

INFORMATION FOR SEQ. ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 3240 base pairs

TYPE: nucleic acid

; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-09-085-957-34

Query Match 94.9%; Score 3236.8; DB 3; Length 3240;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3238; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCCCTCAAGACATCATCAGGTGAAGTGTGGGGCATCCATTGATGCCCAAGATC 60  
 Db 1 ATGCCCTCAAGACATCATCAGGTGAAGTGTGGGGCATCCATTGATGCCCAAGATC 60  
 QY 61 CTAGTGAATGTTTACTTACCAATGGAATGATGATCTTTAGAAATGCTTCGTGAGCT 120  
 Db 61 CTAGTGAATGTTTACTTACCAATGGAATGATGATCTTTAGAAATGCTTCGTGAGCT 120  
 QY 121 ACATTGTAACCTTAAGATGATGATCTTTAAAGAGCAAGAAATACCTCTCCATCA 180  
 Db 121 ACATTGTAACCTTAAGATGATGATCTTTAAAGAGCAAGAAATACCTCTCCATCA 180  
 QY 181 CTTCTCAAGATGATCTTTCAATTTTGTGATGTTTACCAAGAGCAAGAGGAA 240  
 Db 181 CTTCTCAAGATGATCTTTCAATTTTGTGATGTTTACCAAGAGCAAGAGGAA 240  
 QY 241 GAATTTTGTGATGAAACAAGACACTTGTGATCTTCGCTTTTCAACCATTTTAA 300  
 Db 241 GAATTTTGTGATGAAACAAGACACTTGTGATCTTCGCTTTTCAACCATTTTAA 300  
 QY 301 GTTAATTGAACCGATAGGCAACCGTGAAAGAAAGATCTCAATGAGAAATTTGCT 360  
 Db 301 GTTAATTGAACCGATAGGCAACCGTGAAAGAAAGATCTCAATGAGAAATTTGCT 360  
 QY 361 ATGGCATGCGAGTGGCGCAATTTGATGTTTAAAGATCCGTAATACAGGACTCCGA 420  
 Db 361 ATGGCATGCGAGTGGCGCAATTTGATGTTTAAAGATCCGTAATACAGGACTCCGA 420  
 QY 421 AGAAATATTTCTTAATGTTTGTAAAGAGCTGTGATCTTAAAGATCTTAATTCACCTCAT 480  
 Db 421 AGAAATATTTCTTAATGTTTGTAAAGAGCTGTGATCTTAAAGATCTTAATTCACCTCAT 480  
 QY 481 AGTAGAGCAATGATGTCATTCGCGCAATGTAATCTTACACAGAGCTGCCAAGCAC 540  
 Db 481 AGTAGAGCAATGATGTCATTCGCGCAATGTAATCTTACACAGAGCTGCCAAGCAC 540  
 QY 541 ATATATTAATTAATGATGATGAGCCCAATTAATGATGATTTGGTAAATAGTTCTCCA 600  
 Db 541 ATATATTAATTAATGATGATGAGCCCAATTAATGATGATTTGGTAAATAGTTCTCCA 600  
 QY 601 AATAATGACAAGCAGAGATTAATCTGTAAGAAATCAACCATGACTGTGTCCAGAACAGTA 660  
 Db 601 AATAATGACAAGCAGAGATTAATCTGTAAGAAATCAACCATGACTGTGTCCAGAACAGTA 660  
 QY 661 ATTGCTGAAGCAATCAGAAAAAACTAGAAGTGTGCTATCATCTGAACAATTA 720  
 Db 661 ATTGCTGAAGCAATCAGAAAAAACTAGAAGTGTGCTATCATCTGAACAATTA 720  
 QY 721 CTTCTGTTTGAATTAATGAGGCAATCTTTAAAGTGTGAGTGTGATGATG 780  
 Db 721 CTTCTGTTTGAATTAATGAGGCAATCTTTAAAGTGTGAGTGTGATGATG 780  
 QY 781 TTCTTGAAAAATATATCTCTGAGTCAGTATTAAGTATTAAGAAAGCTGTAAATGCTTGG 840  
 Db 781 TTCTTGAAAAATATATCTCTGAGTCAGTATTAAGTATTAAGAAAGCTGTAAATGCTTGG 840  
 QY 841 AGAGTCCCAATTTGAAGATGATGCTTAAGAAAGCTTTATTTCACTGCAATGAGAC 900  
 Db 841 AGAGTCCCAATTTGAAGATGATGCTTAAGAAAGCTTTATTTCACTGCAATGAGAC 900  
 QY 901 TGTTTTACAATGCAATCTTAATCCAGAGCATTTTCCACAGCTTACCATATATGAAATGGA 960  
 Db 901 TGTTTTACAATGCAATCTTAATCCAGAGCATTTTCCACAGCTTACCATATATGAAATGGA 960  
 QY 961 GAAACATCTACAAATCCCTTGGTATTAATAGAGCACTGAGATAAATAATCTTTGT 1020

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Db 961 GAAACATCTACAAATCCCTTGGGTATTAATAGAGACCTCAAAATTAATCTTTGT 1020
Qy 1021 GCAACCTACGCGAATCTTAATATTCGAGACATGACAAAGATTTATGTTGCGAAGATTC 1080
Db 1021 GCAACCTACGCGAATCTTAATATTCGAGACATGACAAAGATTTATGTTGCGAAGATTC 1080
Qy 1081 TACCATGAGAGAGAACCTTATGTGACAACTGAACTCAAAAGATGACTTGTTCAT 1140
Db 1081 TACCATGAGAGAGAACCTTATGTGACAACTGAACTCAAAAGATGACTTGTTCAT 1140
Qy 1141 CCCAGGTGGAATGAATGCTGAATATGATATATACATCTTCTGCTGCTGCT 1200
Db 1141 CCCAGGTGGAATGAATGCTGAATATGATATATACATCTTCTGCTGCTGCT 1200
Qy 1201 CGACTTTGGCTTCCATTTGCTGTTTAAAGCGGAAAGGCTGTAAGAGAAACACTGT 1260
Db 1201 CGACTTTGGCTTCCATTTGCTGTTTAAAGCGGAAAGGCTGTAAGAGAAACACTGT 1260
Qy 1261 CCATTGGCATGGGAAATATTAACCTGTTGATTACACAGACACTTATGATCTGAAAA 1320
Db 1261 CCATTGGCATGGGAAATATTAACCTGTTGATTACACAGACACTTATGATCTGAAAA 1320
Qy 1321 ATGCTTTGAATCTTTGGCCAGTACCTCATGATTTAGAAAGATTTGCTGAACCTTATGCT 1380
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Qy 1381 GTTACTGGATCAAAATCCAAATTAAGAAATCTCATGCTTGAAGTTGAGCTTGCATGCTC 1440
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Db 1441 AGCAGTGTGTAAGTTCCAGATATGTCACTGATTTGAAGAGCATGCAATTTGCTGTA 1500
Qy 1501 TCCCGAGAGAGAGATTTAGCTATTTCCACGAGACTGATTAACAGACTAGTAGAGAC 1560
Db 1501 TCCCGAGAGAGAGATTTAGCTATTTCCACGAGACTGATTAACAGACTAGTAGAGAC 1560
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Db 1621 TCTGAATCACTGAGCAGAGAAAGATTTCTATGAGATTCACAGACATATTTGTAAT 1680
Qy 1681 ATCCCGGAAATTTCAACCAAAATGCTTCTGTGTTAAATGAAATTTAGAGATGAAGTA 1740
Db 1681 ATCCCGGAAATTTCAACCAAAATGCTTCTGTGTTAAATGAAATTTAGAGATGAAGTA 1740
Qy 1741 GCCCAGATGTAATGCTTGTGTAAGATTTGGGCTCCAAATCAAACTGAAACAGGCTATGAA 1800
Db 1741 GCCCAGATGTAATGCTTGTGTAAGATTTGGGCTCCAAATCAAACTGAAACAGGCTATGAA 1800
Qy 1801 CTCTGCACTGTAATTAACCAAGATCTATGCTGAGAGTTTGTGCTTGGCTGCTGAA 1860
Db 1801 CTCTGCACTGTAATTAACCAAGATCTATGCTGAGAGTTTGTGCTTGGCTGCTGAA 1860
Qy 1861 AAATATTTAACAGATGACAAATCTTCTCAGTATTTAATTCAGCTAGTACAGGCTCAAAA 1920
Db 1861 AAATATTTAACAGATGACAAATCTTCTCAGTATTTAATTCAGCTAGTACAGGCTCAAAA 1920
Qy 1921 TATGAACAAATTTGAGTAACCTGCTGTGAGATTTTAACTGAAGAAAGCATGATCATAT 1980
Db 1921 TATGAACAAATTTGAGTAACCTGCTGTGAGATTTTAACTGAAGAAAGCATGATCATAT 1980
Qy 1981 CAAAGATTTGGGCACTTTTCTTTTGGCATTTAAATCTGAGATGCACAATTAACAGTT 2040
Db 1981 CAAAGATTTGGGCACTTTTCTTTTGGCATTTAAATCTGAGATGCACAATTAACAGTT 2040
Qy 2041 AGCCAGAGTTTGGCTTGTGAGTCTTAATGTCTGATGATGAGATGATTTGAAG 2100
Db 2041 AGCCAGAGTTTGGCTTGTGAGTCTTAATGTCTGATGATGAGATGATTTGAAG 2100
Db 2041 AGCCAGAGTTTGGCTTGTGAGTCTTAATGTCTGATGATGAGATGATTTGAAG 2100
Qy 2101 CACCTGAATAGGCAAGTCGAGCAATGAGAAAGCTCATTAATTAATGATCTTCTCAA 2160
Db 2101 CACCTGAATAGGCAAGTCGAGCAATGAGAAAGCTCATTAATTAATGATCTTCTCAA 2160
Qy 2161 CAGAGAGGAGAGATGAAACAAAGATGACAGATGAAGTTTATGTTAGTGACAAATGAG 2220
Db 2161 CAGAGAGGAGAGATGAAACAAAGATGACAGATGAAGTTTATGTTAGTGAGCAAAATGAG 2220
Qy 2221 CGACCGATTTCAATGATGCGCTTACAGAGGCTTCTGCTCTCTTAAACCTGCTCATCA 2280
Db 2221 CGACCGATTTCAATGATGCGCTTACAGAGGCTTCTGCTCTCTTAAACCTGCTCATCA 2280
Qy 2281 CTAGAAACCTCAGGCTTAAAGAGTGCATATATGCTTCTGCAAAAGGCCACTGTG 2340
Db 2281 CTAGAAACCTCAGGCTTAAAGAGTGCATATATGCTTCTGCAAAAGGCCACTGTG 2340
Qy 2341 TTGAATTTGGAGAACCCAGACATATGTCAGAGTTACTGTTTCAAGCAATGATCATC 2400
Db 2341 TTGAATTTGGAGAACCCAGACATATGTCAGAGTTACTGTTTCAAGCAATGATCATC 2400
Qy 2401 TTTAAAAATGGGATGATTTTACGGCAAGATATGCTAAACCTTGAATTAATTCGATTA 2460
Db 2401 TTTAAAAATGGGATGATTTTACGGCAAGATATGCTAAACCTTGAATTAATTCGATTA 2460
Qy 2461 GAAAAATCTGGCAAAATCAAGGCTTGTATCTTCAATGTTACCTTATGTTGCTGCA 2520
Db 2461 GAAAAATCTGGCAAAATCAAGGCTTGTATCTTCAATGTTACCTTATGTTGCTGCA 2520
Qy 2521 ATCGGTGATCTGTGGGACTTATTTAGGTGTGCGAAATCTCACACTATTAATGCAAT 2580
Db 2521 ATCGGTGATCTGTGGGACTTATTTAGGTGTGCGAAATCTCACACTATTAATGCAAT 2580
Qy 2581 CAGTGCAAAAGCGCTTGAAGAGTGCACCTGCAATTCACACCAACATCATCAGTGG 2640
Db 2581 CAGTGCAAAAGCGCTTGAAGAGTGCACCTGCAATTCACACCAACATCATCAGTGG 2640
Qy 2641 CTCAAAAGCAAGAAATTAATATGATGACAGCCATTAACCTGTTTACAGCTTCA 2700
Db 2641 CTCAAAAGCAAGAAATTAATATGATGACAGCCATTAACCTGTTTACAGCTTCA 2700
Qy 2701 TGTGCTGATATCTGTAGTACCTTCAATTTTGGGAATGAGATCGTCAATATGATAC 2760
Db 2701 TGTGCTGATATCTGTAGTACCTTCAATTTTGGGAATGAGATCGTCAATATGATAC 2760
Qy 2761 ATCATGTGAAAGCAATGACAACTGTTTCAATATGATTTTGAACATTTTGGATCAC 2820
Db 2761 ATCATGTGAAAGCAATGACAACTGTTTCAATATGATTTTGAACATTTTGGATCAC 2820
Qy 2821 AAGAAAGAAATTTGGTTTAAACGAGAACTGTGCCATTTGTTTGAACAGAGATTTTC 2880
Db 2821 AAGAAAGAAATTTGGTTTAAACGAGAACTGTGTCCATTTGTTTGAACAGAGATTTTC 2880
Qy 2881 TTAATAGTATTAAGTAAGAGCCCAAGATGACAAAGCAAGAGATTTGAGAGTTT 2940
Db 2881 TTAATAGTATTAAGTAAGAGCCCAAGATGACAAAGCAAGAGATTTGAGAGTTT 2940
Qy 2941 CAGAGATGTTTAAAGGCTTATTAAGCTATTTGACAGATGACAGATGACAGATTTT 3000
Db 2941 CAGAGATGTTTAAAGGCTTATTAAGCTATTTGACAGATGACAGATGACAGATTTT 3000
Qy 3001 CTTTCTCAATGATGCTTGGCTCTGGAATCCAGAACTAATCTTTTGAATGACATGCA 3060
Db 3001 CTTTCTCAATGATGCTTGGCTCTGGAATCCAGAACTAATCTTTTGAATGACATGCA 3060
Qy 3061 TACATTTGAAAGACCTTACCTTATGATTAATCTGAGCAAGAGCTTTGAGATTTTCATG 3120
Db 3061 TACATTTGAAAGACCTTACCTTATGATTAATCTGAGCAAGAGCTTTGAGATTTTCATG 3120
Qy 3121 AAACAAATGATGATGACATCATGCTGTGACAAACAAATGATTTGATCTTCCAC 3180
Db 3121 AAACAAATGATGATGACATCATGCTGTGACAAACAAATGATTTGATCTTCCAC 3180
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QY 3181 ACAATTAAACGATGCTATTGAACTGAAAGATACTGAGAAATGAAAGCTCACTTGGGA 3240  
DB 3181 ACAATTAAACGATGCTATTGAACTGAAAGATACTGAGAAATGAAAGCTCACTTGGGA 3240

## RESULT 7

US-08-162-081B-35  
Sequence 35, Application US/08162081B  
Patent No. 5824492

## GENERAL INFORMATION:

APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph, Otsu, Masayuki; Panayiotou, George; Volinia,  
APPLICANT: Stefano, Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
TITLE OF INVENTION: THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felle & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION NUMBER: US/08/162, 081B

APPLICATION NUMBER: 435

CLASSIFICATION: February 7, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/00761

FILING DATE: 13 April 1993

ATTORNEY/AGENT INFORMATION:

NAME: Pasqualini, Patricia A.

REGISTRATION NUMBER: 34,894

REFERENCE/DOCKET NUMBER: LUD 5256

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ. ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 3207 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-162-081B-35

Query Match 88.2%; Score 3008.6; DB 1; Length 3207;

Best Local Similarity 96.1%; Pred. No. 0;

Matches 3083; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 1 ATGCTTCGAAGACATCATGAGTGAACGTGGGGGCACTCCATGATGCCCCCAAGATC 60  
DB 1 ATGCTTCGAAGACATCATGAGTGAACGTGGGGGCACTCCATGATGCCCCCAAGATC 60  
QY 61 CTAGTGAATGTTTACTACCAATGGAATGATAGTAGTCTTAGATGCTCCGTGAGGCT 120  
DB 61 CTAGTGAATGTTTACTACCAATGGAATGATAGTAGTCTTAGATGCTCCGTGAGGCT 120  
QY 121 ACATTGTAATCTTAAGCATGAACTATTTAAAGAGCAAGAAATCCCTTCATCAA 180  
DB 121 ACATTGTAATCTTAAGCATGAACTATTTAAAGAGCAAGAAATCCCTTCATCAA 180  
QY 181 CTCTTCAAGATGATCTTCTTACATTTTGTAGTGTATCCCAAGAGAGAGAAAGGAA 240  
DB 181 CTCTTCAAGATGATCTTCTTACATTTTGTAGTGTATCCCAAGAGAGAGAAAGGAA 240  
QY 241 GAAATTTTGTATGATGAAACAGACGACTTTGTGATCTTCGGCTTTTCAACCAATTTTAAAA 300

DB 241 GAAATTTTGTATGATGAAACAGACGACTTTGTGATCTTCGGCTTTTCAACCAATTTTAAAA 300  
QY 301 GTAAATGAACCACTAGAGCAACCTGAAAGAAAAGATCTCCATCGAAGAAATGGTTTGGT 360  
DB 301 GTAAATGAACCACTAGAGCAACCTGAAAGAAAAGATCTCCATCGAAGAAATGGTTTGGT 360  
QY 361 ATGGGATGCGAGTGTGCGAATTTGATATGTTTAAAGATCTGTAAGTACAGAGACTTCGGA 420  
DB 361 ATGGGATGCGAGTGTGCGAATTTGATATGTTTAAAGATCTGTAAGTACAGAGACTTCGGA 420  
QY 421 AGAAATTTCTTATATGTTTGTAAAGAGCTGTGATCTTAAAGGATCTTAATTAATCTCAT 480  
DB 421 AGAAATTTCTTATATGTTTGTAAAGAGCTGTGATCTTAAAGGATCTTAAATTAATCTCAT 480  
QY 481 AGTAGAGCAATGATGATCTATCCGCAATGTAAGTATCTTACAGAGCTGCCAAGAGAC 540  
DB 481 AGTAGAGCAATGATGATCTATCCGCAATGTAAGTATCTTACAGAGCTGCCAAGAGAC 540  
QY 541 ATATATATATTAATTGATAGAGGCCAATATATGATGATTTGGGTAAATAGTTTCTCCA 600  
DB 541 ATATATATATTAATTGATAGAGGCCAATATATGATGATTTGGGTAAATAGTTTCTCCA 600  
QY 601 AATATGACAGAGAGATATCTGTAAGATCAACATGACTGTGTGCCAAGCAAGTA 660  
DB 601 AATATGACAGAGAGATATCTGTAAGATCAACATGACTGTGTGCCAAGCAAGTA 660  
QY 661 ATGCTGGAAGCATGCGAAGAAAATACTAGAAAGATGTGCTATCACTGAAACAATTAAAA 720  
DB 661 ATGCTGGAAGCATGCGAAGAAAATACTAGAAAGATGTGCTATCACTGAAACAATTAAAA 720  
QY 721 CTCTGTTTGTAAATATGAGGCAAGTACATTTTAAAGTGTGATGATGATGATGATGATG 780  
DB 721 CTCTGTTTGTAAATATGAGGCAAGTACATTTTAAAGTGTGATGATGATGATGATGATG 780  
QY 781 TTCTTGAAGAAAATATCTCTGAGTCACTATATATGAAGAGCTGTATATGCTTTGGG 840  
DB 781 TTCTTGAAGAAAATATCTCTGAGTCACTATATATGAAGAGCTGTATATGCTTTGGG 840  
QY 841 AGGATGCCCAATTTGAAGATGATGAGTGAAGAAAGGCTTATCTCACTGCCAAGAGAC 900  
DB 841 AGGATGCCCAATTTGAAGATGATGAGTGAAGAAAGGCTTATCTCACTGCCAAGAGAC 900  
QY 901 TGTTTTACATGCGATCTTATTCAGACGATTTCCACAGCTACACCATATATGATGAG 960  
DB 901 TGTTTTACATGCGATCTTATTCAGACGATTTCCACAGCTACACCATATATGATGAG 960  
QY 961 GAAACATCTACAAATCCCTTGGGTTATTAATGAGCACTGAGATTAATAATTTCTTGT 1020  
DB 961 GAAACATCTACAAATCCCTTGGGTTATTAATGAGCACTGAGATTAATAATTTCTTGT 1020  
QY 1021 GCAACTAGTGAATCTTAATATTTGAGACATTTGAGCAAGATTTATGTTGGAACAGGTATC 1080  
DB 1021 GCAACTAGTGAATCTTAATATTTGAGACATTTGAGCAAGATTTATGTTGGAACAGGTATC 1080  
QY 1081 TACCATGAGAGAGAACCTTATGTAAGTGAAGTGAACCTCAAGAGATACCTTTGTCAT 1140  
DB 1081 TACCATGAGAGAGAACCTTATGTAAGTGAAGTGAACCTCAAGAGATACCTTTGTCAT 1140  
QY 1141 CCCAGGTGAATGAATGCTGTAATTAATATATATATATATATATCTTCTCGTGTGCT 1200  
DB 1141 CCCAGGTGAATGAATGCTGTAATTAATATATATATATATATATCTTCTCGTGTGCT 1200  
QY 1201 CGACTTGGCTTCCATTTGCTGTGTAAGGCGGAAAGGCTGTAAGAGAACTGT 1260  
DB 1201 CGACTTGGCTTCCATTTGCTGTGTAAGGCGGAAAGGCTGTAAGAGAACTGT 1260  
QY 1261 CCAATGGCATGGGGAATATTAATCTGTTGATTAACAGACACTAGATCTGAGAAA 1320  
DB 1261 CCAATGGCATGGGGAATATTAATCTGTTGATTAACAGACACTAGATCTGAGAAA 1320  
QY 1321 ATGCTTTGAATCTTTGGCAGTACTGATTAAGAGATTTGCTGAACCTATGTGT 1380  
DB 1321 ATGCTTTGAATCTTTGGCAGTACTGATTAAGAGATTTGCTGAACCTATGTGT 1380

Db 1321 ATGGCTTTGAATCTTTGGCCAGTACTCTATGAGCTAGAGAGATTTGCTGAACCTATTGCT 1380  
Qy 1381 GTTACTGATCAATCCAAATTAAGAACTCCATGCTTAGATGGAGTTTGACTGGTTC 1440  
Db 1381 GTTACTGATCAATCCAAATTAAGAACTCCATGCTTAGATGGAGTTTGACTGGTTC 1440  
Qy 1441 AGCAGTGTGTAAAGTTCCAGATATGTCACTGATTTGAAGAGCATGCCAAATTTGTCTGTA 1500  
Db 1441 AGCAGTGTGTAAAGTTCCAGATATGTCACTGATTTGAAGAGCATGCCAAATTTGTCTGTA 1500  
Qy 1501 TCCCGAGAGAGAGATTTAGCTATTTCCAGAGAGAGCTGAGTAAACAGACTTACTGAGAC 1560  
Db 1501 TCCCGAGAGAGAGATTTAGCTATTTCCAGAGAGAGCTGAGTAAACAGACTTACTGAGAC 1560  
Qy 1561 AATGAATTTAAGGAGAAATGACAAAGAACAGCTCAAGCAATTTCTACACGAGATCTCTC 1620  
Db 1561 AATGAATTTAAGGAGAAATGAGTAAGAACAGCTCCAGAGCAATTTGTACACGAGATCTCTA 1620  
Qy 1621 TCTGAAATCACTGAGAGAGAGAAATTTCTATGAGCTCAAGACATATTTGTAACT 1680  
Db 1621 TCTGAAATCACTGAGAGAGAGAAATTTCTATGAGCTCAAGACATATTTGTAACT 1680  
Qy 1681 ATCCCGGAAATTTCAACCAAAATTTGCTCTGTCTGTTAAATGGAATTTAGAGATGAAGTA 1740  
Db 1681 ATCCCGGAAATTTCAACCAAAATTTGCTCTGTCTGTTAAATGGAATTTAGAGATGAAGTA 1740  
Qy 1741 GCCCAGATGTATGCTGTGTAAGAAATTTGCTCCATCAACCTGAAACAGGCTATGGA 1800  
Db 1741 GCTCAGATGTATGCTGTGTAAGAAATTTGCTCCATCAACCTGAAACAGGCTATGGA 1800  
Qy 1801 CTTCTGAGCTGTAAATTAACCCAGATCTATGAGTTTGAGTTTGTCTGCTGCTGCTGGA 1860  
Db 1801 CTTCTGAGCTGTAAATTAACCCAGATCTATGAGTTTGAGTTTGTCTGCTGCTGCTGGA 1860  
Qy 1861 AAAATTTTAAACAGATGACAACTTTCTCAGATTTAAATTCAGCTAGTACAGTCTTAAA 1920  
Db 1861 AAAATTTTAAACAGATGACAACTTTCTCAGATTTAAATTCAGCTAGTACAGTCTTAAA 1920  
Qy 1921 TATGACCAATATTGAGATTAATGCTGCTGAGATTTTACTGAGAAAGCAATGACAT 1980  
Db 1921 TATGACCAATATTGAGATTAATGCTGCTGAGATTTTACTGAGAAAGCAATGACAT 1980  
Qy 1981 CAAAGATTTGGGCACTTTTCTTTTGGCATTTAAATCTGAGATGCACAATTAACAGTT 2040  
Db 1981 CAAAGATTTGGGCACTTTTCTTTTGGCATTTAAATCTGAGATGCACAATTAACAGTT 2040  
Qy 2041 AGCCAGAGGTTTGGCTGCTTTTGGAGTCTTATTTGTGTCGATGAGTGGATTTTGAAG 2100  
Db 2041 AGCCAGAGGTTTGGCTGCTTTTGGAGTCTTATTTGTGTCGATGAGTGGATTTTGAAG 2100  
Qy 2101 CACCTGAATGGGCAAGTGGAGGCAATGGAAGGCAATTAATTAATGACATTTCTCAA 2160  
Db 2101 CACCTGAATGGGCAAGTGGAGGCAATGGAAGGCAATTAATTAATGACATTTCTCAA 2160  
Qy 2161 CAGAGAGAGAGATGAAACAAAGGTACAGATGAAGTTTATTTAGTGAGCAATGAGG 2220  
Db 2161 CAGAGAGAGAGATGAAACAAAGGTACAGATGAAGTTTATTTAGTGAGCAATGAGG 2220  
Qy 2221 CGACCAAGATTTCAATGATGATGCTCTCAAGGCTTGTCTCTCTTAAACCTGCTCATCA 2280  
Db 2221 CGACCAAGATTTCAATGATGATGCTCTCAAGGCTTGTCTCTCTTAAACCTGCTCATCA 2280  
Qy 2281 CTAGAGAAACCTCAGGCTTAAAGAGTGTGATTAATGCTTGTGAGAAAGGCACTGGG 2340  
Db 2281 CTAGAGAAACCTCAGGCTTAAAGAGTGTGATTAATGCTTGTGAGAAAGGCACTGGG 2340  
Qy 2341 TTGAATTTGGAGAAACCCAGACATGTCAGAGTTACTGTTTCAAGAAATGATGATC 2400  
Db 2341 TTGAATTTGGAGAAACCCAGACATGTCAGAGTTACTGTTTCAAGAAATGATGATC 2400  
Qy 2401 TTTAAAAATGGGAGTATTTAGCGCAAGATATGCTAACCTTCAATTAATTTGATTA 2460  
Db 2401 TTTAAAAATGGGAGTATTTAGCGCGCAAGATATGCTAACCTTCAATTAATTTGATTA 2460

Qy 2461 GAAATATCTGGCAAAATCAAGGCTTGTATCTTGAATGTTTACCTTAATGCTGTCTCA 2520  
Db 2461 GAAATATCTGGCAAAATCAAGGCTTGTATCTTGAATGTTTACCTTAATGATGCTGTCA 2520  
Qy 2521 ATGGTGACTGTGTGGGACTTATTTAGAGTGTGTGCGAAATTTCTACACTATTAAGCAAT 2580  
Db 2521 ATGGTGACTGTGTGGGACTTATTTAGAGTGTGTGCGAAATTTCTACACTATTAAGCAAT 2580  
Qy 2581 CAGTGCAAGGCGGCTTGAAGGTGCACTGACGTTCAACAGCCACACATACATCAGTGG 2640  
Db 2581 CAGTGCAAGGCGGCTTGAAGGTGCACTGACGTTCAACAGCCACACATACATCAGTGG 2640  
Qy 2641 CTCAGAGCAAGAAACAAAGGAGAAATATATGATGACAGCCATGACCTGTTTACAGTTCA 2700  
Db 2641 CTCAGAGCAAGAAACAAAGGAGAAATATATGATGACAGCCATGACCTGTTTACAGTTCA 2700  
Qy 2701 TGTGCTGATATCTGTGTAGTACCTTCACTTTTGGAAATTTGGAATGTCATATGATAC 2760  
Db 2701 TGTGCTGATATCTGTGTAGTACCTTCACTTTTGGAAATTTGGAATGTCATATGATAC 2760  
Qy 2761 ATGATGATGAAGAGATGAGCAACTGTTTCAATATGATTTTGGACACTTTTGGATCAC 2820  
Db 2761 ATGATGATGAAGAGATGAGCAACTGTTTCAATATGATTTTGGACACTTTTGGATCAC 2820  
Qy 2821 AAGAGAGAAATTTGTTTAAAGAGAGCCAGAACTGTCATTTGTTTGAACAGATTTTC 2880  
Db 2821 AAGAGAGAAATTTGTTTAAAGAGAGCCAGAACTGTCATTTGTTTGAACAGATTTTC 2880  
Qy 2881 TTAATATGATTTTGAAGAGAGCCAGAACTGTCATTTGTTTGAACAGATTTTC 2940  
Db 2881 TTAATATGATTTTGAAGAGAGCCAGAACTGTCATTTGTTTGAACAGATTTTC 2940  
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Qy 3001 CTTTCTCAATGATGCTGTGCTCTGGAATGCGAGAACTACATCTTTTGTATGATGCA 3060  
Db 3001 CTTTCTCAATGATGCTGTGCTCTGGAATGCGAGAACTACATCTTTTGTATGATGCA 3060  
Qy 3061 TACATTTGAGAAACCTAGCTTATGATTAATTAATCTGAGAGAGGCTTTGGAGTATTCATG 3120  
Db 3061 TACATTTGAGAAACCTAGCTTATGATTAATTAATCTGAGAGAGGCTTTGGAGTATTCATG 3120  
Qy 3121 AAACAAATGATATGATGACATCATGAGGCTGAGCAACAAATGATGAGATCTTCAC 3180  
Db 3121 AAACAAATGATATGATGACATCATGAGGCTGAGCAACAAATGATGAGATCTTCAC 3180  
Qy 3181 ACAATTAACAGCATGATGAACTGA 3207  
Db 3181 ACAATTAACAGCATGATGAACTGA 3207

RESULT 8  
US-08-780-872-35  
; Sequence 35, Application us/08780872  
; Patent No. 5846824  
; GENERAL INFORMATION:  
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
; APPLICANT: Bales, Waterfield, Michael Derek; Parker, Peter  
; APPLICANT: Joseph, Otsu, Masayuki; Parayotou, George; Volinia,  
; APPLICANT: Stefano; Gout, Iyan Tatavosvitch  
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
; TITLE OF INVENTION: THEIR PREPARATION AND USE  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pelfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022





Db 1681 ATCCCGAAATTCACCCAAATGCTGTCTGTAAATGAGACCTGAGATGAATA 1740  
 Qy 1741 GCCCAGATGTAATGCTGTGTAATAAAGATTGGCTCCCAATCAAACTGAGACAGCTATGGA 1800  
 Db 1741 GCTCAGATGTAATGCTGTGTAATAAAGATTGGCTCCCAATCAAACTGAGACAGCTATGGA 1800  
 Qy 1801 CTTCTGACGTAATTAATTAACAGATCTATGTTGAGGTTTGTGTTGGTCTTGGAA 1860  
 Db 1801 CTTCTGACGTAATTAATTAACAGATCTATGTTGAGGTTTGTGTTGGTCTTGGAA 1860  
 Qy 1861 AAATTTTAAACAGATGACAACTTCTCAGTATTTAATTCAGCTAGTACAGTCTTA 1920  
 Db 1861 AAATTTTAAACAGATGACAACTTCTCAGTATTTAATTCAGCTAGTACAGTCTTA 1920  
 Qy 1921 TATGACATATTTGATGATTAATCTGTTGAGATTTTACTGAAAGAAAGATGACTAAT 1980  
 Db 1921 TATGACATATTTGATGATTAATCTGTTGAGATTTTACTGAAAGAAAGATGACTAAT 1980  
 Qy 1981 CAAGGATTTGGGCACTTTTCTTTTGGCATTTAAATCTGAGATGACAAATTAACAGTT 2040  
 Db 1981 CAAGGATTTGGGCACTTTTCTTTTGGCATTTAAATCTGAGATGACAAATTAACAGTT 2040  
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 Db 2041 AGTCAAGAGTTTGGGCTGCTTTTGGAGTCTATTTGCTGATGATGAGATGATTTGAAG 2100  
 Qy 2101 CACCTGAATGAGCAAGTGAAGCAATGAAAAAGCTCATTAATTAATGACATTTCTCAA 2160  
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 Qy 2161 CAGAGAGGAAGATGAAAAACAACAAAGGTACAGATGAAGTTTATGTTAGCAATGAGG 2220  
 Db 2161 CAGAGAGGAAGATGAAAAACAACAAAGGTACAGATGAAGTTTATGTTAGCAATGAGG 2220  
 Qy 2221 CGACCAATTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280  
 Db 2221 CGACCAATTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280  
 Qy 2281 CTAGGAAACCTCAGGCTTAAAGAGTGTGAATATGATGATGATGATGATGATGATGATGAT 2340  
 Db 2281 CTAGGAAACCTCAGGCTTAAAGAGTGTGAATATGATGATGATGATGATGATGATGATGAT 2340  
 Qy 2341 TTGAATTTGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAAGACATGAGATCATC 2400  
 Db 2341 TTGAATTTGGAGAACCCAGACATCATGTCAGAGTTACTGTTTCAAGACATGAGATCATC 2400  
 Qy 2401 TTTAAAAATGGGAGATTTTACGGGACATATGCTTACCTTCAGATTAATTCGCAATATG 2460  
 Db 2401 TTTAAAAATGGGAGATTTTACGGGACATATGCTTACCTTCAGATTAATTCGCAATATG 2460  
 Qy 2461 GAAATATCTGGCAAAATCAAGGTTTATGATGATGATGATGATGATGATGATGATGATGAT 2520  
 Db 2461 GAAATATCTGGCAAAATCAAGGTTTATGATGATGATGATGATGATGATGATGATGATGAT 2520  
 Qy 2521 ATCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580  
 Db 2521 ATCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580  
 Qy 2581 CAGTGTAAAGAGGCTGTAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2640  
 Db 2581 CAGTGTAAAGAGGCTGTAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2640  
 Qy 2641 CTCAAGACAGAAACAAAGGAAATATATGATGATGATGATGATGATGATGATGATGATGAT 2700  
 Db 2641 CTCAAGACAGAAACAAAGGAAATATATGATGATGATGATGATGATGATGATGATGATGAT 2700  
 Qy 2701 TGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760  
 Db 2701 TGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760  
 Qy 2761 ATCATGTGAAAGAGATGACAACTGTTTCAATATGATGATGATGATGATGATGATGATGAT 2820

Db 2761 ATCATGTGAAAGATGACAACTGTTTCAATATGATGATGATGATGATGATGATGATGAT 2820  
 Qy 2821 AAGAAGAAAAATTTGGTTTAAACGAGAACGTTGCTGATTTGTTTGAACAGAGATTTG 2880  
 Db 2821 AAGAAGAAAAATTTGGTTTAAACGAGAACGTTGCTGATTTGTTTGAACAGAGATTTG 2880  
 Qy 2881 TTAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940  
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 Qy 2941 CAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000  
 Db 2941 CAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000  
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 Db 3001 CTTTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060  
 Qy 3061 TACATTTGAAAGACCTTACCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 3120  
 Db 3061 TACATTTGAAAGACCTTACCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 3120  
 Qy 3121 AAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180  
 Db 3121 AAACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180  
 Qy 3181 ACAATTAACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3207  
 Db 3181 ACAATTAACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3207

RESULT 9  
 US-09-085-957-35  
 ; Sequence 35, Application us/09085957  
 ; Patent No. 6274327  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
 ; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
 ; APPLICANT: Joseph; Oteu, Masayuki; Panayotou, George; Volinia,  
 ; APPLICANT: Stefano; Gout, Ivan Tarasovich  
 ; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
 ; TITLE OF INVENTION: THEIR PREPARATION AND USE  
 ; NUMBER OF SEQUENCES: 50  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Felfe & Lynch  
 ; STREET: 805 Third Avenue  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10022  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: Wordperfect  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/085,957  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/780,872  
 ; FILING DATE: 09-JAN-1997  
 ; APPLICATION NUMBER: 08/162,081  
 ; FILING DATE: February 7, 1994  
 ; APPLICATION NUMBER: PCT/GB93/00761  
 ; FILING DATE: 13 April 1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Pasqualini, Patricia A.  
 ; REGISTRATION NUMBER: 34,894  
 ; REFERENCE/DOCKET NUMBER: LUD 5256  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 688-9200  
 ; TELEFAX: (212) 838-3884



! INFORMATION FOR SRO ID NO: 35:  
! SEQUENCE CHARACTERISTICS:  
! LENGTH: 3207 base pairs  
! TYPE: nucleic acid  
! STRANDEDNESS: single  
! TOPOLOGY: linear  
! US-09-085-957-35

Query Match 88.2%; Score 3008.6; DB 3; length 3207;  
Best Local Similarity 96.1%; Pred. No. 0;  
Matches 3083; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 1 ATGCTCCAGACCATATCATGAGTAACTGTGGGCGCATCCCTGATGCCCCCAAGATC 60  
DB 1 ATGCTCCAGACCATATCATGAGTAACTGTGGGCGCATCCCTGATGCCCCCAAGATC 60  
QY 61 CTAGTGAATGTTTACTACCAATAGATAGTAGCTTTAGATGATGCTCCCGGAGGCT 120  
DB 61 CTAGTGAATGTTTACTACCAATAGATAGTAGCTTTAGATGATGCTCCCGGAGGCT 120  
QY 121 ACATTAGTAATTAAGACATGAACTATTTAAAGACAGAAATAACCTCTCATCAA 180  
DB 121 ACATTAGTAATTAAGACATGAACTATTTAAAGACAGAAATAACCTCTCATCAA 180  
QY 181 CTCTTCAAGATGATCTTTTACATTTTGTAAAGTGTACCCAGAGACAGAAAGGAA 240  
DB 181 CTCTTCAAGATGATCTTTTACATTTTGTAAAGTGTACCCAGAGACAGAAAGGAA 240  
QY 241 GAATTTTATGAAACAAGACGCTTTGATCTTGGGCTTTTCAACCATTTTAAAA 300  
DB 241 GAATTTTATGAAACAAGACGCTTTGATCTTGGGCTTTTCAACCATTTTAAAA 300  
QY 301 GTAATTGAACCAAGAGCAACCGTGAAGAAAAGATCCTCAATGAGAAATTTGTTTGT 360  
DB 301 GTAATTGAACCAAGAGCAACCGTGAAGAAAAGATCCTCAATGAGAAATTTGTTTGT 360  
QY 361 ATGGCGATGCCAGTGTGCGAATTTGATATGTTAAAGATCCTGAAGTACAGAGCTTCCGA 420  
DB 361 ATGGCGATGCCAGTGTGCGAATTTGATATGTTAAAGATCCTGAAGTACAGAGCTTCCGA 420  
QY 421 AGAAATTTCTTAAATGTTTGTAAAGAGCTGTGATCTTAGGATCTTAAATTTCCCTCAT 480  
DB 421 AGAAATTTCTTCAATGTTTGTAAAGAGCTGTGATCTTAGGAGTCTTAAATTTCCCTCAT 480  
QY 481 AGTAGAGCAATGTATGTCTATCCGACATGTAGAACTTTCACAGAGCTGCCAAAGAC 540  
DB 481 AGTAGAGCAATGTATGTCTATCCGACAAATGTAGAACTTTCACAGAGCTGCCAAAGAC 540  
QY 541 ATATATATTAATTTGATAGAGGCAATAATATAGTGTGATTTGGGTATATGTTTCTCA 600  
DB 541 ATATATATTAATTTGATAGAGGCAATAATATAGTGTGATTTGGGTATATGTTTCTCA 600  
QY 601 AATATATGACAAGCAAGATATCTCTGAATAATCAACATGACTGTGGCCAGAAAGTA 660  
DB 601 AATATATGACAAGCAAGATATCTCTGAATAATCAACATGACTGTGGCCAGAAAGTA 660  
QY 661 ATTGCTGAAGCAATCAGAGAAAAAACTGAAGTATGTTGGTATCATCTGAACAATTAAA 720  
DB 661 ATTGCTGAAGCAATCAGAGAAAAAACTGAAGTATGTTGGTATCATCTGAACAATTAAA 720  
QY 721 CTCTGTGTTTAAATATCAGGGCAAGTATATTTTAAAGTGTGTGATGTGAATAC 780  
DB 721 CTCTGTGTTTAAATATCAGGGCAAGTATATTTTAAAGTGTGTGATGTGAATAC 780  
QY 781 TTCTTAGAAAAATATCTCTGAGTCAAGTATATTAAGAGCTGTATATGCTTGGG 840  
DB 781 TTCTTAGAAAAATATCTCTGAGTCAAGTATATTAAGAGCTGTATATGCTTGGG 840  
QY 841 AGGATGCCAATTTGAAGATGATGGCTAAAGAAAGCTTTATTTCGAAGTCCCAATGAC 900  
DB 841 AGGATGCCAATTTGAAGATGATGGCTAAAGAAAGCTTTATTTCGAAGTCCCAATGAC 900  
QY 901 TGTTTTAAATGCGATCTTATTCAGACGCAATTTCCACAGCTACACCATATATGATGAG 960

DB 901 TGTTTTAAATGCGATCTTATTCAGACGCAATTTCCACAGCTACACCATATATGATGAG 960  
QY 961 GAAACATCTCAAAATCCCTTGGGTTATTAATATAGACATCTCAAGATTAATTTCTTGT 1020  
DB 961 GAAACATCTCAAAATCCCTTGGGTTATTAATATAGACATCTCAAGATTAATTTCTTGT 1020  
QY 1021 GCAACCTACGTGAATCAATTAATTCAGACATTCGACAAATTTATGTTTCGACAGATATC 1080  
DB 1021 GCAACCTATGATGATTAATTTTCAGACATTCGACAAATTTATGTTTCGACAGATATC 1080  
QY 1081 TACCATGAGAGAACCTTTATGTGACATGTGAACCTCAAGAGTACTTGTTCAT 1140  
DB 1081 TACCATGAGAGAACCTTTATGTGATTAAGTGAACCTCAAGAGTACTTGTTCAT 1140  
QY 1141 CCCAGGTGAATGAATGGCTGAATTTATGATATATACCTCTGATCTTCTCGGCTGCT 1200  
DB 1141 CCCAGGTGAATGAATGGCTGAATTTATGATATATACCTCTGATCTTCTCGGCTGCT 1200  
QY 1201 CGACTTTGCTTTCAATTTGCTGTGTTAAAGGCGAAGGGTCTAAAGAGAACACTGT 1260  
DB 1201 CGACTTTGCTTTCAATTTGCTGTGTTAAAGGCGAAGGGTCTAAAGAGAACACTGT 1260  
QY 1261 CCAATGGCATGGGAAATATTAATCTTGTGATTAACACAGACACTGATATCTGAAAA 1320  
DB 1261 CCAATGGCCTGGGAAATATTAATCTTGTGATTAACACAGATACTGATATCTGAAAA 1320  
QY 1321 ATGGCTTTGAAATCTTTGGCCAGATCACTGATTAAGAAATTTGCTGAACCCCTATTGCT 1380  
DB 1321 ATGGCTTTGAAATCTTTGGCCAGATCACTGATTAAGAAATTTGCTGAACCCCTATTGCT 1380  
QY 1381 GTTACTGATCAATCAATTAAGAAACCTCAATGCTTAGTGTGAGTTTGACTGTTC 1440  
DB 1381 GTTACTGATCAATCAATTAAGAAACCTCAATGCTTAGTGTGAGTTTGACTGTTC 1440  
QY 1441 AGCAGTGTGTTAAAGTTCCAGATATGTCAGTATTAAGAGCATGCCAATTTGCTGTGA 1500  
DB 1441 AGCAGTGTGTTAAAGTTCCAGATATGTCAGTATTAAGAGCATGCCAATTTGCTGTGA 1500  
QY 1501 TCCCGAAGACAGATTTTATGCTATTTCCACGACAGCTAGTAAACAGACTAGCTAGAC 1560  
DB 1501 TCCCGAAGACAGATTTTATGCTATTTCCACGACAGCTAGTAAACAGACTAGCTAGAC 1560  
QY 1561 AATGAATTAAGGAAATAGCAAGAAACAGCTCAAGCAATTTCTCAACGAGATCTCTC 1620  
DB 1561 AATGAATTAAGGAAATAGTAAAGAAACAGCTCCGACAAATTTGTACAGAGATCTCTC 1620  
QY 1621 TCTGAATCACTGAGCAGAGAAAGATTTTCTATAGAGTCAACAGACATATTTGTAACT 1680  
DB 1621 TCTGAATCACTGAGCAGAGAAAGATTTTCTATAGAGTCAACAGACATATTTGTAACT 1680  
QY 1681 ATCCCCGAATTTTACCCAAATTTGCTGTCTGTTAAATGAAATCTAGAGTGAAGTA 1740  
DB 1681 ATCCCCGAATTTTACCCAAATTTGCTGTCTGTTAAATGAAATCTTAGAGTGAAGTA 1740  
QY 1741 GCCCAGATGATGCTTGGTAAAGATTTGGCCTCAATCAAACTGAACAGGCTATGAGAA 1800  
DB 1741 GCTCAGATGATGCTTGGTAAAGATTTGGCCTCAATCAAGCTGAACAGGCTATGAGAA 1800  
QY 1801 CTCTGGAATGATTAACCCAGATCTATGTTTGAAGTTTGTCTGTGGTCTTTGAA 1860  
DB 1801 CTCTGGAATGATTAACCCAGATCTATGTTTGAAGTTTGTCTGTGGTCTTTGAA 1860  
QY 1861 AATATTTTAAACAGATCAAACTTTCTCAGTATTAATTAATTAAGTACAGGTCTTAAAA 1920  
DB 1861 AATATTTTAAACAGATCAAACTTTCTCAGTATTAATTAATTAAGTACAGGTCTTAAAA 1920  
QY 1921 TATGAACAATATTTGATTAACCTGTTGAGATTTTCTGAAGAAAGCATGACTAAT 1980  
DB 1921 TATGAACAATATTTGATTAACCTGTTGAGATTTTCTGAAGAAAGCATGACTAAT 1980  
QY 1981 CAAAGGATTTGGGCACTTTTCTTTTGGCAATTTAAATCTGAGATGCAATTAAGACGTT 2040

Db	1981	CAAGAGATCGGCACTTTTCTTTTGGCATTTAAATCTGAGATGCAACAATAAAAAGTT	2040
OY	2041	AGCCAGAGGTTGGCTCTGCTTTTGGAGTCTTATGTGCGATGTGGAGTGTATTGAG	2100
Db	2041	AGTCAGAGGTTGGGCTCTCTTTTGGAGTCTTATGTGCGATGTGGAGTGTATTGAG	2100
OY	2101	CACCGAATTAGGCAAGTGCAGGCAATGGAAAAAGCTATTAACTTAACTGACATTCCTAA	2160
Db	2101	CACCTTAATTAGGCAAGTTGAGGCTATGGAAAAGCTCATTTAACTTGACTGACATTCCTAA	2160
OY	2161	CAGAGAGGAAGATGAAACAACAAGGTACAGATGAAATTTTATAGTTAGAGCAATGAG	2220
Db	2161	CAAGAGGAAGAGATGAAACAACAAGGTACAGATGAAATTTTATAGTTAGAGCAATGAG	2220
OY	2221	CGACCAAGATTTTCATGATGATGCCCTTACAGGGCTTGCTCTCTCTTAAACCTGCTCATCA	2280
Db	2221	CGACCAAGATTTTCATGATGATGCTCCAGGGCTTTGCTCTCTCTTAAACCTGCTCATCAG	2280
OY	2281	CTAGGAACCTCAGGCTTAAAGAGTGTGCAATTATATGCTTGTGAAAAAGGCCATGTGG	2340
Db	2281	CTGGGAATCTCAGGCTTGAAGAGTGTGCAATTATATGCTTGTGAAAAAGGCCATGTGG	2340
OY	2341	TTGAATTTGGGAGAACCCAGACATCATGTCAAGATTACTGTTTCGAAACAATGAGATCATC	2400
Db	2341	TTGAATTTGGGAGAACCCAGACATCATGTCAAGATTACTGTTTCGAAACAATGAGATCATC	2400
OY	2401	TTTAAAAATGGGGATGATTTTACGGCAGATATGCTAACACTTCAATTAATTCGTATTATG	2460
Db	2401	TTTAAAAATGGGGATGATTTTACGGCAGAAATATGCTAACCTTCAGATTATTCGATTAATG	2460
OY	2461	GAAAAATATCTGGCAAAATTCAGAGTCTTGATCTTGGAAAGTCACTTAATGATGTCTGTCA	2520
Db	2461	GAAAAATATCTGGCAAAATTCAGAGTCTTGATCTTGGAAATTAATGATGATGTCTGTCA	2520
OY	2521	ATCGGTGACTGTGTGGGACTTATTGAGGTGGTGCAAATTTCTCACATTAATATGCAATT	2580
Db	2521	ATCGGTGACTGTGTGGGACTTATCGAGGTGGTGCAAATTTCTCACATTAATATGCAATT	2580
OY	2581	CAGTGCACAAAGCGGCTTGAAGGTGCACTGCAGTTCACACGCCACATCCTCAGTGG	2640
Db	2581	CAGTGTAAAGAGGCGCTGAAGAGTGCACATGCAGTTTAAACGCCACATCCTCAGTGG	2640
OY	2641	CTCAAGAACAAGAACAAAGGAGAAATATATATGAGCAGTTCGCTGTTTACACGTTCA	2700
Db	2641	CTCAAGAACAAGAACAAAGGAGAAATATATATGAGCGCATGCAATTTGTTTACACGATCA	2700
OY	2701	TGTGCTGATATCTGTGTAGTCACTTCAATTTTGGGAATTTGGAGATTCGTCACAATAGTAAC	2760
Db	2701	TGTGCTGATATTTGTGTGCCACTTCAATTTTGGGAATTTGGAGATTCGTCACAATAGTAAT	2760
OY	2761	ATCATGTGGAAGACGATGAGCAACATGTTTCAATATAGATTTTGGACACTTTTGGATCAC	2820
Db	2761	ATCATGTGTTAAAGATGATGAGCAACATGTTTCAATATAGATTTTGGACACTTTTGGATCAC	2820
OY	2821	AAGAAAGAAAAATTTGTTTATTAAGAGAGGCGGCTTGTGTTTGGACCAAGATTTTC	2880
Db	2821	AAGAAAGAAAAATTTGTTTATTAAGAGAGGCGGCTTGTGTTTGGACCAAGATTTTC	2880
OY	2881	TTAATATGATATTAGTAAAGAGAGCCCAAAATGCAACAAGAGCAAGAAATTTGAGAGGTTT	2940
Db	2881	TTAATATGATATTAGTAAAGAGAGCCCAAAATGCAACAAGAGCAAGAAATTTGAGAGGTTT	2940
OY	2941	CAGGAGATGTGTTTACAGGCTTATCTTACGCTATTTGCACGATGCCCAATCTCTTCATTAAT	3000
Db	2941	CAGGAGATGTGTTTACAGGCTTATCTTACGCTATTTGGCAGATGCCCAATCTCTTCATTAAT	3000
OY	3001	CTTTTCTCAATGATATGCTTGGCTCTGGAATGCGCAACATGCAATCTTTTGAATGATATTGCA	3060
Db	3001	CTTTTCTCAATGATATGCTTGGCTCTGGAATGCGCAACATGCAATCTTTTGAATGATATTGCA	3060
OY	3061	TACATTTGGAAGAAGCCCTAGCCTTAGATATAAACTGAGCAAGAGGCTTTGAGATATTTTCATG	3120
Db	3061	TACATTTGGAAGAAGCCCTAGCCTTTAGATATAAACTGAGCAAGAGGCTTTGAGATATTTTCATG	3120

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QY 3121 AAACAAATGATGATGACATCATCATGCTGGCTGGACCAACAAAATGATTTGATCTTCAC 3180
Db 3121 AAACAAATGATGATGACACACCATGCTGGCTGGACCAACAAAATGATTTGATCTTCAC 3180
QY 3181 ACAATTAACAGCATGATGAACTGA 3207
Db 3181 ACAATTAACAGCATGCTTGAACCTGA 3207

RESULT 10
US-09-392-350-1
; Sequence 1, Application US/09392350
; Patent No. 6133032
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Coweirt
; TITLE OF INVENTION: ANTISENSE MODULATION OF P13 KINASE P110 BETA EXPRESSION
; FILE REFERENCE: RTS-0075
; CURRENT APPLICATION NUMBER: US/09/392.350
; CURRENT FILING DATE: 1999-09-08
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 3213
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3213)
US-09-392-350-1

Query Match 13.5%; Score 460.8; DB 3; Length 3213;
Best Local Similarity 50.4%; Pred. No. 1.9e-118;
Matches 1597; Conservative 0; Mismatches 1467; Indels 106; Gaps 15;

QY 58 ATCTAGTGAATGTTACTACCAAAATGGAATGATAGTACTTATAGAAATGCTCTCGAG 117
Db 88 ATACCTGTGATTTCTTTTGGCCCACTGGGATTTATATCCAGTTGGAGTACCTCGGAA 147
QY 118 GCTCATTATGATTAACATTAAGCATGAATTTTAAAGAGCAAGAAATACCTCTCCAT 177
Db 148 GCTACCATTTCTTATATTAAAGACAATGTTATGAGCAAGATTCACAAATACCCATGTC 207
QY 178 CACTTCTTCAAGATGAACTCTTTTACATTTTGTAAAGTGTATCCCAAGAGCAAGAAAG 237
Db 208 AACCTCCTTATGATGATTAAGTACTCTATATGTTTGCATGTCGATACAGACTCGTATAT 267
QY 238 GAAGATTTTGTATGAAACAAGACGACTTTGTATCTTGGGCTTTTCAACCATTTTTA 297
Db 268 GAGAGGCTTGAAGATGAACAACGAAAGCTGTGATGTCAAGACCTTTTCTTCAGTTCTC 327
QY 298 AAAGTATTTGAACAGTAGAGCAACCGTAGAAGAAAGATCCCAATGAGAAATGTTTT 357
Db 328 AATATTAGACAAAGAGTGTGACCCAGGGGAAAA---ATTAGACTCAAAAATTTGAGTC 384
QY 358 GCTATCGGCATCGCAGTGTGCGAATTTGATATGTTAAAGATCCTGAAGTACAGACTTC 417
Db 385 CTTATAGGAAAGAGTCTGCATGAATTTGATTCCTTGAAGAGATCCTGAAGTAAATGAATTT 444
QY 418 CGAAGAAATATCTTAAATGTTTGAAGAGAGCTGTGATCTTAAAGATCTTAAATCAACT 477
Db 445 CGAAGAAAGAGCCCAATTTAGCA-----GAAAAAATCTGTGCA 486
QY 478 CATAGTAGAGCAATGATGCTATCCGCAATGTAGAAATCTTCACCAAGAGCTCCAAAG 537
Db 487 CTTGGGATTTGTCTGTGATGAGACTGGGTAAACAAACATATCCACCAAGAGCATGAAGCA 546
QY 538 CACATATATTAATTAATTTGATAGAGGCCAAATAATAGTGTGATTTGGGTATATGTTCT 597
Db 547 TCCATTCCTGAAAACTTAGAAGATTAACCTTATGAGGGGAAAGGCTCATGTATGCTTCAT 606
QY 548 CCAATATATGCAAGCAAGATATACCTGAAAAATCAACATGACTGTGTGCCAGAACAA 657

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Db 607 TTGAAAACTCCAGACGCTGTTAGCTTCAAGTCTCTCTAATAGAAATCCATACAA 666  
Qy 658 GTAATGCTGAGCAATCAGAAAAAATAAGAAATGTTGCTATCATCTGAACAATTA 717  
Db 667 GTAATGAAATTTGGCAATC---CAAAAAGTTTGACTTTCATGCGAAGAAAGATGAAGTT 723  
Qy 718 AAACCTCTGTGTTTGAATATCAGGGCACTATTTTAAAGTGTGTGATGTGAA 777  
Db 724 AGCCCTATATAT-----TATGTGTGCAAGTCACCGGAGAGTGAAG 765  
Qy 778 TACTTCTAGAAAAATATCCCTGAGTCAGATATAGATATTAAGAACTGATATATCTT 837  
Db 766 TATGTTTGTGTGATCATCCATATATCAGTTCAGATATCCGAACTGTGTATGATAC 825  
Qy 838 GGGAGAGTCCCAATTTGAAGATGATGCTA---AAGAAAGCTTATTTCAATGTC 892  
Db 826 AGAGCCCTGCCCCATTTTATACCTGTGTGAATGTCGCAAGATCAAGAAATGATAGCA 885  
Qy 893 CAATGAGCTGTTTACATGCGCATTTATTCAGACGCAATTTCCACAGTACACCATATA 952  
Db 886 GAATATGATTCGATAGAGCTGCGCATTAATCGAAATCATCTATCTTCCCTCCATTA 945  
Qy 953 TGAATGAGAAACATCACAATAATCCCTTGGGTATTAATNAGCACTGAGAAATAAA 1012  
Db 946 CCAACCAAGAAAACAGAAATTAATTTCTCATGTTGGGAAAAATAACAACCTTTCCAATT 1005  
Qy 1013 TTCTTTGTGCACCTACGTGAATCTAATAATTCGAGACATTTGACAAAGATTTATGTTGAA 1072  
Db 1006 GTCTTGTTAAGGGAAA--TAACTTAAACAGAGAAACGTAAAGTTCAATGTCAGG 1063  
Qy 1073 CAGGATCTACCATGAGAGAAACCTTATGTGA--CAATGTGAACACTCAAGAGTAC 1129  
Db 1064 CTGCTCTTTTCAATGACTGAGCTCCTGTGTAACCATGTAAGCTCAGAGGTATCAG 1123  
Qy 1130 CTGTGTCATCCCAAGTGAAGTAAGAGTGAATTAATGATATATATCTGATCTTC 1189  
Db 1124 GGAATAATGATCATATTTGGAATGAACACTGGAATTTGATTAATTTTGTGACTTAC 1183  
Qy 1190 CTGCTGCTGCTGACTTGTGCTTTCATTT-----GCTCTGTTAAAGCGGAAAGGTGC 1244  
Db 1184 CAGAAATGCTGATTAATGTTTGTGCTGTATGACAGTTTGTGAATTAAGTAAACCAAGA 1243  
Qy 1245 TAAAGAGAACTGTCCAT-----TGGCATGGGAAATATTAACCTGTGTTG 1291  
Db 1244 AATCAACGAAACATTAATCCCTCTAATATCAGACATCAGAAAGCTGAAAGATGC 1303  
Qy 1292 ATTACACAGACATCTATGATCTGAAAAATGGCTTTGAATCTTTGGCCGATCTCATG 1351  
Db 1304 ATTATCTGTAGGCTGGTAAATACATGATGTTTGAATTTTGAATTAAGCAATTAAGAACTG 1363  
Qy 1352 GATTAGAAATTTGCTGAACCTATTTGTTGCTGATCAAAATCCAAATTAAGAAATCTC 1411  
Db 1364 GAGACATTAATTAACACAGCTGCTCTTCAATTTCTGTGTAACCTGAAAGAAATGTTGATC 1423  
Qy 1412 CATGCTTAGAGTTGAGATTGAGCTGTTGACAGTGTGTAAGTTTCCAGATATGTCAG 1471  
Db 1424 CAATGGAACTGTTCAAAACAATCAATATACGAAAAATGCAACGCTTTCAGATTAAT 1483  
Qy 1472 TGAATGAAGGATGCGCAATTTGCTGTATCCGAGAGAGCAAGATTTAGCTATTTCCACG 1531  
Db 1484 TTCCAAGAAATTAATAACAACCTTATTAATCCCTCCCTTCGATAGATATTTGAAAGG 1543  
Qy 1532 CAGAGCTGAGTACAGACTAGTAGAGACAAATGAATTAAGGAAATTAAGCAAGAACAGC 1591  
Db 1544 CAGCTGAGATTTGAGAGAGTATAGTCTAATGTGTCAAGTCAAGGTGAAAAAAGTTTC 1603  
Qy 1592 -----TCAAGCAATTTCTACACGAGATCTCTCTGAAATCACTGACAGAGAGA 1642  
Db 1604 TTCTGTATGAAGAAATCTTGACAGGAGATCCCTTGTCTCAACGTGTGAAAAATGAAA 1663  
Qy 1643 AAGATTTTCTATGAGAGTCAAGAC--ACTATGTGTATCACTATCTCCGAAATTTCTACCA 1699  
Db 1664 TGATCTTATTTGAACTTTGGCACAAGATGCGAGAGATTTTCCCAATCACTGCGCA 1723

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Qy 1700 AATGCTTCTGTCTGTTAAATGGAATTTAGAGATGAGTAGCCAGATGATATGCTTGG 1759  
Db 1724 AATTAAGCTGTCAATCAAGATGAATTAACCTGAGATGTTGCTCAGCTTCAAGCCGCTGC 1783  
Qy 1760 TAAAGATTTGGCTCCAACTAAACCTGAAACAGGCTATGCACTTCTGGACTGTAAATACC 1819  
Db 1784 TTCAAGATTTGGCCTAACCTGACCCCGGAGGCGCTAGAGCTTGTGATTTCAACTATC 1843  
Qy 1820 CAGATCCATATGTTGAGGTTTGTGTTGCGGCTTGGAAAAATTTTAACAGATGACA 1879  
Db 1844 CAGACAGATACGTTCAAGAAATATGCTGTAGCTGCTCG---CGACAGATAGATGAAG 1900  
Qy 1880 AACTTCTCAGTATTTAATTTCACTAGTACAGGCTCTTAAATATGAACAATATTTGGATA 1939  
Db 1901 AACTTCTCAGATATCTTTTAACTGCACTGTGCAAGTGTAAATATGAGCCTTTCTTGAT 1960  
Qy 1940 ACTTGTGTGAGATTTTATCTGAAGAAACATTTGACTAATCAAGAGATTGGCACTTTT 1999  
Db 1961 GTGCCCTCTCTAGATTTCTATTGAAAAGACACTGTGTGTAATCGAGAGATAGGGCAGTTTC 2020  
Qy 2000 TCTTTGGCAATTAATCTGAGATGCAACAATAACAGTATCCAGAGTTGGCCTGC 2059  
Db 2021 TATTTGGCACTTAGGTGAGAGTGCACATTTCTGCTGTCTGATACAAATTTGTGTCA 2080  
Qy 2060 TTTTGGAGTCTATTTGCTGCAATGGGATGTATTTGAAAGCACTGAATAGGCAAGTCG 2119  
Db 2081 TCTTGAAGATATCTCGGGGAGAGTGTGGGACATGAAGTCTTTCTAAGCAGTTG 2140  
Qy 2120 AGCAATGGAAGCTCATTAATTAAGTCACTGACATTTCTCAACGAGAGAGAGATGAAA 2179  
Db 2141 AAGCACTCAATTAAGTTAAATACTTTAATTAATTAATCAAGATGCCGTGAAGTTAA 2200  
Qy 2180 CAAAAAGATACAGATGAAGTTTGTGTGAGCAAAATGAGCCAGCATTTATGATGAG 2239  
Db 2201 ACAGACCAAGAGGAAAGAGAGGCGATCATCTGTTTAAACGAGTGTCTACCGGAAAG 2260  
Qy 2240 CCTTACAGGCTTGTGCTCTCTCTAACCCTGCTCATCAACATGAGAAACCTGAGCTTA 2299  
Db 2261 CCTCTCTGACCTGCACTGACCCCTGAACCCAGTGTATCTCTCGAAGCTTATGTTG 2320  
Qy 2300 AAGAGTGTGCAATTAATGCTTCTGCAAAAAGGCACTGTGTGAAATGGGAGAACCCAG 2359  
Db 2321 AAAAGTGAATATCATGGAATTCAAAATGAAGCTTTGTGGCTGTGATACAAATPAACAAG 2380  
Qy 2360 ACATCATGTCAGATTAATCTGTTTACAGAACATGAGATCATCTTTAAATATGGGATGAT 2419  
Db 2381 TATTTGTGAGATTTCAAT-----TGAAGTGAATTTTAAATATGATGATTT 2428  
Qy 2420 TACGCAAGATATGCTAATCACTCAATTAATGATTTATGAAAAATATCTGGCAAAATC 2479  
Db 2429 TACGACAGATATGTTGACACTTCCAAATGTTGCGCTTGATGATTAATCTGTGAAAGAG 2488  
Qy 2480 AAGCTTGAATCTTCAATGTTAATCTTATGTTGTCTGTCAATCGGTGACTGTGTGGAG 2539  
Db 2489 CTGCTTGTGATCTTGGAGTGTGCTTATGAGCTGTTTACGAACAGAGATTCGCTGCGCC 2548  
Qy 2540 TTAATGAGGTGTGCAAAATTTCTCACTATTTATGCAAAATTCAGTCCAAAGCGCGC---T 2596  
Db 2549 TCAATGAATGTGACACCTCTGAAAACAATGTCTGACATTCAGCTGAACAGTAGCAATG 2608  
Qy 2597 TGAAGGTGCACTGAGTTCAACAGCCACACACTACATCATGAGGCTCAAGCAAGAACAC 2656  
Db 2609 TGCTCTGCTGAGAGGCTTCAACAAAGATGCTCTTGAACGTGCTTAAAGAAATCAACT 2668  
Qy 2657 AAGAGAAATATATGATGAGAGCCATTTGATACCTGTTTACAGTTCATGTGTGATCTGTG 2716  
Db 2669 CTGGGATAGCTGAGCCAGCCATTTGAGAAATTTTACATGTCCTGTGCTAGCTACTGTG 2728  
Qy 2717 TACCTACCTTCAATTTTGGGAAATTTGAGATGTCACAAATGTAATCATATGATGTAAGAG 2776  
Db 2729 TAGCTTCTTATGTCTTGTGGAATTTGTGACAGACATAGTGAACAACATCATGCTCAAAAAA 2788

OY	2777	ATGGCAACTGTTTCATATPATAATTTTGGACACTTTTGGATCACAAGAAAAAATTTG	2836
Db	2789	CTGGCGACACTCTTCACATGTACTTTGGACATATTTCTTGAATTTCAATCTAAGTTTG	2848
OY	2837	GTTATAAAGAGAACGTGTGCCATTGTGTTTGACACAGAGATTTCTTAATAGTAGTTAGTA	2896
Db	2849	GCATTAAAGAGAGAGAGTGCCTTTATTCTTACCTAGATTTTCATCATGTCAATTCAAC	2908
OY	2897	AAGGAGCCCAAGATGCACAAAAGACAGAGAAATTTGAGAGGTTTCAGAGATGTGTACA	2956
Db	2909	AAGGAAAAACAGG-----AAATACAGAAAAGTTTGCCGGGTTCGCGACAGTTGTGAGG	2962
OY	2957	AGGCTTATCTAGCTATTGGACAGCATGCGCAATCTCTTATAAATTTTCTCATATGATG	3016
Db	2963	ATGCATATCTGATTTTACGACGGCATGGGAAATCTCTTATCACTCTCTTTCGGCTGAGTG	3022
OY	3017	TTGGCTCTGGAATGCGACAACTACATCTTTTATGATGATTCATACATTCGAAAGACC	3076
Db	3023	TGACTGCAAGGCTTCTGAACTCAGATACGTCAAGATATACAGTATCTTAAAGACCTTC	3082
OY	3077	TAGCCTTAGATATAAACTGAGCAGAGGCTTTGGAGTATTTTATGATAACAAATGATGTG	3136
Db	3083	TTGCATTAGGGAAGAGTGAAGAGAGAGCACTCAACAGCTTTAAGCAAAAATTTGATGAG	3142
OY	3137	CACATCATGTGTGCTGCGACAACAAAATAGATTTGATCTTCCACCAATT	3186
Db	3143	CGCTCAGGAAAGCTGCACTACTAAAGTGAATCTGGATGGCCACACAGATT	3192

Db	1862	ACGAGTCTTACCTTGA	CTGCGAGCTGAC	CAAAATTTCTGCTG	GACCGGCGCTTGCC	CAACC	1921
QY	1982	AAAGATTTGGGCACTTTTCTTTTGGCATT	TAATAATGAGATG	CACAAAT	TAACATTA	2041	
Db	1922	GCAAGATGGGCACTTCTTTCTTTTGGCACC	TCCGCTCGAGATG	CACGTGCGCGGTGG		1981	
QY	2042	GCCAGAGTTTGGCGCTTGTGGAGTCT	ATTGTGCGATGTGGATGT	ATTTGAAC		2101	
Db	1982	CCCTGCGCTTGGCGCTCATCCTTGAGGCT	TAACAGGCGACAGACCAC	CAATGAAGG		2041	
QY	2102	ACCTGAATPAGCAGTGGAGGCAATG	AAAAGCTATTAACTTA	ACTGACATTCT	CAAC	2161	
Db	2042	TGCTGATGAAACAGAGGGGAAAGCACT	GACCAACTGAAGCGCTG	ATGACTTGTGTC	CAAGC	2101	
QY	2162	AGGAGAGAAAGATGA	AAACAAAGGTACAGATGA	AGTTTTT	AGTTAGCAATG	AGGC	2221
Db	2102	TGAGCTCTCAGAA	AACCCCAAGCCCAAGACCAAGAG	CGTGA	GTGACTTGATGGGC	2161	
QY	2222	GACCAGATTTTCATG	ATGCGCTTACAGGGCTTGTCTGTCTCT	CTTAACCTTGCTCAT	CAAC	2281	
Db	2162	AGGAGGCTTACTT	GAGGCGCTCTCCACCTG	GAAGTCCCACTGACCC	CAGACCTTGC	2221	
QY	2282	TAGAAACCTCAGGCT	TAAAGAGTGTGAATTA	TGTCTTGCA	AAAAGGCCACTGTG	2341	
Db	2222	TGGCTGAAGTCTG	CTGAGAGTGA	CACTTCA	TGACCTC	CAAGATGAAGCCCTTG	GA 2281

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RESULT 11
US-09-194-640A-2
; Sequence 2, Application US/09194640A
; Patent No. 6482623
; GENERAL INFORMATION:
; APPLICANT: Van Hasebroeck, Bart
; APPLICANT: Waterfield, Michael D.
; TITLE OF INVENTION: No. 6482623el Lipid Kinase
; FILE REFERENCE: 2332-1-002
; CURRENT APPLICATION NUMBER: US/09/194,640A
; CURRENT FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: PCT/GB97/01471
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 9611460.8
; PRIOR FILING DATE: 1996-06-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3387
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-194-640A-2

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Db	2282	TCATGTACAGCAACAGAGAGGACAGCAGCGCGCC-----AGGCTGGCATCATCT	2332
Qy	2402	TTAAAAATGGGGATGATTTACGGGCACAGATATGCTACACTTCAAAATTATTCGATATTATGG	2461
Db	2333	TTAAGAAACGGGGATGACCTCCGGCAGACATATGCTGACCTTCGACAGATGATCCACTCATGG	2392
Qy	2462	AAATATCTGGCAAAATCATAGCTTTGATCTTGGAATGTTAACTTATAGTTCGTGTCAA	2521
Db	2393	ACGTCTCTGTGAACACAGAGAGGGGTGACCTGAGAGATGACCCCTATGGCTGCTCCCA	2452
Qy	2522	TCGGTGCATGTGTGGACTTATTGACGTGTGGCAATTCACACTATTATGCAATTC	2581
Db	2453	CCGGGAGCCGACAGGCGCTCATTTGAGGTGTATCTCGGTTAGACACCATGGCCAACTCC	2512
Qy	2582	A--GTGAAAGCGCGCTTGAAAGGTGCACATGCAGTTCAACAGCCACACACTACATCACTG	2638
Db	2513	AACCTCAACAGAGACCATGTGGCAGCCACACCGCGCTTCAACAAAGATGCCCTGCTCACT	2572
Qy	2639	GGCTCAAAAGCAACAACAAGAGAAATATATATGATGAGCATTTGACCTGTTAACGCTT	2698
Db	2573	GGCTGAAGTCCAAACAACCCGGGGGAGGCCCTGTGATGAGCCATTTGAGGAATTCACCTCTT	2632

Query Match	9.7%	Score 329.8	DB 4	Length 3387
Best Local Similarity 53.2%		Pred. No. 7.1e-82		
Matches 800	Conservative	0	Mismatches 682	Indels 21
			Gaps 4	
Qy	1662	TCCCGAAATTCACCAAAATTCCTTCGTCTGTCTGTTAAATGSAATCTAGAGATGAATG	1741	
Db	1625	TCCCGAGGCGCTACCCGGCTGCTGTGTACCAAGTGSACAAAGCATGAGATGTGG	1684	
Qy	1742	CCGAGATATTGCTTGGTTAAAGATTGGCCCTCCAAATCAAACTGAAACGCTATGSAAC	1801	
Db	1665	CCCAATCTCTACCTGCTGTGCTCTCTTACCGAGACTCCCGCTGAGCGCCCTGGAGC	1744	
Qy	1802	TTCTGAGCTGAATTACCCAGATCCATATGTTTCAGAGTTTGTGTTGGTGTCTGSA	1861	
Db	1745	TGCTAGACTCAGCTTCCCGCATGCCAGTAGGCTCTTGCGCATCAAGTCGCTCGGA	1804	
Qy	1862	AATATTAAAGATACAACTTCTCTGATTTAAATTCAGCTAGTAAAGTCCTAAT	1921	
Db	1805	AA--CTACGAGCATAGAGCTGTTCACAGTACTGCTCAGCTGTGAGAGTGCTCAAGT	1861	
Qy	1922	ATGAACAATATTGGATATACCTGCTGTGAGATTTTAACTGAGAAACATTTGACTATC	1981	

Db 2633 CCTGTGCTGGGTATTTGTCTGTGGCCACATATGTGCTGGGCATTTGGCGATCGGCCACACGGACA 2692  
 Qy 2759 ACATCATGGTGAAGACGATGACACACTGTTTCATATAGATTTTGGACACTTTTGGATC 2818  
 Db 2693 ACATCATGATCCGAGAGATGGGGCAGCTGTTCACATATGATTTTGGCCACTTTCTGGGGA 2752  
 Qy 2819 ACAAGAGAAAAAATTTGGTATATTAACGAGACGTTGCCATTGTTTGCACAGAGATT 2878  
 Db 2753 ATTTCCAGACCCAACTTTGGAAATCAACCGCGAGCGTGTCCATTATCTCACTAGACT 2812  
 Qy 2879 TCTTAATATGATTTAGTAAAGAGCCCAAGATGACAAAGACAGAGAAATTTGAGAGT 2938  
 Db 2813 TTGTCCATGTGATTTACAGAGG-----GAAGACTAATAATATGTGAGAAAAATTTGAACGCT 2866  
 Qy 2939 TTCAAGAGATGTGTTACAGGCTTATCTAGCTATTGCACGCAATGCCAATCTCTTAATA 2998  
 Db 2867 TCCGGGGCTACTGTGAAGAGGCTTACACCAATCTCTGGGGCCGACGGGCTTCTTCTCC 2926  
 Qy 2999 ATCTTTTCTCAATGATGCTTGGCTCTGGAAATGCCAGAACTTCAATCTTTTGTATGACATTG 3058

Db 2927 ACCCTTTGCCCTGATCGGGCGGAGCCCTGCTGAGCTCAGCTCTCCAAAGACATCC 2986  
QY 3059 CATACATTCGAAAGACCCCTAGCCTTAGATAAACTGAGCAAGGCTTTGGAGATTTC 3118  
Db 2987 AGATCTCAAGAGACTCCCTGCACTGGGGAAAAAGAGAGAGGCACTGAGACACTTC 3046  
QY 3119 TGAACAACATGATGATGACATCATGTGGCTGGACACAAAAAATGATTTGATCTTC 3178  
Db 3047 GAGTGAAGTTTAAAGAAACCCCTCCGTGAGAGCTGAAACCAAAAGTGAATGCTGGCCC 3106  
QY 3179 ACA 3181  
Db 3107 ACA 3109

## RESULT 12

US-09-357-070-1  
; Sequence 1, Application US/09357070  
; Patent No. 6046049  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF P13 KINASE P110 DELTA EXPRESSION  
; FILE REFERENCE: RFS-0076  
; CURRENT APPLICATION NUMBER: US/09/357,070  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 1  
; LENGTH: 3868  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (197)..(3331)  
US-09-357-070-1

## Query Match

Best Local Similarity 53.2%; Score 329.8; DB 3; Length 3868;  
Matches 800; Conservative 0; Mismatches 682; Indels 21; Gaps 4;

QY 1682 TCCCCGAAATTTCTACCCCAATTTGTTCTGTCTGTTAATGGAATTTCTAGAGATGAATAG 1741  
Db 1821 TCCCGAGGCGCTAGCCCGCTGCTGTGTACCAAGTGGAAACAAAGCATGAGATGTGG 1880  
QY 1742 CCCAGATGTAATGCTGTGTAAGAAAGATTGGCCCTCCAAATCCAAACCTGAACAGGCTATGGAA 1801  
Db 1881 CCCAGATGCTCTACCTCTGTCTGTCTGCTGGCGGAGCTGCCGCTCTGAAGGCCCTGAGAC 1940  
QY 1802 TTCTGACCTGTAATTTACCCAGATCTATGTGTTGAGGTTTGTCTGTCTGTCTGTGAAA 1861  
Db 1941 TGTCTAGACTTCAGCTTCCCGATGGCCAGTAGGCTCTTCCGATCAAGTCTGCGGGA 2000  
QY 1862 AATATTTAACAGATGAACAACTTTCTAGATATTTAATTCAGCTATGTCAGGCTCTTAAT 1921  
Db 2001 AA--CTGACGAGAGATGAGAGTGTTCAGATACCTGTGCACTGTGTCAGGTCCTCAAGT 2057  
QY 1922 ATGAACAATATTTGGAATACCTGTTGAGATTTTACTGAAATAAAGCAATGACTATC 1981  
Db 2058 ACGATCTCTACCTGAGCTGAGAGCTGACCAATCTCTGCTGGAACGGGCCCTGGCCAAAC 2117  
QY 1982 AAAGATTTGGGCACTTTTCTTTTGGCATTTAAATCTGAGATGACATTAACAGTTA 2041  
Db 2118 GCAAGATCGGCACTTCTTTTCTGGAACCTCGGCTCGAGATTCAGTGGCGGTGG 2177  
QY 2042 GCCAGAGTTTGGCTCTTTTGGAGTCTATGTCGTGCTGCAATGTGGATGTATTGAAGC 2101  
Db 2178 CCTGCGCTTCGGCTCATCTGTGAGGCTTACCTGCAAGGCGAGAGACCAACACATGAGG 2237  
QY 2102 ACCTGAATTAGCAAGTGGAGCAATGGAACAAAGCTCATTAATTAAGTGAATCTTCAAC 2161  
Db 2238 TGCTGATGAAGCAAGGGGAAAGCACTGAGCAAACTGAAAGGCCCTTAATGATCTGTCAAGC 2297  
QY 2162 AGGAGAGAAAGATGAACAAACAAAGGTACAGATGAAGTTTATGTTAGCAATGAGGC 2221

Db 2298 TGAGCTCTCAGAAAGACCCCCAGGCCAGACCAAGGAGCTGATGCACTTGTGATGCGGC 2357  
QY 2222 GACCAATTTCTAGGATGACCTTACAGGGCTTGTGCTGCTCTTAAACCCGTCATGAAC 2281  
Db 2358 AGGAGGCTTACCTAGAGGCTCTTCCCACTGAGTCCCACTGACCCAGACCTTGC 2417  
QY 2282 TAGAAACCTCAGGCTTTAAAGATGTCGAATTAATGCTTGTGCAAAAAGGCCACTGTGT 2341  
Db 2418 TGGCTGAAGTCTGGTGAACAGTGACCTTCAATGAGCTCCAAAGATGAACCCCTGTGGA 2477  
QY 2342 TGAATTGGAGAACCCAGACATATGTCAAGTTACTGTTTCAGAACATGATCATCT 2401  
Db 2478 TCATGTACAGCAACGAGGAGCGAGCGCCGCGC-----AGCGTGGGCATCATCT 2528  
QY 2402 TTTAAATTTGGGATGATTTACGGCAAGATATGCTAACCTTCAATTAATTCATTTG 2461  
Db 2529 TTAAGAAAGGAGATGATCTCCGCGAGCAATGCTGACCTGCAAGATGATCAGCTCATGG 2588  
QY 2462 AAAATATCTGCAAAATCAAGATCTTGTATCTTGAATGTTACCTTATGTTGTCTGCA 2521  
Db 2589 ACGTCTGTGGAAGCAGAGGAGGCTGACCTGAGAGATGACCCCTATGAGCTGCTCCCA 2648  
QY 2522 TCGTGACTGTGTGGACTTATTGAGGTGTGCAAAATCTCACTATTATGCAAAATTC 2581  
Db 2649 CCGGGGACCGCAGAGGCTCATTTGAGGTGTACTCCGTTGACACACCATGCGCAACATCC 2708  
QY 2582 A---GTGCAAGGCGCTTAAAGTGCATGCAAGTTCAACAGCCACACACTCATAGT 2638  
Db 2709 AACTCAACAAAGACCAATGAGAGCAGCACGCCCTTCAACAAAGAGCCCTGCTCACT 2768  
QY 2639 GGCTCAAAAGACAAGAAACAAAGAGAAATATATGATGAGCAGCATTAAGCTTTTACAGCT 2698  
Db 2769 GCGTGAAGTCCAAAGACCCGGGAGGCGCTGATGAGCATTTGAGAGATTTACCTCT 2828  
QY 2699 CATGTCTGATACCTGTGATGCTTCACTTCAATTTGGAAATGAGATGTCACAAATGTA 2758  
Db 2829 CMTGTCTGCTATTTGTGTGGCCATATGTGCTGGGCATTTGGCATGCGCACAGCACA 2888  
QY 2759 ACATCATGTGAAAGAGATGACAACTGTTTCAATATAGATTTTGGACACTTTTGGATC 2818  
Db 2889 ACATCATGATCCGAGAGAGTGGCAGCTGTTCACATTTGATTTGGCACCTTTCTGGGA 2948  
QY 2819 ACAAGAAAGAAATTTGTTATTAACGAGAAAGTGTGCAATTTGTTTGAACAGGAT 2878  
Db 2949 ATTTCAAGACCAAGTTTGAATCAACCGCAGAGGTGTCCATTCATCTCACCACACT 3008  
QY 2879 TCTTAATGTGATTAAGTAAGAGAGCCCAAGATGCAACAAAGAGAAATTTGAGAGT 2938  
Db 3009 TTGTCAATGTGATTTACAGAGG-----GAAAGCTAATTAATGAGAAATTTGAACGT 3062  
QY 2939 TTCAGAGATGTGTACAGAGCTTATATCTAGCTATTTGACAGCATGCCAATCTCTTA 2998  
Db 3063 TCCGGGGCTTACTGTGAAGGGCTTACACCAATCTGTGGGCGCCACGGGCTTCTCTTCC 3122  
QY 2999 ATCTTTTCTAATGAGGCTTGGCTGGAATGCGAAGCTACATCTTTGATGACATG 3058  
Db 3123 ACCCTTTTGGCTTGAATGCGGCGGCGAGCTGCTGTGACTGACGTGCTCCAAAGACATCC 3182  
QY 3059 CATACATTCGAAAGACCTTACCTTATGATTAACATGACGAGGCTTTGGAGATTTC 3118  
Db 3183 AGATCTCAAGGACTCCCTGTGCACTGGGGAACAAAGAGAGGAGGCACTGAAGCACTTC 3242  
QY 3119 TGAACAACATGATGATGACATCATGTGTGCTGAGACACAAAAATGATTTGATCTTC 3178  
Db 3243 GAGTGAAGTTTAAAGCAAGCCCTCGTGAAGCTGGAACCAAAAGTGAATCTGCGCC 3302  
QY 3179 ACA 3181  
Db 3303 ACA 3305

## RESULT 13

US-08-777-405A-1  
Sequence 1, Application US/08777405A  
Patent No. 5858753  
GENERAL INFORMATION:  
APPLICANT: Chantry, David  
APPLICANT: Hoekeita, Merl F.  
APPLICANT: Holzman, Douglas A  
TITLE OF INVENTION: No. 5858753el Lipid Kinase  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
STREET: 6300 Sears Tower/233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,405A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5858753and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/33441  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6350  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5220 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 196..3327  
US-08-777-405A-1

Query Match 9.7% Score 329.8: DB 2: Length 5220;  
Bee local similarity 53.2% Pred. No. 8.8e-82;  
Matches 800: Conservative 0; Mismatches 682; Indels 21; Gaps 4;

Qy 1682 TCCCGAATTTCTACCCAAATTTGCTTCTGTGTTAAATGGAATTTCTAGATGAAATG 1741  
Db 1820 TCCCGAGAGCGCTGACCCGCGCTGCTGTGTCACCAAGTGGAAACAAGATGAGATG 1879  
Qy 1742 CCCAGATGATTTGCTTGTAAAGATTGGCTTCCAAATCAAACTGAAACAGGCTATGAA 1801  
Db 1880 CCCAGATGCTTACCTGTGCTGCTCTGCGGAGCTGCCGCTCTGAGCCCTGAGAGC 1939  
Qy 1802 TTTCGATGTAATTAACCAATCTTATGCTTTCAGATTTTGTCTTGGTGTCTTGGAA 1861  
Db 1940 TGCTAGACTGAGCTTCCCAATGGCAAGTAGGCTCTTCCCAATGCTGCTGCGGA 1999  
Qy 1862 AATATTTAAGATGACAACTTTCTCAGTATTTTAATTCAGTAGTACAGGCTCTAAAT 1921  
Db 2000 AA---CTACGAGACATGACGCTGCTCCAGTACCTGCTGAGTGTGAGGTGCTCAAGT 2056  
Qy 1922 ATGAACAATTTTGGATACTTGTGTGAGATTTTAACTGAAGAAACATTGACTAATC 1981  
Db 2057 ACGAGTCTTACCTGAGCTGCGAGCTGACCAAAATTCCTGCTGAGCCGCGCTGAGCAAC 2116  
Qy 1982 AAAGATTTGGGACCTTTTCTTTTGGCATTTAAATTCGAGATGACAAATAAACAGTTA 2041  
Db 2117 GCAAGATGGGACATTTCTTTTCTGTGGACCTCCGCTCCGAGATGACGTGCGGTGGTG 2176

Qy 2042 GCCAGAGCTTTGGCTGCTTTTGGATCTTATTTGTGCTGATGTGGATGATTTTGAAGC 2101  
Db 2177 CCTGGCCCTTGGGCTCATCTCTGAGGCTTACTGAGGGGAGAGACCCACACATGAAGG 2236  
Qy 2102 ACCGTGATGAGCAAGTGGAGGCAATGGAAGAAGCTCATTAATCTTAACCTGATCTCAAC 2161  
Db 2237 TGCTGATGAAGCAGGGGGAAGCACTGAGCAAACTGAAAGGCCCTGAATGACTTGTCAAGC 2296  
Qy 2162 AGGAGAGAAAGATGAAACCAAAAGGTACAGATGAAATTTTATTTAGTTGAGCAATGAGGC 2221  
Db 2297 TGAGCTCTCAGAAAGACCCCAAGCCCAAGACCAAGAGCTGATGACATTTGATGAGCGC 2356  
Qy 2222 GACCAATTTCTAGATGATGCTTACAGGGCTTGTCTCTCTTAAACCTGCTCATTAAC 2281  
Db 2357 AGAGGCTTACTTGAAGGCTCTTCCACCTGCAAGTCCCATCTGACCAAGCAAGCACTTGC 2416  
Qy 2282 TAGAAACCTCAGCTTAAAGATGTGAAATTTATGTTCTTGTGCAAAAAGGCCACTGTGT 2341  
Db 2417 TGCTGTAAGTCTGGTGAACAGTGAACCTTCAATGACCTCAAGATGAAGCCCTGTGA 2476  
Qy 2342 TGAATTTGGGAAACCCAGACATCATGTCAAGATTACTGTTTCAAGAACATGAGATCATCT 2401  
Db 2477 TCATGTACAGCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2527  
Qy 2402 TTTAAATTTGGGATGATTTTACGCGAAGATATGCTTACACTTCAATTTATTTATTTG 2461  
Db 2528 TTAAGAACGGGAGATGACCTCCGCGAGACATGTGACCTTGCAGATGATCAGCTCATGG 2587  
Qy 2462 AAAATATCTGGCAAAATCAAGTCTTGAATCTTGAATTTGAATTTGATGATGATGATG 2521  
Db 2588 ACGTCTGTGGAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2647  
Qy 2522 TCGGTGATGCTGTGAGGACTTATTTGAGGTGTGCGAAATTTCTCAACTATTTATGCAATTC 2581  
Db 2648 CCGGAGACCCAGAGGCTCATTTAGAGGTGATCTCCGTTAGACACCATGCGCAACATCC 2707  
Qy 2582 A--GTCAAAAGCGGCTTGAAGGTGCTGCTGACATGTTCAACAGCCACACTACATCAGT 2638  
Db 2708 AACTCAACAAGAGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2767  
Qy 2639 GGCTCAAGACAAAGAAAGAGAAATATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2698  
Db 2768 GGCTGAAGTCCAAAGACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2827  
Qy 2659 CATGTGCTGATGATGCTGATGCTTCAATTTTGGAAATTTGAGATGCTGCAATATGTA 2758  
Db 2828 CTTGTGCTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 2887  
Qy 2759 ACATCATGTGTAAGAGAGATGAGACAACTGTTTCAATATAGATTTTGAACACTTTTGGATC 2818  
Db 2888 ACATCATGATCCGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2947  
Qy 2819 ACAAGAAAGAAATTTTGTATTAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2878  
Db 2948 ATTCAAGACCAATTTTGAATCAACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3007  
Qy 2879 TCTTAATAGTATTAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2938  
Db 3008 TTGTTCATGTGATTCAGAGAGG-----GAAAGTATTAATAGTGAAGAAATTTGAAGGT 3061  
Qy 2939 TTAAGAGATGTGTTACAGAGGCTTATGATGATGATGATGATGATGATGATGATGATGATG 2998  
Db 3062 TCCGGGGCTACTGTAAGAAAGGCTTACACATCTGCGGGCCGAGGAGGAGGAGGAGGAGGAG 3121  
Qy 2999 ATCTTTTCTCAATATGCTTGTGCTTGTGAATGCTGCAAGCTTCAATCTTTTGAATGACTG 3058  
Db 3122 ACCCTTTGCTGATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3181  
Qy 3059 CATACATTTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3118  
Db 3182 AGTATCTCAAGAGATCCCTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3241  
Qy 3119 TGAACAATAGATGATGACATCATCATGATGATGATGATGATGATGATGATGATGATGAT 3178

Db 3242 GAGTGAAGTTTAAAGAAAGCCCTCGTGAAGAGCTGGAAACCAAGTAACTGGCTGGCCC 3301  
Qy 3179 ACA 3181  
Db 3302 ACA 3304

RESULT 14  
US-08-977-871A-1  
; Sequence 1, Application US/08977871A  
; Patent No. 5882910  
; GENERAL INFORMATION:  
; APPLICANT: Chantix, David  
; APPLICANT: Hoechst, Merl F.  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: No. 5882910el Lipid Kinase  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall O'Toole Garstein Murray & Borun  
; STREET: 6300 Sears Tower/233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/977,871A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/777,405  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5882910and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/33441  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5220 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 196..3327  
; US-08-977-871A-1

Query Match 9.7%; Score 329.8; DB 2; Length 5220;  
Best Local Similarity 53.2%; Pred. No. 8.8e-82;  
Matches 800; Conservative 0; Mismatches 682; Indels 21; Gaps 4;

Qy 1682 TCCCCGAATTTTACCAAAATGGCTTGTCTGTTAATGGAATTTAGAGATGAATAG 1741  
Db 1820 TCCCGAGAGGGCGTACCCCGCTGCTGTGTGACCAAGTGAACAAAGATGAGATGTGG 1879  
Qy 1742 CCGAGATGATATGGTGTGTAAGATGGCCCTCAATCAAACTGAACAGGCTATGGAAC 1801  
Db 1880 CCGAGATGATATGGTGTGTAAGATGGCCCTCAATCAAACTGAACAGGCTATGGAAC 1839  
Qy 1802 TTCTGAGCTGTAATTTACCGAGATCTATAGTTCAGAGTTTTCGTTCCGTTGCTTGA 1861  
Db 1940 TGTAGACTTCAGCTTCCGATGCGACGATGAGCTCTTTCGATCAATGAGCTGCGGA 1999

Qy 1862 AATATTTAACAAGTGAACAACTTTCAGATTTAATTAAGCTAGTACAGGCTCTAAAT 1921  
Db 2000 AA---CTGACGAGCAGATGAGCTGTTCAGTACCTGTGACAGCTGTGACAGTCTCAAGT 2056  
Qy 1922 ATGACAAATATTGGATTAATCTGCTGTGATTTTACTGAAGAAAGATTAAGTAAATC 1981  
Db 2057 ACAGTCTTACTGAGCTGAGAGCTGACCAAAATTCCTGTGACCGGGCCCTGGCAACC 2116  
Qy 1982 AAGAGATGGGCACTTTTCTTTTGGCATTAAATCTGAGATGACAAATMAAACAGTTA 2041  
Db 2117 GCAAGATCGGCCCACTTCTTTCTGTGCACTCCGCTCCAGATGACAGTCCGCTGGTGG 2176  
Qy 2042 GCCAGAGTTTGGCTCTTTTGGAGTCTTATGTCGTGTCAGTGGAGATGATTTGAAGC 2101  
Db 2177 CCTGGCTTCGGCTCTATCTGAGAGCTTACAGAGGGGACACCCACCATGAAAGG 2236  
Qy 2102 ACCTGAATAGGCAATGAGAGCAATGGAAGAGTCACTTAATCTGACATCTCAAC 2161  
Db 2237 TGCTGATGAAGCGGGGGAAGCACTGAGCAAACTGAAGGCCCTGAATGACTTGTCAAGC 2296  
Qy 2162 AGGAGAGAAAGATGAACACAAAGGTAACAGATGAAGTTTATGTTAGCAATGAGAGC 2221  
Db 2297 TGAGCTCTCAGAAAGACCCCAAGCCCAAGACCAAGAGCTGATGCACTGTGATGGCG 2356  
Qy 2222 GACCAGATTTCAATGATGCTCCCTACAGAGGCTTGTCTCTCTAAACCTGCTCATCAAC 2281  
Db 2357 AGGAGGCTTACCTAGAGAGCCCTCTCCCACTGCAAGTCCCACTGACCCACGACACCTGC 2416  
Qy 2282 TAGAAACCTCAGGCTTAAAGATGTCGAATTAATGCTTCTGCAAAAAGGCCACTGTG 2341  
Db 2417 TGGCTGAAGTCTGCGTGAAGCACTGCACTTCAATGAGTCAAGATGAAGCCCTGTGGA 2476  
Qy 2342 TGAATTGGGAGACCCAGACATCATGTCAGAGTTACTGTTTCAGAAATGAGATCATCT 2401  
Db 2477 TCATGTACAGCAACGAGAGGCGAGCGCGCGC-----AGCGTGGGATCATCT 2527  
Qy 2402 TTAATAATGGGATGATTTACGGCAAGATATGCTAACCTTCAATTAATTTGATTAAG 2461  
Db 2528 TTAAGAACGGGATGACCTCCGCAAGACATGCTGACCTGACAGATGATCAGCTCATG 2587  
Qy 2462 AAAATATCTGGCAAAATCAAGTCTTGTATTTGGAATGTTACTTATGTTGTTCTGCA 2521  
Db 2588 ACCTCTGTGGAAGCAGAGAGGCTGACCTGAGATGACCCCTTATGCTGCTCCCA 2647  
Qy 2522 TCGGTAGCTGTGGGACTTATGAGTGGTGGCAATTTCTCACATTAATGCAATTC 2581  
Db 2648 CCGGGAGCCGACAGGCTCATTTAGAGTGTACTCCGTTACAGACCATGCCAATCC 2707  
Qy 2582 A--GTGCAAAAGCGGCTTGAAGGTGCACTGCAAGTTCAACAGCCACACATCAATCAGT 2638  
Db 2708 AACTCAACAAAGACAAATGAGCCAGCCAGCCGCTTCAACAAAGATGCCCTGCTCACT 2767  
Qy 2639 GGCTCAAAAGCAAGAAACAAAGGAAATATATGATGACAGCTTGAACCTGTTTACAGTT 2698  
Db 2768 GGCCTGAAGTCCAAAGAACCGGGGAGGCTGTGATGAGCAATGAGAGTTCACCTCT 2827  
Qy 2699 CATGCTGTGATCTGTGATGATGATCTTCAATTTTGGGAATGAGATGCGTCAATAGTA 2758  
Db 2828 CCTGTGTGCTATTTGTGTGCGCAATATGTGCTGAGCATGTGCGAATGCGACAGGACA 2887  
Qy 2759 ACATCATGTGTAAGAGCAGATGACAACTGTTTCATATGATTTTGGACACTTTTGGATC 2818  
Db 2888 ACATCATGATCCAGAGAGAGTGGCACTGTTCACATGATTTTGGCACTTTCTGGGGA 2947  
Qy 2819 ACAAGAAAGAAATTTGTTATTAACGAGACGTGTGCCATTTGTTTGAACAGGAT 2878  
Db 2948 ATTCAAGACCAAGTTTGGATCAACCGGAGGTTGCCATTCATCCATCACTTATGACT 3007  
Qy 2879 TCTTAATAGTATTAATTAAGAGGCCCAAGAAATGCAAAAGACAAAGATTTGAGAGGT 2938  
Db 3008 TTGTTCATGTGATTCAGCAGGG-----GAGACTAATTAATGAGAAATTTGAACG 3061  
Qy 2939 TTCAGAGATGTGTTCAAGGCTTATCTATGCTATGACAGCATGCGCAATCTCTGATA 2998

Db 3062 TCCGGGGCTACTGTGAAAGGGGCTACACCATCTGCGCGCCAGGGGCTTCTTCCCTCC 3121  
Qy 2999 ATCTTTCTCAATGCTGTGGCTCTGGAATGCCAGAACTAOMATCTTTATGACATG 3058  
Db 3122 ACCCTTTGCTGCTGTGATGCGGGGCGGAGGCTGCTGACCTGCTCCAAAGACATCC 3181  
Qy 3059 CATACATTCGAAAGACCTTACCTTAGATTAATACTGAGCAAGGCTTTGAGTATTTCA 3118  
Db 3182 AGTATCTCAAGACATCTCCCTGACATGGGGAAACAGAGAGAGGCACTGAAGCACTTCC 3241  
Qy 3119 TGAACCAATGATGATGATCAATCATGCTGCTGACACAAATAATGATTTGATCTTCC 3178  
Db 3242 GAGTGAATTTAAGCAAGCCCTCCGTGAGACTGGAAAAACCAAGTAACTGGCGTGGCC 3301  
Qy 3179 ACA 3181  
Db 3302 ACA 3304

## RESULT 15

US-09-225-951-1  
Sequence 1, Application US/09225951  
Patent No. 5985589  
GENERAL INFORMATION:  
APPLICANT: Chantry, David  
APPLICANT: Hoekstra, Merl F.  
APPLICANT: Holzman, Douglas A  
TITLE OF INVENTION: No. 5985589el Lipid Kinase  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESS: Marshall O'Toole Gerstein Murray & Borun  
STREET: 6300 Sears Tower/233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/225,951  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5985589and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/33441  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6180  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5220 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 196..3327  
US-09-225-951-1

Query Match 9.7%; Score 329.8; DB 2; Length 5220;  
Best Local Similarity 53.2%; Pred. No. 8.8e-82;  
Matches 800; Conservative 0; Mismatches 682; Indels 21; Gaps 4;

Qy 1682 TCCCCGAATCTACCCAAATGCTTCTGCTGTTAAATGGAATTTAGAGATGAATAG 1741  
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Qy 1742 CCCAGATGATATGCTTGTGTAATAAGATTGCTCCAAATCAAACTGGAACAGGCTATGGAAC 1801  
Db 1880 CCCAGATGATCTACTGCTGTGCTGCTGCGCGAGAGTGCCTGCTGAGCGCCCTGGAGC 1939  
Qy 1802 TTTCTGAGCTGTAATTAACCGAGATCTATGATGAGGTTTGTGCTGCTGCTGGA 1861  
Db 1940 TGCTAGACTTCAAGCTTCCCGAATGGCCAGTAGGCTCTTGGCATCAATGCTGGGGA 1999  
Qy 1862 AATATTTAAGAGATGACAAACTTTCTCAGATTTTAATTAATTCAGTAGTACAGTCTTAAT 1921  
Db 2000 AA---CTGAGGAGAGATGAGCTGTTCAGTACTGCTGCAAGCTGTGTCAAGT 2056  
Qy 1922 ATGAACAATATTTGATTAATCTGTTGTGAGATTTTACTGAAAGAAAGCATTTGATATC 1981  
Db 2057 ACAGTCTCTACCTGAGCTGCGAGCTGACAAATTCCTGCTGACCGGGCCCTGGCCAAC 2116  
Qy 1982 AAAGGATTGGCACTTTTCTTTTGGCATTTAAATGTGATGACACAAATAAAAAGTTA 2041  
Db 2117 GCAAGATCGGCCACTTCTCTTCTGCACTCCGCTCCGAGATGACATGCTCGGTGG 2176  
Qy 2042 GCCAGAGTTTGGCTGCTTTTGGAGCTATTGTGCTGATGAGGATGATTTGAAGC 2101  
Db 2177 CCTGCGCTTGGCTGCTATCTGAGGCTTACTGACGGGCGAGACCCACCATGAAAGC 2236  
Qy 2102 ACCTGAATAGGCAAGTGCAGGCAATGGAAGAGCTCAATTAATTAATGATGATTTCTCAAC 2161  
Db 2237 TGCTGATGAAGCAGGGGGAAGCACTGAGCAAACTGAAAGGCCCTGGAATGATCTGTCAAGC 2296  
Qy 2162 AGGAGAGAGAGATGAACCAAAAGGTACAGATGAAGTTTATGTTGAGCAAAATGAGGC 2221  
Db 2297 TGAGCTCTCAGAAAGCCCCCAAGCCCCAGACCAAGAGCTGATGACATTTGTGATGGGC 2356  
Qy 2222 GACCAGATTCATGATGATGACCTTACAGGCTTGTGCTGCTCTTAAACCTGCTCATGAC 2281  
Db 2357 AGGAGCTTACTGAGAGCCCTCTCCACCTGCAAGTCCCATCTGACCTCCAGCACTTGC 2416  
Qy 2282 TAGGAACTCAGGCTTAAAGAGTGTGAATTAATGCTTTGCAAAAAGGCCACTGTGT 2341  
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Qy 2342 TGAATTTGGGAACCCAGACATCATGTCAAGATTACTGTTTCAGAACATGAATCATCT 2401  
Db 2477 TCATGTACAGCAACGAGAGGCAAGGCGAGCGCGCC-----AGGTGGGATCATCT 2527  
Qy 2402 TTAAATAATGGGATGATTTACGGCAAGATGCTTAACCTTCAATTAATTCGATTTAGG 2461  
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Qy 2462 AAAATATCTGGCAAAATCAAGGCTTGTGATCTTGAATGTTACCTTATGTTGTCTGTCA 2521  
Db 2588 ACCTCTGTGTAAGACAGAGAGGGGCTGGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 2647  
Qy 2522 TCGTGAATGTGTGGAAGTATTTGAGGTGTGGAATTTCTACACATTAATGAATTC 2581  
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Qy 2699 CATGTGCTGATACTGTGATGACTTCAATTTTGGGAATTTGAGATGTCACAAATATGTA 2758  
Db 2828 CTGTGTGCTGATTTGTGTGCGCACATATGTGCTGGGCAATTTGGCAATCGGCAAGCACA 2887  
Qy 2759 ACATCATGTGAAAGAGATGAGCACTGTTTCAATATATGATTTTGGACACTTTTGTGATC 2818  
Db 2888 ACATCATGATCCGAGAGATGGGAGCTGTTCACATGATTTTGGCCACTTCTTGGGGA 2947



QY	2819	ACAGAAGAAAATTTGGTATATAACAGAACGTGTGCATTGTGTTGACACAGGATT	2878
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QY	2879	TCTTAATAGTATTAGTAAAGAGCCCAAGATGCACAAAGACAAGAAATTTGAGAGT	2938
Db	3008	TTGTTCATGTGATTACGACGAGG-----GAAAGCATTAATATATGAGAAATTTBAGCGT	3061
QY	2939	TTTCAGGAGATGTGTTACAAGCTTATCTAGCTATTTCGACAGCTGCCAATCTTTCTAA	2998
Db	3062	TCCGGGGGTACTGTGAAGAGGGCTACACCAATCTCGCGGCTGCACGGGCTTCTCTTCCTCC	3121
QY	2999	ATCTTTTCTCAATGATGCTGGCTCTGGAATGCCAGAACTACATCTTTTATATACATGTG	3058
Db	3122	ACCTCTTTGCCCTGATGTGCGGGGCGACGGCTGCTCTGAGCTACGTCTCCAAAGACATCC	3181
QY	3059	CATACATTGGAAGACCCCTAGCCTTAGATTAACATGACAGAGGCTTTGGAGTATTCA	3118
Db	3182	AGTATCTCAAGGACTCCCTGTGCACATCGGGGAAAACAGAGAGAGGCACTGAAGACATTCC	3241
QY	3119	TGAACCAAAATGAATGATGCACATCATGTGCTGCTGACACAAAAAATGGATTGGATCTTCC	3178
Db	3242	GAGTGAAGTTTAAGGAAGCCCTCCGTGAGAGCTGAAAACCAAAAGTGAATCGCTGGGCC	3301
QY	3179	ACA 3181	
Db	3302	ACA 3304	

Search completed: November 7, 2003, 13:16:03  
Job time : 169.161 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 04:07:07 ; Search time 574.767 Seconds

(without alignments)  
16024.736 Million cell updates/sec

Title: US-09-325-095-32

Perfect score: 3412  
Sequence: 1 ATGCTCCAGACCATCATC.....TAAACTAGTTCATTCAAAA 3412

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_19Jun03:\*

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- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
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- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*
- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3407.2	99.9	3412	14	AAO51156 Human p110 CDNA.
2	3407.2	99.9	3424	24	ABL59523 Human phosphatidy
3	3407.2	99.9	3424	24	ABL514365 CDNA encoding huma
4	3137	91.9	3498	15	AAO57012 Ptdins 3-kinase 11
5	3008.6	88.2	3207	14	AAO51155 p110 CDNA. Homo s
6	564	16.5	741	21	AAA02190 Human colon cancer
7	460.8	13.5	3213	21	AAO65690 Human p13 kinase p
8	460.8	13.5	3213	24	ABV78026 Hypoxia-regulated

C	10	452	13.2	4074	22	AA137431	CDNA encoding huma
	11	452	13.2	4074	22	ABA07289	Human musculoskele
	12	452	13.2	4074	22	ABA07290	Human pancreatic c
	13	452	13.2	4074	22	AAK89934	Human digestive sy
	14	452	13.2	4074	22	AAK89935	Human digestive sy
C	15	452	13.2	4074	25	ABK60419	CDNA encoding nove
	16	380.6	11.2	412	25	ABK37274	Bovine EST associa
	17	329.8	9.7	3387	19	AAV16533	CDNA encoding mamm
	18	329.8	9.7	3868	21	AAV13154	Human phosphatidy
	19	329.8	9.7	3868	24	ABK84750	Human CDNA differe
	20	329.8	9.7	3868	24	AAK54363	CDNA encoding huma
	21	329.8	9.7	5220	19	AAV13140	Human phosphatidy
	22	329.8	9.7	5220	20	AAV15932	CDNA sequence enco
	23	329.8	9.7	5220	21	AAZ23882	Human PI 3-kinase
	24	317	9.3	3525	24	ABK84381	Human CDNA differe
	25	305.4	9.0	3773	23	ABL07215	Drosophila melanog
	26	295.6	8.7	5162	20	AAV74104	Human G-protein re
	27	295.6	8.7	5162	21	AAZ86814	Human p120 regulat
	28	295.6	8.7	5397	24	ABL59522	Human phosphatidy
	29	295.6	8.7	5397	24	AAZ4367	CDNA encoding huma
	30	291.8	8.6	4134	17	AAZ58545	Human phosphatidy
	31	291.8	8.6	4137	17	AAZ58546	Human phosphatidy
	32	278.8	8.2	3808	19	AAV04634	Porcine phosphoino
	33	278.8	8.2	3808	20	AAV74100	Porcine G-protein
	34	278.8	8.2	3808	21	AAZ86813	Pig p120 regulator
	35	236.8	6.9	1074	23	AAZ73988	DNA encoding novel
	36	224.2	6.6	5285	18	AAZ60199	Phosphatidy inosi
	37	223	6.5	5061	19	AAV42920	CDNA encoding a hu
	38	223	6.5	5061	25	ABT17093	Androgen-independe
	39	192.4	5.6	4491	23	AAZ71517	DNA encoding novel
	40	192.4	5.6	4491	24	ABN59725	Novel human coding
	41	168.2	4.9	5990	24	ABK62570	Rat sequence diffe
C	42	164	4.8	4498	23	AAZ68360	DNA encoding novel
C	43	164	4.8	4747	22	ABA08693	Human p13-kinase h
C	44	164	4.8	4747	22	AAH99523	Human protein enco
	45	154.6	4.5	170	24	ABL36640	Human colon tumour

#### ALIGNMENTS

RESULT 1		AAO51156 standard; CDNA, 3412 BP.	
ID	AAO51156		
AC	AAO51156;		
DT	25-MAR-2003 (updated)		
DT	12-APR-1994 (first entry)		
XX			
DE	Human p110 CDNA.		
XX			
KW	Phosphoinositide kinase; PI; p85 subunit; screening; agonist;		
KW	antagonist; cell proliferation; inhibition; prophylaxis; therapy;		
KW	platelets; neutrophil activity; 3-phosphorylated phosphoinositides;		
KW	ds.		
OS	Homo sapiens.		
XX			
XX			
FT	Key	Location/Qualifiers	
FT	CDS	1..3207	
FT		/tag= a	
FT		/note= "p13- kinase p110"	
XX			
PN	WO9321328-A1.		
XX			
PD	28-OCT-1993.		
XX			
PF	13-APR-1993;	93WO-GB00761.	
XX			
XX	13-APR-1992;	92GB-0008135.	
XX			



Db 1621 TCTGAATCACTGACGACGAGAAAGATTTTCTATGAGTCCACAGACACTATTGTGAAT 1680  
Qy 1681 ATCCCCGAATTTCTACCCAAATTTGCTTCTGTCTGTTAAATGAGATTTAGAGATGA 1740  
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Db 1801 CTTCTGAGCTGTAATTTACCCAGATCTCTATGTTGCAAGTTTGTGTTGGTCTTGGA 1860  
Qy 1861 AAATATTTACAGATGACAACTTTCTCAGATTTTAATTCAGCTAGTACAGTCTTAA 1920  
Db 1861 AAATATTTACAGATGACAACTTTCTCAGATTTTAATTCAGCTAGTACAGTCTTAA 1920  
Qy 1921 TATGAAACAATATTTGGATTAAGTGTGAGATTTTAACTGAGAAAGCATTTGACTAAT 1980  
Db 1921 TATGAAACAATATTTGGATTAAGTGTGAGATTTTAACTGAGAAAGCATTTGACTAAT 1980  
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Qy 2041 AGCCAGAGTTGGGCTGCTTTTGGAGTCTTATGTCGATGTCAGATGATTTGGAAG 2100  
Db 2041 AGCCAGAGTTGGGCTGCTTTTGGAGTCTTATGTCGATGTCAGATGATTTGGAAG 2100  
Qy 2101 CACCTGAATAGGCAAGTCGAGGCAATGGAAGCTCATTAATTAATTAATTAATTAAT 2160  
Db 2101 CACCTGAATAGGCAAGTCGAGGCAATGGAAGCTCATTAATTAATTAATTAATTAAT 2160  
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Db 2161 CAGGAGAGAGAGATGAAACAAACAAAGATGACAGATGAGATTTTACTGACAAATGAG 2220  
Qy 2221 CGACAGATTTTATGAGATGCTTACAGGCTTGTGCTGCTCTTAAACCTGCTATCA 2280  
Db 2221 CGACAGATTTTATGAGATGCTTACAGGCTTGTGCTGCTCTTAAACCTGCTATCA 2280  
Qy 2281 CTGAGAAACCTCAGGCTTAAAGATGTCATTAATTAATTAATTAATTAATTAAT 2340  
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Db 3361 TAAATGTAACGCAACAGGTTTGTATGACCTTAACCTAGTTCAATTTCAAA 3412  
RESULT 2  
ABL59523  
ID ABL59523 standard; cDNA; 3424 BP.  
XX  
AC ABL59523;  
XX  
DT 16-JUL-2002 (first entry)  
XX  
DE Human phosphatidylinositol-3-kinase catalytic alpha cDNA SEQ ID NO:23.  
XX  
KW Human; phosphatidylinositol-3-kinase catalytic alpha; enzyme;  
KW tumour; lipid associated gene; lipid metabolism; lipid synthesis;  
KW Chromosome 3q26.3; gene; ss.  
OS Homo sapiens.  
XX  
PN MO200227028-A1.  
XX  
PD 04-APR-2002.  
XX  
PF 27-SEP-2001; 2001WO-US30366.  
XX  
PR 28-SEP-2000; 2000US-0676052.  
XX  
PA (ATAT-) ATRIRGIN TECHNOLOGIES INC.  
XX  
PI Skinner MK, Paton JL, Chaudhary J;

XX WPI; 2002-402054/43.  
XX Identifying tumor characteristics in a tissue sample taken from a  
PT patient, involves determining the copy number or expression level of  
PT genes associated with lipid metabolism, synthesis or action -  
XX  
PS Example 1; Page 82-83; 113pp; English.  
XX  
XX The present invention describes a method for identifying tumor  
CC characteristics, comprising measuring a copy number or expression level  
CC of at least two genes associated with lipid metabolism, synthesis, or  
CC action in cells from a patient tissue sample, and comparing the results  
CC with a copy number or expression level of the genes in a normal cell.  
CC Also described is an array of nucleic acid polymers immobilised on a  
CC solid support, comprising a solid support, at least two different nucleic  
CC acid polymers which are each specific for a different gene associated  
CC with lipid metabolism, synthesis or action, where each nucleic acid  
CC polymer is located at a predetermined position on the solid support, and  
CC the array comprises nucleic acid polymers which are specific for less  
CC than 100 genes other than the selected genes. The method is useful for  
CC determining tumour characteristics in a tissue sample taken from a  
CC patient. The present sequence represents a human lipid-associated gene  
CC related cDNA sequence, which is used in the exemplification of the  
CC present invention.  
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 other;  
Query Match 99.9%; Score 3407.2; DB 24; Length 3424;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3409; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ATGCTCCAGACCATCATGAGTGAACGTGGGGCATCCATCTGATGCCCAAGATC 60  
DB 13 ATGCTCCAGACCATCATGAGTGAACGTGGGGCATCCATCTGATGCCCAAGATC 72  
QY 61 CTAGTGGAAATGTTTACTACCAATGGAATGATGATCTTAGATGCTCCGTAGGCT 120  
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QY 121 ACATTAGTAATAAGCAAGTAACTATTAAAGAAAGAAATACCTCTCCATCA 180  
DB 133 ACATTAGTAATAAGCAAGTAACTATTAAAGAAAGAAATACCTCTCCATCA 192  
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QY 241 GAATTTTGTAGTAAAGCAAGACACTTTGTGATCTTCGGCTTTTCAACATTTTAA 300  
DB 253 GAATTTTGTAGTAAAGCAAGACACTTTGTGATCTTCGGCTTTTCAACATTTTAA 312  
QY 301 GTAATGAACAGTAGGCAACCGTGAAGAAAGATCTCAATGAGAAATGGTTTGTCT 360  
DB 313 GTAATGAACAGTAGGCAACCGTGAAGAAAGATCTCAATGAGAAATGGTTTGTCT 372  
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DB 373 ATCGGATGCCAGTGTGCAATTTGATGTTAAAGATCTGAAATGAGCACTTCCGA 432  
QY 421 AGAATATTTCTTAATGTTTGTAAAGAGCTGTGATCTTAAGGATCTTAATCACTCAT 480  
DB 433 AGAATATTTCTTAATGTTTGTAAAGAGCTGTGATCTTAAGGATCTTAATCACTCAT 492  
QY 481 AGTAGAGCAATGATGCTATCGGACATGTAAGATCTTCCAGAGCTGCAAGAC 540  
DB 493 AGTAGAGCAATGATGCTATCGGACATGTAAGATCTTCCAGAGCTGCAAGAC 552  
QY 541 ATATATTAATTAATTTGGATAGAGCCCAATATATAGTGTATTTGGTAAATTTCTCCA 600  
DB 553 ATATATTAATTAATTTGGATAGAGCCCAATATATAGTGTATTTGGTAAATTTCTCCA 612  
QY 601 AATATATGACAGCAAGATTAATCTGAAATCAACCATGACTGTGTCCAGAACAGTA 660

DB 613 AATATGACAGCAAGATTAATCTGAAATCAACCATGACTGTGTCCAGAACAGTA 672  
QY 661 ATGCTGAAGCAATCAGAAAAAACTGAAGTATGTTGCTTATCTGAACATTTAA 720  
DB 673 ATGCTGAAGCAATCAGAAAAAACTGAAGTATGTTGCTTATCTGAACATTTAA 732  
QY 721 CTCTGTGTTTAAATATCAGGGCAAGTACATTTTAAAGTGTGATGATGAATAC 780  
DB 733 CTCTGTGTTTAAATATCAGGGCAAGTACATTTTAAAGTGTGATGATGAATAC 792  
QY 781 TTCTTAAGAAAAATATCTCTGTGATGAATATTAAGAGCTGTATATGCTTGGG 840  
DB 793 TTCTTAAGAAAAATATCTCTGTGATGAATATTAAGAGCTGTATATGCTTGGG 852  
QY 841 AGAGTCCCAATTTGAAGATGATGCTTAAAGAAACCTTATTTCACTGCAATGAC 900  
DB 853 AGAGTCCCAATTTGAAGATGATGCTTAAAGAAACCTTATTTCACTGCAATGAC 912  
QY 901 TGTTTTACATGCCATCTTATTTCCAGAGCATTTTCCAGAGTACCAATATATGATGA 960  
DB 913 TGTTTTACATGCCATCTTATTTCCAGAGCATTTTCCAGAGTACCAATATATGATGA 972  
QY 961 GAAACATCTAAGAAATCCCTTTGGGTATTAATATAGCACTGATATAAATTTCTTGT 1020  
DB 973 GAAACATCTAAGAAATCCCTTTGGGTATTAATATAGCACTGATATAAATTTCTTGT 1032  
QY 1021 GCACCTACGTAATCTTAATTTTGAAGATTTGAGATTTATGTTGCAAGATATC 1080  
DB 1033 GCACCTACGTAATCTTAATTTTGAAGATTTGAGATTTATGTTGCAAGATATC 1092  
QY 1081 TACCATGAGAGAAACCTTATGTCAGATGGAACACTCAAGAGTACTTGTTCAT 1140  
DB 1093 TACCATGAGAGAAACCTTATGTCAGATGGAACACTCAAGAGTACTTGTTCAT 1152  
QY 1141 CCCAGTGGAAATGATGCTGAATATATATATATCTTCCGATCTTCTGCTGCT 1200  
DB 1153 CCCAGTGGAAATGATGCTGAATATATATATATCTTCCGATCTTCTGCTGCT 1212  
QY 1201 CGACTTTCCTTCAATTTGCTCTGTAAAGGCGAAAGGGGCTTAAAGAGAAACACTGT 1260  
DB 1213 CGACTTTCCTTCAATTTGCTCTGTAAAGGCGAAAGGGGCTTAAAGAGAAACACTGT 1272  
QY 1261 CCATTGGATGGGAAATATAACTTGTGATTAACAGACACTCTAGTATCTGAAAA 1320  
DB 1273 CCATTGGATGGGAAATATAACTTGTGATTAACAGACACTCTAGTATCTGAAAA 1332  
QY 1321 ATGCTTTGAATCTTTGGCCAGTACCTCATGATTAAGAAATTTGCTGAAACCTTATGCT 1380  
DB 1333 ATGCTTTGAATCTTTGGCCAGTACCTCATGATTAAGAAATTTGCTGAAACCTTATGCT 1392  
QY 1381 GTTACTGTGATCAATCCAAATTAAGAAACCTCATGCTAGAGTTGAGTGTGCTTC 1440  
DB 1393 GTTACTGTGATCAATCCAAATTAAGAAACCTCATGCTAGAGTTGAGTGTGCTTC 1452  
QY 1441 AGCAGTGTGTAAGATTTCCAGATATGTCAGTATTAAGAGATGCCAATTTGCTGTA 1500  
DB 1453 AGCAGTGTGTAAGATTTCCAGATATGTCAGTATTAAGAGATGCCAATTTGCTGTA 1512  
QY 1501 TCCGAGAGAGAGATTTAGCTATTTCCAGAGAGCTGATTAACAGACTAGCTAGAGAC 1560  
DB 1513 TCCGAGAGAGAGATTTAGCTATTTCCAGAGAGCTGATTAACAGACTAGCTAGAGAC 1572  
QY 1561 AATGAATTAAGGAAAAATGAAGAAAGAGCTCAAGCAATTTTCAACGAGATCTCTC 1620  
DB 1573 AATGAATTAAGGAAAAATGAAGAAAGAGCTCAAGCAATTTTCAACGAGATCTCTC 1632  
QY 1621 TCTGAATCACTGAGCAGAGAAAGATTTCTATGAGTCAAGACACTATTTGTAACT 1680  
DB 1633 TCTGAATCACTGAGCAGAGAAAGATTTCTATGAGTCAAGACACTATTTGTAACT 1692  
QY 1681 ATCCCGAAATTTCAACCAATTTGCTTGTCTGTTAATGAATTTAGAGATGAAGTA 1740

Db 1693 ATCCCGAAATTCACCCAAATTCCTCTGCTGTTAAATGGAATTCAGATGAAGTA 1752  
 Qy 1741 GCCCAGATGATATGCTGTGTAAGATATGGCTCCCAATCAAACTGAACAGGCTATGGA 1800  
 Db 1753 GCCCAGATGATATGCTGTGTAAGATATGGCTCCCAATCAAACTGAACAGGCTATGGA 1812  
 Qy 1801 CTTCTGAGCTGTAATTAACCCAGATCCATGTTGCAAGTTTCTGTTCCGTTGTTGGA 1860  
 Db 1813 CTTCTGAGCTGTAATTAACCCAGATCCATGTTGCAAGTTTCTGTTCCGTTGTTGGA 1872  
 Qy 1861 AAATATTAACAGATGACAAATCTTCTCAGATTTAATTCAGCTGTGACAGGCTCTAAA 1920  
 Db 1873 AAATATTAACAGATGACAAATCTTCTCAGATTTAATTCAGCTGTGACAGGCTCTAAA 1932  
 Qy 1921 TATGAACAATATTTGGATTAATCTGCTTGTGAGATTTTAACTGAGAAAGCATTTGACTAAT 1980  
 Db 1993 TATGAACAATATTTGGATTAATCTGCTTGTGAGATTTTAACTGAGAAAGCATTTGACTAAT 1992  
 Qy 1991 CAAGGATTTGGGACCTTTTCTTTTGGCATTTTAAATCTGAGATGACAAATTAACAGTT 2040  
 Db 1993 CAAGGATTTGGGACCTTTTCTTTTGGCATTTTAAATCTGAGATGACAAATTAACAGTT 2052  
 Qy 2041 AGCCGAGTTTGGGCTGCTTTTGGAGTCTTATTTGCTGTCATGTTGGATGTTATTTGAAG 2100  
 Db 2053 AGCCGAGTTTGGGCTGCTTTTGGAGTCTTATTTGCTGTCATGTTGGATGTTATTTGAAG 2112  
 Qy 2101 CACCTGAATATGAGCAAGTGCAGGCAATGAGAAAGCTCATTAATCTTAAGTACATTTCTCAA 2160  
 Db 2113 CACCTGAATATGAGCAAGTGCAGGCAATGAGAAAGCTCATTAATCTTAAGTACATTTCTCAA 2172  
 Qy 2161 CAGGAGAGAGAGATGAACACAAAAGGTACAGATGAAAGTTTAAAGTTAGCAAAATGAGG 2220  
 Db 2173 CAGGAGAGAGAGATGAACACAAAAGGTACAGATGAAAGTTTAAAGTTAGCAAAATGAGG 2232  
 Qy 2221 CGACCAAGTTTATGATGATGATGCTTACAGGCTGCTGCTCTCTTAAACCTCTCTCATCA 2280  
 Db 2233 CGACCAAGTTTATGATGATGATGCTTACAGGCTGCTGCTCTCTTAAACCTCTCTCATCA 2292  
 Qy 2281 CTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTAATGTTCTTGTCAAAAAAGGCGCATGTGG 2340  
 Db 2293 CTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTAATGTTCTTGTGTCAAAAAAGGCGCATGTGG 2352  
 Qy 2341 TTGAATTTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTTCAGAAACATGAGATCATC 2400  
 Db 2353 TTGAATTTGGGAGAACCCAGACATCATGTCAGAGTTACTGTTTTCAGAAACATGAGATCATC 2412  
 Qy 2401 TTTAAATATGCGGATGATTAAGGCAAGATATGCTTAACCTTCAATTAATTTGATATATG 2460  
 Db 2413 TTTAAATATGCGGATGATTAAGGCAAGATATGCTTAACCTTCAATTAATTTGATATATG 2472  
 Qy 2461 GAAATATCTGGCAAAATCAAGGCTGTGATCTTCGAATGTTAAGCTTATGATGTTGCTGTCA 2520  
 Db 2473 GAAATATCTGGCAAAATCAAGGCTGTGATCTTCGAATGTTAAGCTTATGATGTTGCTGTCA 2532  
 Qy 2521 ATCGGTGATCTGTGGGACTTATTAAGGTGTGTGCAAAATCTCACAATAATTAATGCAAAAT 2580  
 Db 2533 ATCGGTGATCTGTGGGACTTATTAAGGTGTGTGCAAAATCTCACAATAATTAATGCAAAAT 2592  
 Qy 2581 CAGTCAAAAGGCGGCTTGAAGGTGACCTGCACTTCAACGCAACACACTACATCAGTGG 2640  
 Db 2593 CAGTCAAAAGGCGGCTTGAAGGTGACCTGCACTTCAACGCAACACACTACATCAGTGG 2652  
 Qy 2641 CTCAAAGACAAAGACAAAGGAAATATATATGATGAGGCACTGACCTGTTTACAGTTCA 2700  
 Db 2653 CTCAAAGACAAAGACAAAGGAAATATATATGATGAGGCACTGACCTGTTTACAGTTCA 2712  
 Qy 2701 TGTGCTGATACCTGCTGATGCTTCACTTATTTGGAAATGAGATGCTGACAAATATGTAAC 2760  
 Db 2713 TGTGCTGATACCTGCTGATGCTTCACTTATTTGGAAATGAGATGCTGACAAATATGTAAC 2772  
 Qy 2761 ATCATGTTGAAAGACATGATGACAACTGTTTCAATATGATTTTGGACACTTTTGGATCAC 2820  
 Db 2773 ATCATGTTGAAAGACATGATGACAACTGTTTCAATATGATTTTGGACACTTTTGGATCAC 2832

Qy 2821 AAGAGAAAAATTTGTTATTAACGAGACGTGTGCCATTTGTTTGAACACAGATTTTC 2880  
 Db 2833 AAGAGAAAAATTTGTTATTAACGAGACGTGTGCCATTTGTTTGAACACAGATTTTC 2892  
 Qy 2881 TTAATATGATTTAGTAAAGAGACCCCAAGATGACAAAGACAAAGAAATTTGAGAGTTT 2940  
 Db 2893 TTAATATGATTTAGTAAAGAGACCCCAAGATGACAAAGACAAAGAAATTTGAGAGTTT 2952  
 Qy 2941 CAGGATGTTGTTACAGGCTTATCTAGCTATTGTCAGAGATGACCAATCTCTCTTAAT 3000  
 Db 2953 CAGGATGTTGTTACAGGCTTATCTAGCTATTGTCAGAGATGACCAATCTCTCTTAAT 3012  
 Qy 3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCGAGAACTACAAATCTTTTATGATGACATTCGA 3060  
 Db 3013 CTTTCTCAATGATGCTTGGCTCTGGAATGCGAGAACTACAAATCTTTTATGATGACATTCGA 3072  
 Qy 3061 TACATTCGAAAGACCTTACGCTTATGATTAATACTGACGAAGGCTTTGGATTTTCATG 3120  
 Db 3073 TACATTCGAAAGACCTTACGCTTATGATTAATACTGACGAAGGCTTTGGATTTTCATG 3132  
 Qy 3121 AAACAAATGATGATGACATCATGATGCTGGAACAACAAATGATGATTCGATC 3180  
 Db 3133 AAACAAATGATGATGACATCATGATGCTGGAACAACAAATGATGATTCGATC 3192  
 Qy 3181 ACAATTAACAGCATGCTTGAATGAAGATTAATCTGAGAAATGAAAGCTCACTCTGGA 3240  
 Db 3193 ACAATTAACAGCATGCTTGAATGAAGATTAATCTGAGAAATGAAAGCTCACTCTGGA 3252  
 Qy 3241 CACTACACTGCACTGTTATTAATCTCTGACAGGCAAGACCGATTCATAGGAATTCGAC 3300  
 Db 3253 TTTCCACTGCACTGTTATTAATCTCTGACAGGCAAGACCGATTCATAGGAATTCGAC 3312  
 Qy 3301 AATCATGAAGACCTTGAATTAATGAGCAAGCAAGCAATTAATTAATTAATTAATTA 3360  
 Db 3313 AATCATGAAGACCTTGAATTAATGAGCAAGCAAGCAATTAATTAATTAATTAATTA 3372  
 Qy 3361 TAATGTAACGCAAGAGGTTTGAATGACCTTAACTAGTTCAATTTCAAA 3412  
 Db 3373 TAATGTAACGCAAGAGGTTTGAATGACCTTAACTAGTTCAATTTCAAA 3424

RESULT 3  
 AAS14365  
 ID AAS14365 standard; cDNA; 3424 BP.  
 XX  
 AC AAS14365;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE cDNA encoding human p110alpha isoform of PI3-kinase.  
 XX  
 KW Human; phosphatidylinositol 3-kinase; PI3K; p110alpha isoform;  
 KW LAMP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;  
 KW autoimmune disease; inflammatory bowel disease; bacterial pneumonia;  
 KW Type I diabetes mellitus; cytostatic; immunosuppressive; ss.  
 OS Homo sapiens.  
 FT Key Location/Qualifiers  
 FT CDS 13..3219  
 FT /tag=a  
 FT /product="p110alpha isoform of PI3-kinase"  
 FN WO200185986-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 10-MAY-2001; 2001WO-US15065.  
 XX  
 PR 10-MAY-2000; 2000US-203346P.  
 XX  
 PA (ICOS-) ICOS CORP.





Db 1633 TCTGAATCACTGACAGAGAAAGATTTCTATGAGTCACAGACACTATTGTCTACT 1692  
Qy 1681 ATCCCGAAATTCATCCCAAATTTGCTTGTCTGTTAAATGGAAATTCAGATGAAGTA 1740  
Db 1693 ATCCCGAAATTCATCCCAAATTTGCTTGTCTGTTAAATGGAAATTCAGATGAAGTA 1752  
Qy 1741 GCCCAGATGTATGCTTGGTAAAGATTTGGCTCCAAATCAACCTGAACAGGCTATGGA 1800  
Db 1753 GCCCAGATGTATGCTTGGTAAAGATTTGGCTCCAAATCAACCTGAACAGGCTATGGA 1812  
Qy 1801 CTTCTGACTGTAAATTAACCAATCTATGTTCCAGGTTTGTCTGTTGGTGGTGGAA 1860  
Db 1813 CTTCTGACTGTAAATTAACCAATCTATGTTCCAGGTTTGTCTGTTGGTGGTGGAA 1872  
Qy 1861 AAATATTTAACAAGATGACAAACCTTCTCAGTATTTAATTCAGCTAGTACAGGCTCTAAA 1920  
Db 1873 AAATATTTAACAAGATGACAAACCTTCTCAGTATTTAATTCAGCTAGTACAGGCTCTAAA 1932  
Qy 1921 TATGAACAATATTTGGATTAATCTGCTGTGAGATTTTAACTGAGAAACATTTGACTAAT 1980  
Db 1933 TATGAACAATATTTGGATTAATCTGCTGTGAGATTTTAACTGAGAAACATTTGACTAAT 1992  
Qy 1981 CAAAGATTTGGGACCTTTTCTTTTGGCATTTAAATCTGAGATGACATTAACAGTT 2040  
Db 1993 CAAAGATTTGGGACCTTTTCTTTTGGCATTTAAATCTGAGATGACATTAACAGTT 2052  
Qy 2041 AGCCAGAGTTTGGGCTGCTTTTGGAGTCTATTTGCGTGCATGCGGAGTGTATTTGAAG 2100  
Db 2053 AGCCAGAGTTTGGGCTGCTTTTGGAGTCTATTTGCGTGCATGCGGAGTGTATTTGAAG 2112  
Qy 2101 CACTGAATATGAGCAAGTCAGGCAATGGAAGCTCATTAATCTTAACCTGACTCTCAA 2160  
Db 2113 CACTGAATATGAGCAAGTCAGGCAATGGAAGCTCATTAATCTTAACCTGACTCTCAA 2172  
Qy 2161 CAGGAGAGAGAGATGAAAACAATAAGTACAGATGAAGTTTGTAGCAATGAGG 2220  
Db 2173 CAGGAGAGAGAGATGAAAACAATAAGTACAGATGAAGTTTGTAGCAATGAGG 2232  
Qy 2221 GCACGAGATTTATGAGATGCTTACAGGCTTGTCTGCTCTCTAATCCTGCTCATGAA 2280  
Db 2233 GCACGAGATTTATGAGATGCTTACAGGCTTGTCTGCTCTCTAATCCTGCTCATGAA 2292  
Qy 2281 CTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTAATGCTTCTGCAAAAAGCCAGCTGG 2340  
Db 2293 CTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTAATGCTTCTGCAAAAAGCCAGCTGG 2352  
Qy 2341 TTGAATTTGGAGAACCCAGACATCATGTGAGATTACTGTTTCAAGAACATGAGATCATC 2400  
Db 2353 TTGAATTTGGAGAACCCAGACATCATGTGAGATTACTGTTTCAAGAACATGAGATCATC 2412  
Qy 2401 TTTAAATAATGGGAGATGATTTAGGGCAAGATATGCTTAACCTTCAATTAATTTGGTATTAG 2460  
Db 2413 TTTAAATAATGGGAGATGATTTAGGGCAAGATATGCTTAACCTTCAATTAATTTGGTATTAG 2472  
Qy 2461 GAAATATATCTGCAAAATCAAGGCTTGAATCTTGCAGATTTAATCTTATGTTGCTGTCA 2520  
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Qy 2521 ATCGGTACTGTGTGGGACTTATTTAGAGTGTGCGAAATTTCTCACTATTAATGCAAT 2580  
Db 2533 ATCGGTACTGTGTGGGACTTATTTAGAGTGTGCGAAATTTCTCACTATTAATGCAAT 2592  
Qy 2581 CAGTCCAAAGGCGGCTTGAAGTGCATGCGAGTTCAACAGCAACACATAATCAGTGG 2640  
Db 2593 CAGTCCAAAGGCGGCTTGAAGTGCATGCGAGTTCAACAGCAACACATAATCAGTGG 2652  
Qy 2641 CTCAAAGACAAGACAAGAGAAATATATGATGACGACATGACCTGTTTACAGCTTCA 2700  
Db 2653 CTCAAAGACAAGACAAGAGAAATATATGATGACGACATGACCTGTTTACAGCTTCA 2712  
Qy 2701 TGTGCTGATCTGTGTACTTACTTCAATTTTGGGAATTTGAGATGTCACAAATAGTAAAC 2760

Db 2713 TGTGCTGATCTGTGTACTTACTTCAATTTTGGGAATTTGAGATGTCACAAATAGTAAAC 2772  
Qy 2761 ATCATGTGAAAGACGATGACAACTGTTTCATATAGATTTTGGACACTTTTGGATCAC 2820  
Db 2773 ATCATGTGAAAGACGATGACAACTGTTTCATATAGATTTTGGACACTTTTGGATCAC 2832  
Qy 2821 AAGAAAGAAAATTTGGTTATTAACGAGACGTGTGCCATTTGTTTGAACACAGATTTTC 2880  
Db 2833 AAGAAAGAAAATTTGGTTATTAACGAGACGTGTGCCATTTGTTTGAACACAGATTTTC 2892  
Qy 2881 TTAATAGATTTAGTAAAGAGCCCAAGATGCAACAAAGACAAAGAAATTTGAGAGTTT 2940  
Db 2893 TTAATAGATTTAGTAAAGAGCCCAAGATGCAACAAAGACAAAGAAATTTGAGAGTTT 2952  
Qy 2941 CAGGAGATGTGTTCAAGGCTTATCTAGCTTATTCAGACAGCATGCCAATCTCTTCAAT 3000  
Db 2953 CAGGAGATGTGTTCAAGGCTTATCTAGCTTATTCAGACAGCATGCCAATCTCTTCAAT 3012  
Qy 3001 CTTTTCGCAATGATGCTTGGCTCTGGAAATGCCAGAACTTACATCTTTTGAATGACATTTGCA 3060  
Db 3013 CTTTTCGCAATGATGCTTGGCTCTGGAAATGCCAGAACTTACATCTTTTGAATGACATTTGCA 3072  
Qy 3061 TACATTCGAAAGACCCCTAGCCTTATAGATTAATACTGACAAAGGCTTTGGAGTATTTCAATG 3120  
Db 3073 TACATTCGAAAGACCCCTAGCCTTATAGATTAATACTGACAAAGGCTTTGGAGTATTTCAATG 3132  
Qy 3121 AAACAAATGAATGATGACATCATGCTGCTGAGCAACAAATAATGATTTGATCTTCAC 3180  
Db 3133 AAACAAATGAATGATGACATCATGCTGCTGAGCAACAAATAATGATTTGATCTTCAC 3192  
Qy 3181 ACAATTAACAGCATGATGATTAACCTGAAAGATTAACCTGAAAGATGATCTTCGGA 3240  
Db 3193 ACAATTAACAGCATGATGATTAACCTGAAAGATTAACCTGAAAGATGATCTTCGGA 3252  
Qy 3241 CACTACATCTGACCTTAAATTAATCTCTGACAGGCAAAACCGATTTGATGATTTGAC 3300  
Db 3253 TTCCACATCTGACCTTAAATTAATCTCTGACAGGCAAAACCGATTTGATGATTTGAC 3312  
Qy 3301 AATCCATGAACGCAATTAATTAATTAACGACAGAAACGAATTAATTAATTAATTAAT 3360  
Db 3313 AATCCATGAACGCAATTAATTAATTAACGACAGAAACGAATTAATTAATTAATTAAT 3372  
Qy 3361 TAATGTAAACGCAACAGGCTTTGATGACCTTAAATAGTTCAATTTCAAA 3412  
Db 3373 TAATGTAAACGCAACAGGCTTTGATGACCTTAAATAGTTCAATTTCAAA 3424

RESULT 4  
AA057012  
ID AA057012 standard; cDNA to mRNA; 3498 BP.  
XX  
AC AA057012;  
XX  
DT 25-MAR-2003 (updated)  
DT 31-AUG-1994 (first entry)  
XX  
XX  
XX PtdIns 3-kinase 110 kD catalytic subunit cDNA.  
KW 110 kD catalytic subunit; phosphatidylinositol 3-kinase;  
KW transformation; Schizosaccharomyces pombe; nmt promoter; thiamine;  
KW PtdIns 3-kinase; assay; detection; cell growth; regulation; cancer;  
KW blood vessel plaques; ss.  
XX  
OS Bos taurus.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..3207  
FT /\*tag= a  
FT /product= P110  
XX  
XX W09403609-A1.  
XX  
PD 17-FEB-1994.

XX 05-AUG-1993; 93WO-GB01651.  
XX  
XX 05-AUG-1992; 92GB-0016654.  
XX  
XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
XX  
XX Goode NT, Nurse PM, Parker PUJ, Waterfield MD;  
XX MPI; 1994-065697/08.  
XX P-PSDB; AAR46294.  
XX  
XX Eukaryotic cells transformed with mammalian phospholipid or  
PT protein kinase DNA - useful in assays for compounds involved in  
PT cell growth regulation and for treating cancers  
XX  
XX Disclosure; Fig 1; 71pp; English.  
XX  
XX This sequence encodes the 110 kd catalytic subunit of the phosphatidy1  
CC inositol (Ptdins) 3-kinase. This sequence was transformed into  
CC Schizosaccharomyces pombe cells under the regulatory control of the  
CC nmt promoter in an embodiment of the invention. In the presence of  
CC choline the promoter is inactive and the cells carrying the Ptdins  
CC catalytic subunit plasmid grow as the parental strain. In the absence  
CC of choline the nmt promoter functions and the Ptdins 3-kinase  
CC catalytic subunit is induced. Ptdins activity is substantially  
CC increased under these conditions. Cells containing constructs such as  
CC this, are useful in assays for detecting compounds involved in cell  
CC growth regulation. It is also used as the basis for detecting  
CC compounds for treating cancers and the formation of blood vessel  
CC plaques.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
CC  
CC Sequence 3498 BP; 1148 A; 627 C; 721 G; 1002 T; 0 other;  
SQ  
Query Match 91.9%; Score 3137; DB 15; Length 3498;  
Best Local Similarity 95.5%; Pred. No. 0;  
Matches 3261; Conservative 0; Mismatches 145; Indels 7; Gaps 3;  
QY 1 ATGCCCTCCAAAGACATCATCAGTGAACCTGTGGGGCATCCACTGTAGCCCCCAAGAAC 60  
DB 1 ATGCCCTCCAAAGACATCATCAGTGAACCTGTGGGGCATCCACTGTAGCCCCCAAGAAC 60  
QY 61 CTAGTGAATGTTTACTACCAATGGAATGATGATGATGATGATGATGATGATGATGATG 120  
DB 61 CTAGTGAATGTTTACTACCAATGGAATGATGATGATGATGATGATGATGATGATGATG 120  
QY 121 ACATTAGTACTATAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180  
DB 121 ACATTAGTACTATAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180  
QY 181 CTTCCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
DB 181 CTTCCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
QY 241 GAATTTTTTGAAGAAACAGACACTTTGTGATCTTCGGCTTTTCAACCAATTTTAAAA 300  
DB 241 GAATTTTTTGAAGAAACAGACACTTTGTGATCTTCGGCTTTTCAACCAATTTTAAAA 300  
QY 301 GTAATTTGAACCAAGTGGCAACCGTGAAGAAAGATCTCAATCGAATAATGGTTTGTCT 360  
DB 301 GTAATTTGAACCAAGTGGCAACCGTGAAGAAAGATCTCAATCGAATAATGGTTTGTCT 360  
QY 361 ATCGGATGCCAGTGTGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATG 420  
DB 361 ATCGGATGCCAGTGTGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATG 420  
QY 421 AGAAATATTTCTTAATGTTTGAAGAGCTGTGATCTTAAGGATCTTAATTCACCTCAT 480  
DB 421 AGAAATATTTCTTAATGTTTGAAGAGCTGTGATCTTAAGGATCTTAATTCACCTCAT 480  
QY 481 AGTAGAGCAATGTATGTATCGGCAATGTAGATCTTTCACGAGAGTCCCAAGCAC 540

DB 481 AGTAGAGCAATGTATGTATCTCCAAATGTAGAACTTTCACGAGAGTCCCAAGCAC 540  
QY 541 ATATATATAAATTGGATAGAGCCCAATATATAGTGTGATTTGGTAAATAGTTCTCCA 600  
DB 541 ATATATATAAATTGGATAGAGCCCAATATATAGTGTGATTTGGTAAATAGTTCTCCA 600  
QY 601 AATATGACACAGACAGATATCTGAAATATCAACCATGACTGTGTGCCAGACAGTA 660  
DB 601 AATATGACACAGACAGATATCTGAAATATCAACCATGACTGTGTGCCAGACAGTA 660  
QY 661 ATTGCTGAAGCATACAGAAAAAACTGAAATATGTTGCTCATCTGAAATATTA 720  
DB 661 ATTGCTGAAGCATACAGAAAAAACTGAAATATGTTGCTCATCTGAAATATTA 720  
QY 721 CTCTGTGTTTGAATATCAGGCAAGTATTTTAAAGTGTGATGATGATGATGATGATG 780  
DB 721 CTCTGTGTTTGAATATCAGGCAAGTATTTTAAAGTGTGATGATGATGATGATGATG 780  
QY 781 TTCTTGAAAAATATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 840  
DB 781 TTCTTGAAAAATATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 840  
QY 841 AGGATGCCAATTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900  
DB 841 AGGATGCCAATTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900  
QY 901 TGTTTTACATGCCATCTTATTCAGAGCATTTTCAGAGCATCATATATGATGATGATG 960  
DB 901 TGTTTTACATGCCATCTTATTCAGAGCATTTTCAGAGCATCATATATGATGATGATG 960  
QY 961 GAAACATCTACAAAATCCCTTGGGTATTAATAGACATCAGAAATAAAATCTTTGT 1020  
DB 961 GAAACATCTACAAAATCCCTTGGGTATTAATAGACATCAGAAATAAAATCTTTGT 1020  
QY 1021 GCAACCTAGGAAATCTAATTTGAGACATGTCAGAAATTTATGTTGCAAGATGATG 1080  
DB 1021 GCAACCTAGGAAATCTAATTTGAGACATGTCAGAAATTTATGTTGCAAGATGATG 1080  
QY 1081 TACCATGAGAGAAACCTTATGTGACATGTAACATCTCAAAAGATACCTTTGCCAAT 1140  
DB 1081 TACCATGAGAGAAACCTTATGTATGTATGATGATGATGATGATGATGATGATGATG 1140  
QY 1141 CCCAGTGAATGAATGCTGATATATATATATATATATATATATATATATATATATAT 1200  
DB 1141 CCCAGTGAATGAATGCTGATATATATATATATATATATATATATATATATATATAT 1200  
QY 1201 GCACTTGGCTTTCATTTGCTGTGTAAGGCGAAAGGGGCTAAAGAGGAACAATCT 1260  
DB 1201 GCACTTGGCTTTCATTTGCTGTGTAAGGCGAAAGGGGCTAAAGAGGAACAATCT 1260  
QY 1261 CCATTGGATGGGAAATATAAATCTGTTGATTAACAGACACTCTAGTATCTGAAAA 1320  
DB 1261 CCATTGGATGGGAAATATAAATCTGTTGATTAACAGACACTCTAGTATCTGAAAA 1320  
QY 1321 ATGCTTTGATCTTTGGCCAGTACCTATGATGATGATGATGATGATGATGATGATGAT 1380  
DB 1321 ATGCTTTGATCTTTGGCCAGTACCTATGATGATGATGATGATGATGATGATGATGAT 1380  
QY 1381 GTTACTGATCAATCCAAATTAAGAAACCTCATGATGATGATGATGATGATGATGATG 1440  
DB 1381 GTTACTGATCAATCCAAATTAAGAAACCTCATGATGATGATGATGATGATGATGATG 1440  
QY 1441 AGCAGTGTGTTAAATGTTCCAGATATGTGATGATGATGATGATGATGATGATGATGAT 1500  
DB 1441 AGCAGTGTGTTAAATGTTCCAGATATGTGATGATGATGATGATGATGATGATGATGAT 1500  
QY 1501 TCCGAGAGAGAGATTTAGCTATTTCCAGAGAGCTGAGTACAGACTAGCTAGAGAC 1560  
DB 1501 TCCGAGAGAGAGATTTAGCTATTTCCAGAGAGCTGAGTACAGACTAGCTAGAGAC 1560  
QY 1561 AATGAATTAAGGAAAAAGACAAAGAACAGCTCAAAAGCAATTTTCAACGAGATCTCTC 1620  
DB 1561 AATGAATTAAGGAAAAAGACAAAGAACAGCTCCAGCAATTTTGAACGAGATCTCTCTA 1620

QY	1621	TCGAAATCACTGAGCAGAGAGAAGATTTTCTATGAGACTCAACACACTATTGTGTAACT	1680
Db	1621	TCTGAAATCACTGAGCAGAGAGAAGATTTTCTGTGAGACCACACACATAATTGTGTAACT	1680
QY	1681	ATCCCCGAAATTCTACCCAAATTGGTCTGCTGCTGTTAAATGGAAATTCAGAGATGAAGTA	1740
Db	1681	ATCCCCGAAATTCACCCAAATTGGTCTGCTGCTGTTAAATGGAACTCAGAGATGAAGTA	1740
QY	1741	GCCCAATGATATTCCTGGTAAAGAAATGGGCTCCCAATCAAACTGAAACAGGCTATGGAA	1800
Db	1741	GCTCAGATGTACTGCTGGTAAAGAAATTTGGGCTCCCAATCAAACTGAAACAGGCTATGGAG	1800
QY	1801	CTTCTGGACTGTAAATTAATCCCAATCTTATGTTGCAAGGTTTTGCTGTTCCGTCTGGAA	1860
Db	1801	CTTCTGGACTGTCAAAATTTACCACAGATCCCTATGTTTCAGAGTTTTGCTGTTCCGTCTGGAA	1860
QY	1861	AAATATTTAACGATGACAAACTTTCTCAGTATTTAATTCAGAGCTAGTACAGTCCCTAAA	1920
Db	1861	AAATATTTAACGATGACAAACTTTCTCAGTACTTAATTCAGCTATGTCAGAGTACTAAA	1920
QY	1921	TATGAACAATAATTTGGATPACTTGTGTGAGATTTTACTGAAGAAAGCAATTGACTAAT	1980
Db	1921	TATGAACAAGTATTTGGATPAACCTGCTGTGAGATTTTACTCAAAAAGCTPAACTAAT	1980
QY	1981	CAAGAGATTGGCACTTTTCTTTTGGCATTTAAATCTGAGATGACAAATPAACGTT	2040
Db	1981	CAAGAGATCGGTCATTTTCTTTTGGCATTTAAATCTGAGATGCAACAAATPAACGTT	2040
QY	2041	AGCCAGAGSTTTGGCTGCTTTTGGAGTCTATTGTGCTGATATGGGATGTATTGGAG	2100
Db	2041	AGTCAGAGSTTTGGCTGCTTTTGGAGTCTATTGTGCTGATATGGGATGTATTGTAAG	2100
QY	2101	CACCTGAATAGCAAGTGCAGAGCAATGAAAAAGCTATTAACCTAACGATTCCTAAA	2160
Db	2101	CACCTTAATAGGCAAGTGAAGGCTATGAAAAAGCTATTAACCTAACGATTCCTAAA	2160
QY	2161	CAGAGAGAAAGATGAAACACAAAAGGTACAGATGAAGTTTATAGTTAGCAATATGAG	2220
Db	2161	CAAGGAAAGAAAGATGAAACACAAAAGGTATCAAGATGAAGTTTATAGTTAGCAAAATGCG	2220
QY	2221	CGACCAGATTCATGATGATGCCCTACAGGGCTTGCTGTCCTCTPAAACCTCGTCATCA	2280
Db	2221	CGACCAGATTCATGATGATGCTCTCAGGGCTTTCTGTCTCTCTPAAACCTCGTCATCAG	2280
QY	2281	CTAGGAAACCTCAGGCTTAAAGATGTGAAATTATGTCTTCTGCAAAAAGCCACTGTGG	2340
Db	2281	CTGGGAAATCTCAGGCTTAAAGAGTGTGAAATTAATGTCTTCTGCAAAAAGCCACTGTGG	2340
QY	2341	TTGAATTTGGGAGAACCCAGACATCATGTCAAGATTAATCTGTTTCAGAACATGAGATCATC	2400
Db	2341	TTGAATTTGGGAGAACCCAGACATCATGTCAAAATTAATCTTTCAGAACAAAGAGATCATC	2400
QY	2401	TTTAAATAATGGGGATGATTTTACGGCAAGATATGTCTCAACCTTCAAAATTAATCGATTATG	2460
Db	2401	TTTAAATAATGGGGATGATTTTACGGCAAGATATGTCTCAACCTTCAAGATTATTCGACTTA	2460
QY	2461	GAAAAATATCTGGCAAAATCAAGATCTTGATCTTGCATGTTTACCTTAATGATGTGTGTCA	2520
Db	2461	GAAAAATATCTGGCAAAATCAAGATCTTGTATCTTGCATGTTTACCTTAATGATGTGTGTCA	2520
QY	2521	ATCGGTGACTGTGTGGCACTTATGAGTGTGTGGCAAAATTTCTCAACATTAATATGCAAAAT	2580
Db	2521	ATCGGTGACTGTGTGGCACTTATCAAGATGTGTGGCAAAATTTCTCAACATTAATATCAAAAT	2580
QY	2581	CAGTGCAAAGCGGCTGTGAAAGGTGTCACTGCAGTTCAACAGCCACACACTCATCATGTTGG	2640
Db	2581	CAGTGTAAAGAGGCGCTGAAGGTGTCACTGCAGTTTAAACACCCACACACTCATCATGTTGG	2640
QY	2641	CTCAAAAGCAAGAACAAAGAGAAATATATATATGCAAGCCATTTGACTGTGTTTACAGTTTCA	2700
Db	2641	CTCAAAAGCAAGAACAAAGGGGAAATATATATATGATGCGGCCATTCGATTTGTTTACACGATCA	2700

Oy		2701	TGTGCTGGATAC	TGTGTAGCTTCACTTCATTTTGGGAATTGGAAATCGTCACATAAGTAAC	2760
Db		2701	TGTGCTGGATAT	TGTGTAGCTTCCACCCTCATTTTTGGGAATTGGAAATCGTCACATAAGTAAT	2760
Oy		2761	ATCATTGGGAAGA	GCATGAGCAACTGCTTTCACTAATTTTGACACTTTTGGATCAC	2820
Db		2761	ATCATTGGTTAA	GATGATGACAACCTGTTCTATATTAATTTTGGACCTTTTGGATCAC	2820
Oy		2821	AAGAAGAAAAA	ATTTGGTTATPAAACGAGAACGTTGSCATTTGTTTTGACACAGATTTTC	2880
Db		2821	AAGAAGAAAAA	ATTTGGTTATPAAACGAGAACGCCGCGCTTTGTTTGAACAAGATTTTC	2880
Oy		2881	TTAATAGTAGTA	TTAGTAAAGAGCCCAAGATGCAAAAGACAAAGAAATTTGAGAGGTTT	2940
Db		2881	TTAATAGTAGTA	TTAGTAAAGAGCCCAAGATGCAAAAGACAAAGAAATTTGAGAGGTTT	2940
Oy		2941	CAGAGATGCTTT	CAAGGCTTACTCTAGCTATTTGACAGCATGCGCATCTTCATATAAT	3000
Db		2941	CAGAGATGCTTT	CAAGGCTTACTCTAGCTATTTGACAGCATGCGCATCTTCATATAAT	3000
Oy		3001	CTTTTCTCAAT	GATGATGCTTGGCTCTGGAATGCGCAACCTCAATCTTTTGAATGACATGCA	3060
Db		3001	CTTTTCTCAAT	GATGATGCTTGGCTCTGGAATGCGCAACCTCAATCTTTTGAATGACATGCA	3060
Oy		3061	TACATTGGAAG	AGCCCTAGCCCTTAGATPAAAACCTGAGCAAGAGGCTTTGGAGTATTTGATG	3120
Db		3061	TACATTGGAAG	AGCCCTAGCCCTTAGATPAAAACCTGAGCAAGAGGCTTTGGAGTATTTGATG	3120
Oy		3121	AAACCAAATGA	TATGATGCATCATGCTGGCTGGAACAACAAAATGGAATTGGATCTTCCAC	3180
Db		3121	AAACCAAATGA	TATGATGCACACCATGCTGGCTGGAACAACAAAATGGAATTGGATCTTCCAC	3180
Oy		3181	ACAATTAAAC	GACATGCACTGTAACCTGAGAAAGATACTGAGAAATGAAAGCTCACTCTGGA	3240
Db		3181	ACAATTAAAC	GACATGCACTGCTTTAACTGAATATATATCTAATTAAGCT----CAGTATCTGGA	3225
Oy		3241	CACTACACTG	CACTGTTAATTAATCTCTGACGAGGCAAGACCCGATTTGATAGGAATTGCAC	3300
Db		3236	TTCTACACTG	CACCTGTTAATTAATCTCTGCAACGAGCAAGACTGATTTGATAGGAATTGCAC	3295
Oy		3301	AATCATGAA	CAGCATTTG--ATTACACGAAGAACAGAAATTAATCTATATTAATTTAA	3359
Db		3296	AATCATGAA	CAGCATTTGAAATTTACGACAAGAACAGAAATTAATCTATATTAATTTAA	3355
Oy		3360	ATAATGTAA	ACGCAACGAGGTTGATAGCACTTAACTAGTCATTTCAAAA	3412
Db		3356	ATAATGTAA	ACGCAACGAGGTTGATAGCAC-TAACTAGTCATTTCAAAA	3407
<b>RESULT 5</b>					
AAO51155					
ID	AAO51155	standard;	CDNA:	3207 BP.	
XX	AAO51155;				
XX					
DT	25-MAR-2003	(updated)			
DT	09-JAN-2003	(updated)			
DT	12-APR-1994	(first entry)			
XX					
DE	p110 CDNA.				
XX					
KW	Phosphoinositide kinase; PI; p85 subunit; screening; agonist;				
KW	antagonist; cell proliferation; inhibition; propylaxis; therapy;				
KW	platelets; neutrophil activity; 3-phosphorylated phosphoinositides;				
XX	ss.				
OS	Homo sapiens.				
XX					
PH	Key	location/Qualifiers			
FT	CDS	1..3207			
FT		/tag= a			
FT		/note= "pi3- kinase p110"			
XX					



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Db      1501  TCCCGTGAAGCAGATTAGTTATTCCTGAGGAGCTGATGACGACTGACTAGAGAC 1560
Qy      1561  AATGATTAAGGAAAATAGCAAAAGACAGCTCAAGCAATTTCTACAGAGATCCTGC 1620
Db      1561  AATGATTAAGGAAAATAGTAAGAACAGCTCCAGCAATTTGTCAGAGATCCTCTA 1620
Qy      1621  TCTGAATCTAGCAGAGAGAAAAGATTTCTATGAGAGTCAGACACTATTGTGTA 1680
Db      1621  TCTGAATCTAGCAGAGAGAAAAGATTTCTGATGAGCCACAGACACTATTGTGTA 1680
Qy      1681  ATCCCGAAATCTACCCAAATTTGCTCTGTCTGTTAAATGGAATTTGAGATGA 1740
Db      1681  ATCCCGAAATCTACCCAAATTTGCTCTGTCTGTTAAATGGAATTTGAGATGA 1740
Qy      1741  GCCCAGATGATTTGCTGTTAAAGATGGCCCTCCATCAATCAAGCTGAA 1800
Db      1741  GCTCAGATTAAGCTGTTGTTAAAGATGGCTCCATCAAGCTGAAAGGCTATGAG 1800
Qy      1801  CTTCGTGACTGTAATTAACCAAGTCTATGTTGAGGTTGCTGTTGCTGTTGAA 1860
Db      1801  CTTCGTGACTGCAATTAACCAAGTCTATGTTGAGGTTGCTGTTGCTGTTGAA 1860
Qy      1861  AAATATTTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGT 1920
Db      1861  AAATATTTTAACAGATGACAAACTTTCTCAGTATTTAATTCAGCTAGTACAGT 1920
Qy      1921  TATGAACAATATTTGGATTAAGTCTGAGATTTTCTGAGAGAAACATTTGACTAT 1980
Db      1921  TATGAACAATATTTGGATTAAGTCTGAGATTTTCTGAGAGAAACATTTGACTAT 1980
Qy      1981  CAAGAGATGGGACACTTTTCTTTTGGCAATTTAAATCTGAGATGACAAATCA 2040
Db      1981  CAAGAGATGGGACACTTTTCTTTTGGCAATTTAAATCTGAGATGACAAATCA 2040
Qy      2041  AGCCGAGGTTTGGCTGCTTTTGGAGTCTTATGTCGATGAGGAGTGTATTTGA 2100
Db      2041  AGTCAGAGGTTTGGCTGCTTTTGGAGTCTTATGTCGATGAGGAGTGTATTTGA 2100
Qy      2101  CACCTGAATATGAGCAAGTGGAGGCAATGGAAGAGCTCATTAACCTGACATTC 2160
Db      2101  CACCTGAATATGAGCAAGTGGAGGCAATGGAAGAGCTCATTAACCTGACATTC 2160
Qy      2161  CAGGAGAGAGAGATGAAACACAAAAGATGACAGATGAAATTTTATGAGCAAA 2220
Db      2161  CAGGAGAGAGAGATGAAACACAAAAGATGACAGATGAAATTTTATGAGCAAA 2220
Qy      2221  CGACCAAGATTTATGATGATGCCCTTAACAGGCTTGTCTCTTAAACCTGCT 2280
Db      2221  CGACCAAGATTTATGATGATGCCCTTCAAGGCTTGTCTCTTAAACCTGCTCAT 2280
Qy      2281  CTAGGAAACCTCAGGCTTAAAGAGTGTGCAATTAATGCTTCTGCAAAAAGG 2340
Db      2281  CTGGAAGATCTCAGGCTTGAAGAGTGTGCAATTAATGCTTCTGCAAAAAGG 2340
Qy      2341  TTGAATTTGGGAGAACCCAGACATCATGTGAGATTTACTTTTCAGAACATGA 2400
Db      2341  TTGAATTTGGGAGAACCCAGACATCATGTGAGATTTACTTTTCAGAACATGA 2400
Qy      2401  TTTAAAAATGGGATGATTTACGGCAAGATATGCTAACACTTCAAAATTA 2460
Db      2401  TTTAAAAATGGGATGATTTACGGCAAGATATGCTAACACTTCAAAATTA 2460
Qy      2461  GAAATATCTGGCAAAATCAAGCTCTGATCTTCCAAATTTACCTTAAGTGT 2520
Db      2461  GAAATATCTGGCAAAATCAAGCTCTGATCTTCCAAATTTACCTTAAGTGT 2520
Qy      2521  ATCGGTGACTGTGTGGACTTATTAAGGTGTGCAAAATTTCCACACTTA 2580
Db      2521  ATCGGTGACTGTGTGGACTTATTAAGGTGTGCAAAATTTCCACACTTA 2580
Qy      2581  CAGTCAAAAGCGGCTTGAAGGTGCACTGCAATTCAGGCAACACTACATG 2640

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Db      2581  CAGTCAAAAGCGGCTTGAAGGTGCACTGCAATTTAAACGCCACACTC 2640
Qy      2641  CTCAAGACCAAGAACAAAGAGAAATATATGATGAGCAGCATGACCTGTTA 2700
Db      2641  CTCAAGACCAAGAACAAAGGGAATATATGATGAGGCGCATGATTTGTTAC 2700
Qy      2701  TGTGCTGATATCTGTGTAGTACTTCACTTTTGGGAATTTGAGATGTCAT 2760
Db      2701  TGTGCTGATATTTGTGTGTCACCTTCAATTTTGGGAATTTGAGATGTCAT 2760
Qy      2761  ATCATGTGGAAGAGAGATGACACTGTTTCAATATAGATTTTGGACACT 2820
Db      2761  ATCATGTGGAAGAGATGACACTGTTTCAATATAGATTTTGGACACTTTT 2820
Qy      2821  AAGAGAAAATTTGTTATTAACGAGAGTGTGCCATTTGTTTGAACAGAT 2880
Db      2821  AAGAGAAAATTTGTTATTAACGAGAGTGTGCCATTTGTTTGAACAGAT 2880
Qy      2881  TTAATAGTATTAAGTAAAGAGCCCAAGATGACAAAGAGAAATTTGAG 2940
Db      2881  TTAATAGTATTAAGTAAAGAGCCCAAGATGACAAAGAGAAATTTGAG 2940
Qy      2941  CAGGAGATGTGTACAGGCTTATCTAGCTATTGACAGCATGCCAATCTCT 3000
Db      2941  CAGGAGATGTGTACAGGCTTATCTAGCTATTGACAGCATGCCAATCTCT 3000
Qy      3001  CTTTCTCAATGATGCTTGGCTGGAATGGCAGAACTACAAATCTTTGATG 3060
Db      3001  CTTTCTCAATGATGCTTGGCTGGAATGGCAGAACTACAAATCTTTGATG 3060
Qy      3061  TACATTCGAAAGACCTTACCTTATGATTAACCTGACAGAGCTTTGAG 3120
Db      3061  TACATTCGAAAGACCTTACCTTATGATTAACCTGACAGAGCTTTGAG 3120
Qy      3121  AAACAAATGAATGATGACATCATGATGCTGTCGACACAAATAATGAT 3180
Db      3121  AAACAAATGAATGATGACACCATGATGCTGTCGACACAAATAATGAT 3180
Qy      3181  ACAATTAACGACATGCACTGAACCTGA 3207
Db      3181  ACAATTAACGACATGCTTGAACCTGA 3207

RESULT 6
AAA02190
ID AAA02190 standard; cDNA, 741 BP.
XX
XX AAA02190;
AC
XX
XX
DT 19-MAY-2000 (first entry)
XX
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2181.
XX
XX Human; colon cancer; tumour; diagnosis; gene expression product;
XX probe; detection; cancerous state; metastasis; identification;
XX breast cancer; oestrogen receptor-positive breast cancer; therapy;
XX oestrogen receptor-negative breast cancer; lung cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX
XX MO9958675-A2.
PN
XX
XX 18-NOV-1999.
PD
XX
XX 13-MAY-1999; 99WO-US10602.
PF
XX
XX 14-MAY-1998; 98US-0085426.
PR 15-MAY-1998; 98US-0085537.
PR 15-MAY-1998; 98US-0085696.
PR 21-OCT-1998; 98US-0105234.
PR 27-OCT-1998; 98US-0105877.
XX
XX (CHIR ) CHIRON CORP.
PA

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PA (HYSF-) HYSFO INC.  
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J,  
PI Reinhard C, Glese K, Randazzo F, Kennedy GC, Pot D, Kassam A,  
PI Lamsom G, Drmanac R, Civenjakov R, Dickson M, Drmanac S, Labat I,  
PI Leshkowitz D, Kita D, Garcia V, Jones LM, Stache-Crain B,  
XX MPI, 2000-126369/11.  
XX  
XX Polynucleotide library used to determine cancerous states of mammalian  
PT cells -  
XX  
XX Claim 1, Page 850; 1097pp; English.  
XX  
XX AAA00010 to AAA02716 represent polynucleotides isolated from cDNA  
CC libraries constructed from human colon cancer cell lines. The present  
CC invention also describes a method of detecting differentially expressed  
CC genes correlated with a cancerous state of a mammalian cell, comprising  
CC detecting at least one differentially expressed gene product in a test  
CC sample derived from a cell suspected of being cancerous, where detection  
CC of the differentially expressed gene product is correlated with a  
CC cancerous state of the cell from which the test sample was derived.  
CC The polynucleotides sequences can be used in a method for detecting  
CC differentially expressed genes correlated with a cancerous state of a  
CC mammalian cell. The polynucleotides can also be used as probes for  
CC detecting and mapping related genes. They can be used in diagnosis and  
CC prognosis of diseases and disorders (e.g. identification of  
CC pre-metastatic or metastatic cancerous states, stages of cancer, or  
CC responsiveness of cancer to therapy). This is particularly for breast  
CC cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-  
CC negative breast cancer, lung cancer, and colon cancer.  
XX  
XX Sequence 741 BP; 221 A; 137 C; 154 G; 208 T; 21 other;  
SQ  
Query Match 16.5%; Score 564; DB 21; Length 741;  
Best Local Similarity 93.0%; Pred. No. 6.3e-138;  
Matches 661; Conservative 0; Mismatches 41; Indels 9; Gaps 7;  
QY 2182 CAAAGGTAAGATGAGTTTGTAGTGAAGCAATGAGGCGACAG-ATTTCATGATGC 2240.  
DB 18 CAAAGGTAAGATGAGTTTGTAGTGAAGGCGACAGCAAAATTTCATGATGC 77  
QY 2241 CCTACAGGGCTTGC-TGTCTCTCTTAACCTCTCTCATCACTAGCAAACTTAGCTTA 2299  
DB 78 TCTACAGGGCTTCTTCTCTCTTAACCTCTCTCATCACTAGCAAACTTAGCTTA 137  
QY 2300 AAGAGTGTGAATATGATCTTCTGCAAAAAGGCGACGTGTGTAATGGAGAACCCAG 2359  
DB 138 AAGAGTGTGAATATGATCTTCTGCAAAAAGGCGACGTGTGTAATGGAGAACCCAG 197  
QY 2360 ACATCATGTCAAGTACTCTTTCAGAACATGAGATCATCTTTAAAAATGGGATGAT 2419  
DB 198 ACATCATGTCAAGTACTCTTTCAGAACATGAGATCATCTTTAAAAATGGGATGAT 257  
QY 2420 TACGGCAAAATATGCTTAACACTTCAAAATTTGTTATGAAAAATATCTGGCAAAATC 2479  
DB 258 TACGGCAAAATATGCTTAACACTTCAAAATTTGTTATGAAAAATATCTGGCAAAATC 317  
QY 2480 AAGGTTGATCTTGAATGTAACCTTATGTTGTGTCATCGGTGACTGTGGGAC 2539  
DB 318 AAGGTTGATCTTGAATGTAACCTTATGTTGTGTCATCGGTGACTGTGGGAC 377  
QY 2540 TTATTGAGGTGTGCGAAATTTCTACACTATTATGCAAAATTCAGTCAAGGCGGCTTA 2599  
DB 378 TTATTGAGGTGTGCGAAATTTCTACACTATTATGCAAAATTCAGTCAAGGCGGCTTA 437  
QY 2600 AAGGTGCACTGCACTTCAACAGCGACACACTACATAGTGGCTCAAAAGCAAGAACAA 2658  
DB 438 AAGGTGCTC-CTGCAAGTTCACAGCGACACACTACATAGTGGCTCAAAAGCAAGAACAA 496  
QY 2659 GGAGAAATATATGATGACAGCACTGACCTGTTTAC-CGTTGATGTCGTGATACGTGT 2717  
DB 497 GGAGAAATATATGATGACAGCACTGACCTGTTTAC-CGTTGATGTCGTGATACGTGT 556

QY 2718 AGCTACCTTCATTTTGG-GAATTGAGATGTCACAAATAGTAACATCATGCTGGAAGACG 2776  
DB 557 AGCTACCTTCATTTTGGCGAAATTTGAGATGTCACAAATAGTAACATCATGAGCAAGACG 616  
QY 2777 ATGCACTGTTTCAATAGATTTTGGACACTTTTGGATCACAAGAGAAAAATTTG 2836  
DB 617 ATGCACTGTTTCAATAGATTTTGGACACTTTTGGATCACAAGAGAAAAATTTT 676  
QY 2837 GTTATTAACGAGAACGTGTG--CCATTGTTTGGACACAGGATTTCTTA 2884  
DB 677 GGTATTAACGAGAACGATGTCATTTTGTGTTGACACGCAATTCCTTA 727  
RESULT 7  
AAC65690  
ID AAC65690 standard; DNA; 3213 BP.  
XX  
XX AAC65690;  
AC  
XX 16-FEB-2001 (first entry)  
DT  
XX  
DE Human p13 kinase pllobeta DNA.  
XX  
XX Human; p13 kinase p110 beta; antisense inhibition; primer: cytostatic;  
XX antiinflammatory; antiinfective; ds.  
XX  
XX Homo sapiens.  
XX  
XX US6133032-A.  
PN  
XX 17-OCT-2000.  
PD  
XX  
XX 09-SEP-1999; 99US-0392350.  
PF  
XX  
XX 09-SEP-1999; 99US-0392350.  
PR  
XX  
XX (ISIS-) ISIS PHARM INC.  
PA  
XX  
XX Monia BP, Cowser LM;  
PI  
XX  
XX MPI; 2000-686014/67.  
DR  
XX  
XX P-PSDB; AAB11124.  
PT  
XX  
PT Antisense compound 8-30 nucleobases in length targeted to a start codon  
PT of the coding region of human p13 kinase pllobeta, useful for  
PT inhibiting the expression of the human polynucleotide -  
PS  
XX Example 1; Column 43-50; 34pp; English.  
XX  
XX This invention describes a novel antisense compound (I) 8-30 nucleobases  
XX in length targeted to a start codon or nucleobases 4-1174 of the coding  
XX region of human p13 kinase pllobeta (II), in which (I) specifically  
XX hybridizes with and inhibits the expression of (II). The products of the  
XX invention have cytostatic, antiinflammatory and antiinfective activity.  
XX (I) is useful for inhibiting the expression of (II) in human cells or  
XX tissues. The antisense compound can be utilized for diagnostics,  
XX therapeutics, prophylaxis and as research reagents and kits. The  
XX antisense compounds may also be useful prophylactically, e.g. to prevent  
XX or delay infection, inflammation or tumor formation. The antisense  
XX compounds are useful for research and diagnostics, because these  
XX compounds hybridize to nucleic acids encoding (II).  
SQ  
Sequence 3213 BP; 979 A; 612 C; 704 G; 918 T; 0 other;  
Query Match 13.5%; Score 460.8; DB 21; Length 3213;  
Best Local Similarity 50.4%; Pred. No. 1.8e-110;  
Matches 1597; Conservative 0; Mismatches 1467; Indels 106; Gaps 15;  
QY 58 ATCTGAGGATGTTTACTACCAATGAGATGATGACTTTAGATGCTCGGTGAG 117  
DB 88 ATCTGAGGATGTTTCTTTGTCACCTGGATTTATATCACTGAGACTCTCGGAA 147

QY 118 GGTACATTAGTACTATTAAGCATGACTATTTTAAAGAAAGAAATACCTCTCAT 177  
Db 148 GGTACACTTTCTTAATTAATGAGCATGTATGGAAGCAAGTTCACAAATACCCAAATGTTCC 207  
QY 178 CAACCTCTTCAAGATGAATCTTCTTAACATTTTGTGTAAGTGTACCCAAAGACAGAAAG 237  
Db 208 AACCTCTTATGATATTTGACTCTTAATATGTTGGCATGTGTAAATCAGACTCTGTATAT 267  
QY 238 GAAGATTTTTTGTATGAAACAAGACGCTTTGTGATCTTGGCTTTTCAACATTTTAA 297  
Db 268 GAGAGGCTTGAAGATGAAGAACAGAGACTCTGTGATGTACAGACTTTTCTTCAAGTCTTC 327  
QY 298 AAAGTAATTTGAACAGTAGCAACCGTGAAGAAAGATCTTCAATCAGAGAAATGGTTT 357  
Db 328 AAATTAAGTACAAGAGTGTGACCCAGGGGAAAA--ATTAGACTCAAAAAATTGGAGTC 384  
QY 358 GGTATCGGATGCCAGTGGCGAATTTGATATGTTAAAGATCTTGAAGTACAGACTTC 417  
Db 385 CTTATAGGAAAAAGTCTGATGAATTTGATCTTGAAGATCTGAAATTAATGAATTT 444  
QY 418 CGAAGAAATATTTCTTAATGTTTGAAGAGCTGTGATCTTACGGATCTTAATTCACCT 477  
Db 445 CGAAGAAAAATCGCAATTCAGCGA-----GGAAAAATTCCTGTCA 486  
QY 478 CATAGTAGCAATGTATGTCTATCCGCACATGTAGAAATCTTACCCAGAGCTGCCAAG 537  
Db 487 CTGTGGGATTTGTCTGATGTAGTGGCTTAACAAACATATCCACAGAGCATGAACA 546  
QY 538 CACATATATTAATTTGATAGAGCCAAATATATGTGTATTTGGTATATGTTTCT 597  
Db 547 TCCATCCCTGAAACCTTAGAAGATAAATTATGGGGGAAAGCTCATCTACCTGTTCAT 606  
QY 598 CCAATTAATGACAGACAGAAATATCTGAAATCAACCATGATCTGTGCGAGAACAA 657  
Db 607 TTTGAAAACTGCAAGAGCGTGTTAGCTTTCAAGTGTCTCCATTAATGAAATCTTATCAAA 666  
QY 658 GTAATTTGCTGAAGCATCAGAAAAAAACTAGAGATGTGCTATCATCTGAACAATTA 717  
Db 667 GTAATGAATTTGGCAATC---CAAAAAAGTTGATCATTCATGGAAGGAATGTAAGTT 723  
QY 718 AAACCTGTGTGTTTGAATATCAGGGCAAGTACATTTTAAAGTGTGTGATGTATGA 777  
Db 724 AGCCCTATGAT-----TATGTGTGCAAGTCAAGCGGGAGATGATGA 765  
QY 778 TACTTCTAGAAAAAATATCTCTGAGTCAGTATATATATAGAAGCTGTATTAATGCTT 837  
Db 766 TATGTTTTTGGATCAATCACTAATTCAGTTCCAGTATATCCGAACTGTGTGATGAAC 825  
QY 838 GGGAGAGATGCCAATTTGAAAGATGTGCTA-----AGAAAAAGCTTTATTTCTCAACTGC 892  
Db 826 AGAGCCCTGCCCATTTTATATCTTGTGGAATGCTGCAGATCAAGAAAAATGTATGAACA 885  
QY 893 CAATGAGCTGTTTACATGCATCTTATTTCCAGAGCATTTCCACAGCTACACATATA 952  
Db 886 GAAATGATTTGCCATGAGGCTGCCAATATCGAAATTCATCTAATCTTCTTCCATTA 945  
QY 953 TGAATGAGAAACATCTCAAAAATCCCTTGGTTATATAATAGAGACTCAGATTAATAA 1012  
Db 946 CCACCAAAAGAAACAGAAATTAATTTCTCATGTTTGGAAAAATACAAACCTTTCCAAAT 1005  
QY 1013 TTTCTTTGCAACCTTACGTGAATCTAAATATTCAGACATATGACAAGATTTATGTTGCA 1072  
Db 1006 GTCTTGTGTTAAGGAAA--TAAACTTAACAGAGAAACCTTAAAGTTCATGTCAAGG 1063  
QY 1073 CAGGTATCTACATGAGAGAAACCTTATGTGA---CAATGTGAACACTCAAGAGATAC 1129  
Db 1064 CTGGCTTTTTCATGTACTGTGCTCTGTGTAAACCATCGTAAGCTCAGAGGTATCAG 1123  
QY 1130 CTGTTTCAATCCAGGTGGAATGAATGGCTGAATTAATATATATATCTCTGATCTTC 1189  
Db 1124 GAAAAAATGATATATTTGAAATGAACACTGGAATTTGATATATTTGTGTGCTTAC 1183  
QY 1190 CTCGTGTGCTGACTTGTGCTTTCATTT-----GCTCTGTAAAGGCCGAAAGGCTGC 1244

Db 1184 CAAGATGAGCTCGATTAATGTTTGTGTTTATGCAAGTTTGGATTAAGTAAAAACGAGA 1243  
QY 1245 TAAAGAGAACACTGTCAT-----TGGCATGGGGAATATTAACCTGTTTG 1291  
Db 1244 AATCAAGAAAACTATTAATCCCTCTTAATATCAACATCAGGAAGCTGAAAAAGTGC 1303  
QY 1292 ATTACACAGACACTCTAGTATCTGAAAAAATGAGCTTTGAATCTTTGGCAGTACCTCATG 1351  
Db 1304 ATTATCTGTAGCGTGGGTAAATACGATGTTTTTGACTTTAAAGACAAATTTGAACCTG 1363  
QY 1352 GATTAGAAATTTGCTGAACCCATTTGGTGTACTGTGATCAATCCAAATTAAGAAACTC 1411  
Db 1364 GAGACATATATTAACAGAGCTGTCTTATTTCTGATGAACCTCGAAGAAATGTTGAATC 1423  
QY 1412 CATGCTTAGAGTTGAGTTTACTGTGTACAGAGTGTGTAAAGTTCCAGATATGTACG 1471  
Db 1424 CAATGGAACTGTTCAAACAAATCCATATCTGAAATGCAACAGCTTTGCATTTAAT 1483  
QY 1472 TGATTTGAAGAGCATGCCAATTTGTCTGTATCCCGAAGACAGATTTAGCTATTCCACG 1531  
Db 1484 TTCCAGAGAAATTAATAACACCTTATTTATACCTCCCTTGATTAAGATTAATGAAAAAG 1543  
QY 1532 CAGACTGAGTACAGACTAGCTAGACAAATGAATTAAGGAAAAATGACAAAGAACAGC 1591  
Db 1544 CAGCTGAGATTTGCAAGCAGTGTATGTGCTAATGTGTCAAGTCAAGTGGAAAAAGTTTC 1603  
QY 1592 -----TCAAGCAATTTCTACAGAGATCCCTCTCTGGAATTCATGACGAGAGA 1642  
Db 1604 TTCTGTATTTGAAAAAATCTTGAACAGGATCCCTGTCTCACTGTGTGAAAAATGAAA 1663  
QY 1643 AAGATTTTCTATGAGTACAGAC--ACTATTTGTATCTATCCCGCAAAATTTACCA 1699  
Db 1664 TGATCTTATTTGCACTTTGGACAAAGCTGCCGAAATTTTCCACAAATCACGTCGAA 1723  
QY 1700 AATGCTTCTGTCTGTAAATGGAATTTCTAGAGTAAGTAAGCCGATGTATGCTTGG 1759  
Db 1724 AATTACTGTGCAATCAAGTGAATTAACCTTAGAGATGTTGCTCAGCTTCAGGGCTGC 1783  
QY 1760 TAAAGATTTGGCCTCCCAATCAAACTGAAACAGGCTATGGAATCTTGAAGCTATATAC 1819  
Db 1784 TTCAATTTTGGCTTAACCTGCCCCCGGAGGCCCCCTAGACTTCTGATTTCAACTATC 1843  
QY 1820 CAGATCTATGATTTGAGAGTGTGCTGTGCTGCTGGAATAATTAACAGATGACA 1879  
Db 1844 CAGACCAATGATTTGAAATATGTCTGTAGGCTGCTG---CGACAGATGAGTATGAAG 1900  
QY 1880 AACTTTCTCAGTATTTAATTCAGCTAGTACAGGCTCTAAAAATGAAACAAATTTGATA 1939  
Db 1901 AACTTTCTCAATATCTTTTACAACTGTGCAAGTGTAAATATGAGCTTTTCTTGAAT 1960  
QY 1940 ACTGCTGTAGATTTTACTGAAGAAAGCATGTACATTAACAAAGATTTGGGCACTTT 1999  
Db 1961 GTGCCCTCTTAATCTTATTAAGAAAGCACTGTGTAATCGAGGATAGGGCAGTTTC 2020  
QY 2000 TCTTTTGGCATTTAAATCTGAGATGACAAATTAAGAGCTTGAAGGTTTGGCTGC 2059  
Db 2021 TATTTTGGCATTTATGCTCAAGATGCAATTCCTGCTGTCTCAATACAAATTTGGTGTCA 2080  
QY 2060 TTTTGGAGTCTATTTGTGTCATGTGAGATGTATTTTGAACAACCTGAAATGCAAGTGC 2119  
Db 2081 TCTTTGAAGCATATCGCGGGGAAGTGTGGGCAATGAAGTGTCTTTCTAAGCAGTTTG 2140  
QY 2120 AGGCAATGAAAAAGCTCAATTAATCTGATCTCAAAACAGAGAGAAAGATGAAA 2179  
Db 2141 AAGCACTCAATTAAGTTAAAACTTTAAATAGTTTAATCAAACTGAATGCCGTGAAGTTAA 2200  
QY 2180 CAAAAAAGTACAGATGAAGTTTATGTTAGTGAACAAATAGGCGAACCAATTTCAATGATG 2239  
Db 2201 ACAGAGCCAAAGGAAAGAGGCAATGATACCTGTTTAAACAGAGTCTTATCCGGGAAG 2260  
QY 2240 CCTACAGGGCTGTGTCTCTCTTAAACCTGTCTCATCACTAGAAACCTCAAGGCTTA 2299



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Db      2261 CCCTCTCTGACGTCAGTCACCCCTGAAACCATGTTATCTCTCAGAACTCTATGTTG 2220
Qy      2300 AAGAGTGTGGAATATATGCTCTTTCGCAAAAAGCCACTGTGTGTAATGGGAGAACCCAG 2359
Db      2321 AAAGGTGCAAAATACATGATGATTCGAAATGAAAGCCTTTGTGGCTGATACAAATACAGG 2380
Qy      2360 ACATCATGTCAGAGTTACTGTTTCAGAAACAATGATCATCTTTAAAAATGGGAGTATT 2419
Db      2381 TATTTGGTGAAGATTGAGT-----TGAGTGAATTTTAAAAATGGTGAATGATT 2428
Qy      2420 TACGGCAAGATATGCTAACACTTCAAATTTATGTTATGAAAAATATGCAAAATC 2479
Db      2429 TACGACAGATATGTTGACACTTCGAAATGTTGCTTATGATGATTTACTCTGAAAGAGAG 2488
Qy      2480 AAGGCTTATCTTTCGAATGTTAACTTATGTTGTCTGTCATACGCTGATGTTGGGAGC 2539
Db      2489 CTGGTTTGGATCTTGGGATGTTGCTTATGCTGTTTAGCAACAGAGATCGCTCGGCC 2548
Qy      2540 TTAATGAGGTGGTGGCAAAATTCACACATTTATGCAAAATTCAGTCAAAAGCGCG--T 2596
Db      2549 TCAATGAGTTGTGACACCTCTGAAAACAATGCTGACATTCAGCTGAACAGTAGCAATG 2608
Qy      2597 TGAAGGTGACGTCAGCTTCAACAGCCACACACTAGATGAGTGCCTCAAAAGACAGAA 2656
Db      2609 TGGCTGCTCAGAGAGCTTCGCAAAAGATGCCCTTCTGAACTGGCTTAAAGAAATACAACT 2668
Qy      2657 AAGGAAATATATATGATGAGCCATTCCTGTTTACAGCTTCATGCTGATGATCTG 2716
Db      2669 CTGGGATATACCTGAGCCGAGCATTTGAGGAATTTACAGTGTCTGTGGCTGATCTG 2728
Qy      2717 TAGCTATCTTCAATTTGGGAATTTGAGATGCTACATATGTAACATCATGCTGAAAGAG 2776
Db      2729 TAGCTTCTTATGCTCTTGGGATTTGTGACAGACATGATGACAAACATCATGCTCAAAA 2788
Qy      2777 AAGGCAACGTTTTCATATGATTTTGGACACTTTTGGATCACAAGAAAGAAAATTTG 2836
Db      2789 CTGGCAGCTCTTCACATTTGACATTTCTTGAAATTTCAAAATCTTAAGTTTG 2848
Qy      2837 GTTATTAACAGAACGTCGTCCATTTGTTTTCACAGAGATTTCTTATAGTATTAGTA 2896
Db      2849 GCATTAAAGGAGGAGAGGAGCTTTTATTTCTTATGATATTTTCAATCCATGTCATTCAC 2908
Qy      2897 AAGGAGCCCAAGATGACAAAGACAGAGATTTGAGAGGTTTCAGAGATGTTTACA 2956
Db      2909 AAGGAAAAACAG-----AAATACGAAAAGTTGGCGGTCCGCCAGTGTGTGAGG 2962
Qy      2957 AAGCTTATCTAGCTATTGACAGAGCAATCTCTTCAATTAATCTTTCTCAATGATGC 3016
Db      2963 ATGCATATTTGATTTTACAGCGCATGGGAATCTTTCATCACTCTTTGCGCTGATGT 3022
Qy      3017 TTGGCTCTGGAATGCCAGAACTACATCTTTTGATGACATGTCATTCATTCGAAGAGCC 3076
Db      3023 TGACTGCAAGGGCTTCCTGAATCTACATGATCAATGATATTAAGAGATCTC 3082
Qy      3077 TAGCTTATGATTAAGCTGAGCAAGAGCTTTGGAGTATTTCAATGAACAAATGATGATG 3136
Db      3083 TTGCAATTTAGGGAAGAGTGAAGAAAGACCTCAAAAGTTTAAAGCAAAAATTTGATGAG 3142
Qy      3137 CACATCATGCTGTCGACAAACAAAATGATTTGATCTTTCACACAAAT 3186
Db      3143 CGCTCAGGGAAGCTGAGCTTAAAGTAACTGGATGGCCCAACAGATT 3192

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RESULT 8  
ABV78026  
ID ABV78026 standard; DNA; 3213 BP.

XX ABV78026;  
XX 12-NOV-2002 (first entry)  
XX  
XX Hypoxia-regulated protein coding sequence #46.  
DE  
XX

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KW Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
KW antiinflammatory; vulnery; gynecological; ophthalmological; vaccine;
KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;
KW ischemic condition; reperfusion injury; retinopathy; neonatal stress;
KW preeclampsia; atherosclerosis; inflammatory condition; wound healing;
KW inflammation; erythropoiesis; hair loss; human; gene; ds.
OS Homo sapiens.
PN WO200246465-A2.
PD 13-JUN-2002.
PF 10-DEC-2001; 2001WO-GB05458.
PR 08-DEC-2000; 2000GB-0030076.
PR 08-FEB-2001; 2001GB-0003156.
PR 25-OCT-2001; 2001GB-0025666.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
PI White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
PI Rayner WN;
DX WPI; 2002-627238/67.
XX
XX PT Identifying a gene involved in disease for treating hypoxia-regulated
XX PT conditions, comprises comparing the transcriptome/proteome of two cell
XX PT types under different conditions and identifying a differentially
XX PT regulated gene -
XX PS Claim 37; Page 363-364; 538pp; English.
XX
XX CC The present invention relates to methods for identifying genes and
XX CC proteins that are implicated in a specific disease or physiological
XX CC condition. The method comprises comparing the transcriptome/proteome of a
XX CC specialised cell type implicated in a disease or condition with that of a
XX CC second specialised cell type, under two experimental conditions, and
XX CC identifying a gene that is differentially regulated in the two
XX CC specialised cell types under experimental conditions. ABV7873-ABV78116
XX CC and ABP5061-ABP5257 were identified using the methods of the invention.
XX CC The coding sequences and proteins are useful for treating a disease in a
XX CC patient, for manufacture of a medicament for treating hypoxia-regulated
XX CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
XX CC biological response to hypoxia conditions, or hypoxic-associated
XX CC pathology in a patient. The coding sequences and proteins are also useful
XX CC for monitoring the therapeutic treatment of a disease or physiological
XX CC condition, such as cancer, ischemic conditions, reperfusion injury,
XX CC retinopathy, neonatal stress, preeclampsia, atherosclerosis, inflammatory
XX CC conditions, wound healing, inflammation, erythropoiesis or hair loss.
SQ Sequence 3213 BP; 979 A; 612 C; 704 G; 918 T; 0 other;

```

Query Match 13.5%; Score 460.8; DB 24; Length 3213;  
Best local Similarity 50.4%; Pred. No. 1.8e-110;  
Matches 1597; Conservative 0; Mismatches 1467; Indels 106; Gaps 15;

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Qy      58 ATCTAGGGAATGTTTACTACCAATGAAATGATGAGCTTGAATGCTCCGTGAG 117
Db      88 ATACCTGAGATTTCTTTTGGCCACTGGATTTATATTCAGTTGAGAGTACTCTGGGAA 147
Qy      118 GCTACATTAGTAATCTAATAGCATGAACTATTTAAAGAACAAAGAAATACCTCTCAT 177
Db      148 GCTACATTCTTATATTAAGAGATGTTATGAAAGCAAGTTCAACATTAACCAATGTTTC 207
Qy      178 CACTTCTTCAAGATGAATCTTTTCACTTTTGTAGTGTTCACCAAGAAAGCAAGAG 237
Db      208 AACTCTTATGAGATATGAGCTCTATATGTTGATGTGGAATCAGACTGCTGTATAT 267
Qy      238 GAAGAAATTTTGAAGAAACAAAGAGACTTGTGTGATCTTGGCTTTTCAACCAATTTTA 297
Db      268 GAGGAGCTTGAAGATGAAGAACGAAAGACTGTGTATGTCAAGACTTTTCTTCAATCTC 327

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QY	238	AAAGTAATTGAA	CCGATGACCA	CCGTGAAGAA	AAAGATCCTCAATCGAGAA	TTGGTTT	357
Db	328	AAATTAATGAC	CAAGAA	AGTTGTGAT	CAACCCAGGGGAAAA	---ATTAGACTCAAAAATTTGGAGTC	384
QY	358	GCTATCGGAT	CCCACTGTCGGA	TTTGATATGTTTAA	AGATCCGTAAGTACAGACCTTC		417
Db	385	CTTATAGGAAA	AAAGGCTTCGATGAA	TTTGATTTCTTGA	AGGATCCGGAATTAATGATTT		444
QY	418	CGAAGAAATAT	CTTAATGTTTGTAA	AGAGCTGAGATCTTAGGATCTTAATTCACCT			477
Db	445	CGAAGAAAAAT	CGGCAATTCAGCA	-----GGAAAAATTCCTGTCA			486
QY	478	CATAGTAGACA	TATGTATATCCGCACA	TGTGAATCTTCA	CCAGAGCTGCCAAG		537
Db	487	CTTGGGATGCT	CTTGGATGAGTAC	TGGCTAAAAACAACATATCCAC	CAAGATGACCA		546
QY	538	CACATATATTA	ATAATTTGATAGAGCCAA	ATAATAGTGTGATTTGGTATAGTTCT			597
Db	547	TCCATCCCTGAAA	AACTTAGAGATAAA	CTTTATGGGGGAAACCTCATCTACTCTGTCAAT			606
QY	598	CCAAATTAATGA	CAAGCAGAGATATCTCGAAATCA	CAACATGACGTGTGCAGAACAA			657
Db	607	TTTGA AAACTGC	CAGACGCTGTTAGCTTCAAGTGTCTCTTAATGAACTCTATCAAA				666
QY	658	GTAATTTGCTGA	NGCAATCAGAAAAAA	CTAGAAGTATGTTGCTATCATCTGAACATTA			717
Db	667	GTAATTAATTA	TGGCAATC---CAAAAACGTTGACATTA	CTGGGAAGGATGAGTT			723
QY	718	AAACTCTGTGTTT	AGAAATATCAGGGCAAGTACATTTTAAAGTGTGTGATGTAA				777
Db	724	AGCCCTATGAT	-----TATGTGTGCAAGTACAGCGGAGAGTGA				765
QY	778	TACTTCTAGAAA	AAATATCTCTGAGTCAGTAAATGATATATAAGAGCTGATTAATGCT				837
Db	766	TATGTTTGGGAT	CAATCCATTAATTCAGTTCAGATATATCCGAACGTGTGTGATGAAC				825
QY	838	GGAGAGATGCC	CAATTTGGAAGTGAATGCTA-----AAGAAAGCTTTATTTCTCAACGTGC				892
Db	826	AGAGCCCTG	CCCCATTTTATCTTGTGGAAATCTCGAAGATCAAGAAATGTATGACAA				885
QY	893	CAATGACACTG	TTTACATGCACTCTTATTCAGACGCAATTTCCACAGCTAACCACTATAT				952
Db	886	GAAATGATTTGCC	ATGAGGCTGCATTAATCGAAATTCATCTTAATCTTCTTCCATTA				945
QY	953	TGAATGAGAAA	CATCTACAAAAATCCCTTGGGTTAATAATGAGCACTCAGAAATPAAAA				1011
Db	946	CCACCAAAAGAAA	CAACGAAATTTTCTCTATGTTTGGAAAAATATACACCTTTTCCAAAT				1001
QY	1013	TTCTTTGTGCA	ACTACGTGAATCTAAATATTCGAGACATTGACAAAGATTTATGTTGCA				1072
Db	1006	GCTTGTGTTAA	AGGAAA---TAAACTTAAACAGAGGAAATCTTAAAGTTCAATGTCAAGG				1061
QY	1073	CAGGTATCTA	CCATGAGAGAACCTTATGTGA---CAATGTGAACACTCAAAGATAC				1122
Db	1064	CTGGCTTTTTCAT	GTAAGTACGTGCTCTCTGTGTAAACCACTCTAAGCTCAGAGGTATCAG				1122
QY	1130	CTGTGTCAAAT	CCCAAGTGAATGAGCTGAATTAATGATATATATACATTCCTGATCTTC				1188
Db	1124	GGAAAAATGAT	ATATTTGGAAATGAACCACTGGAATTTGATATTAATATTTGTGACTTAC				1188
QY	1190	CTCGTCTGCTG	CACTTGGCTTTCCATTT-----GCTCTGTAAAGCGCGAAAGGATGC				1244
Db	1184	CAAGAAATGCTG	ATTATGTTTGTGCTTTATGCAATTTTGATATAAGTAAABAAACGAAGA				1244
QY	1245	TAAAGGAA	CACGTGCTAT-----TGCATGGGGAATATATAAATTGTTTG				1297
Db	1244	AATCAACGAAA	CTATTAATCCCTCTAAATATACAGCCATCAGAAAGCTGAGAAAATGTC				1303
QY	1292	ATTACACAGACA	CTCTAGATCTGAAAAAATGGCTTTGAAATCTTTGGCCAGTACGCTATG				1351
Db	1304	ATTATCTGTAC	CGTGGGTAATACGATGGTTTTTGATCTTTAAAGCAATTTGAGACTG				1361
QY	1352	GATTGAAAGAT	TGTGTAACCTTATGTTGTATCTGATCAATCCAAATTAAGAACTC				1411

Db	1364	GAGACATATATTTACACAGCTGATCTTTCATTTCTCGATGAATCTGAAAGAAATGTTGAATC	1422
Qy	1412	CATGCTTAGAGTTGGAGTTTGACGTGTTTCACACAGTGTGTAAAGTTCCACATATGTCAG	1471
Db	1424	CAATGGGAACTGTTCAAAACAAATCCATATCTAGAAATGCACAGCTTTGCATGTTAAAT	1483
Qy	1472	TGATTGAAGACATGCCAATTGGTCTGTATCCCGAAGACAGATTTAGTATTTCCACG	1531
Db	1484	TTCCAGAGAAATAAAAAACACCTTATATTACCCCTCGTTGATPAAGTTATTTGAANAAG	1543
Qy	1532	CAGGACTGAGTAAACAGACTAGCTAGAGCAATGAAATTAGGAAAAATGACAAAGAACGC	1591
Db	1544	CAGCTGAATTTGCAAGCAGTATAGTGTCTAATGTGTCAAGTCGAGGTGAAAAAAGTTTC	1603
Qy	1592	-----TCAAAGCAATTTCTACAGAGATCCCTCTCGAATATCATCTAGCAGGAGA	1644
Db	1604	TTCTCTGATTAAGAAAGAAATCTTGGACAGAGATCCCTGTCTCAACTGTGTAAATATGAA	1667
Qy	1643	AAGATTTTCTATGAGAGTCACAGAC---ACATTTGTGTACTATCCCGAAATTTCTACCCA	1699
Db	1664	TGAGACTTATTTGGACTTTTGCGACAAAGCTCCGAGAAATTTCCCAACATCATCTGCCAA	1722
Qy	1700	AATTGCTTCTGTCTGTTAAATGGAATTTCTAGATGAAAGTACCAGATGTATTGCTTGG	1755
Db	1724	AATTACTGCTCAATCAAGTGAATTAACCTTGGAGATGTTGCTCAGCTTCAGGCGCTGC	1783
Qy	1760	TAAAGATTTGGCCCTCCAAATCAAACTGGAACAGGCTATGGAACTTTGACACTGTATTAAC	1819
Db	1784	TTCAATTTTGGCTTAAACCTGACCCCGCGAGGCCCTAGACCTTCTGATTTTCAACTATTC	1843
Qy	1820	CAGATCTCATGTTGAGAGTTTGGCTGTTCGGTGTGGAAGAAATATTTAACAGATGACA	1879
Db	1844	CAGACCAATAGCTTGAAGATATGTCTGTAAGCTGCTG---CGACAGTGTAGTATGGAAG	1900
Qy	1880	AACCTTCTCAGTATTTAAATCAGCTAGTACAGGTCTTAAATATGAACAATATTTGGATA	1939
Db	1901	AACTTCTCATATCTTTTAACTGAGCTGGGCAAGTGTAAATATGAGCCTTTTCTTGAT	1960
Qy	1940	ACTTGCTGTGAGATTTTACTGGAAGAAAGATTGACATATCAACAAAGATTTGGCACTTT	1999
Db	1961	GTGCCCTCTAGATTCCTATTAGAAAGACATTTGTAATCTGGAGGATAGGGCAGTTTC	2020
Qy	2000	TCTTTTGGCATTTTAAATCTGAGATGTCACATATTAACACGTTAGCCAGAGTTTGGCCTGC	2058
Db	2021	TATTTTGGCATTTTAGTCAAGATGTCATTTCTGCTGCTCAGTACAAATTTGCTGCA	2088
Qy	2060	TTTTGAGCTCCTATTGCTGTCATGTGGATGTATTTGAAACACCTGAATAGGCAAGTCG	2119
Db	2081	TCCTTGAAGCATACGCCGGGGAAGTGTGGGGCACATGAAGTGTCTTCTAAGCAGGTG	2148
Qy	2120	AGGCAATGGAAGAGCTCATTTACTTAATGACATTTCTAAACAGAGAGGAAGATGAA	2179
Db	2141	AAGCACTCAATTAAGTTAAACCTTTAAATAGTTTAATCAAACTGAATGCCGTGAAGTTAA	2200
Qy	2180	CACAAAAGCTACAGTGAAGTTTTTATGTGAGCAAAATAGGCGACAGATTTCTAGATG	2239
Db	2201	ACAGAGCCAAAGGAGAGGAGCCATGCTACCTGTTTAAACAGAGTCTTATCCGGGAAG	2266
Qy	2240	CCCTTACAGAGGCTTGTCTCTCTCTTAAACCTCTGTCATCAACTAGAAACCTCAGGCTTA	2299
Db	2261	CCCTCTGACCTGGAGTCAACCCGTGAAGCCATGTGTTATCTCTCAGAACTTATGTG	2328
Qy	2300	AAGAGTGTGCAATATATGCTTCTGCAAAAGGCCACATGTGGTGAATTTGGAGAACCCAG	2358
Db	2321	AAAAGTGAATTAATGATATTCAAAAATGAAGCCTTTGTGCTGTGTATCAATATTAACAAG	2380
Qy	2360	ACATCATGTCAAGATTAATCTGTTTCAAGCAATGATCATCTTTAAAAATGGGAGTAT	2419
Db	2381	TATTTGGTGAAGATTCAGT-----TGAGTGAATTTTAAAAATGTGTATGAT	2428
Qy	2420	TAGGCAAGATATGCTAACACTCAATATATGCTATATATGAAAAATATCTGGCAAAATC	2479

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Db 2429 TACGACAGATATGTTGACACTCCAAATGTCGCCCTTGATGATTTTACTCTGGAAAGAG 2488
Qy 2480 AAGGCTTGATCTTTCGAATGTTAACCCTTATGTTGTCGTCAATCGGTGACTGTGTGGAC 2539
Db 2489 CTGGTTTGATCTTTCGAATGTTGCTTATGGCTGTTAGCAACAGAGATCGTCTGGCC 2548
Qy 2540 TTTATGAGTGGTGCAGAAATTCACACTTATTCGAATTTCACTGCAAAAGGCGC---T 2596
Db 2549 TCATTGAAATGTGGACACCTCGAAACAAATGCTGACATTCGCTGAACAGTAGCAATG 2608
Qy 2597 TGAAGGTGACAGCTGCAAGTTCAACAGCACACACTACATCGTGTCAAAAGCAAGACA 2656
Db 2609 TGGCTGCTGACAGAGCTTCACAAAGATGCCCTTCTGAACTGGCTTAAAGATCAAACT 2668
Qy 2657 AAGGAGAAATATATGATGACAGCCATTGACCTGTTTACAGCTTCATGCTGATCTGTG 2716
Db 2669 CTGGGGATGACCTCGACCGAGCATTGAGGAATTTACAGTCTCTGTGGCTACTGTG 2728
Qy 2717 TAGCTACCTTCAATTTGGGAATTTGGAGATGTCACAAATGTAACATCATGTGTGAAGCG 2776
Db 2729 TAGCTTCTATGCTCTTGGGATTTGTGACAGACATAGTGCAACATCATGTGTCAAAAAA 2788
Qy 2777 AAGGACACTGTTTCAATATGATTTTGGACACTTTTGGATTCACAGAAAGAAATTTG 2836
Db 2789 CTGGCCAGCTCTTCCACATTTGACATTTGACATATTTCTGAAATTTCAAACTTAAGTTTG 2848
Qy 2837 GTTATTAACAGAACGTGTGCCATTTGTTTGAACAGAGATTTCTTAATAGTATTA 2896
Db 2849 GCATTAAAGGGAGCGAGTGCCCTTTATTTCTTACCTATGATTTTCAATGTCATTTCAAC 2908
Qy 2897 AAGGAGCCCAAGATGCAAAAGACAGAAATTTGAGAGTTTCAGAGATGTGTACA 2956
Db 2909 AAGGAAAAACAG-----AAATACGAAAGAAAGTTTGCCGGTCCGCCAGTGTGTGAGG 2962
Qy 2957 AGGCTATCTAGCTATTTGACAGAGCCAACTCTTCAATTAATCTTTCTCAATGATGC 3016
Db 2963 ATGCATATCTGATTTTACAGCGGACATGGAGATCTTCTTCACTCTTTGGCTGATGT 3022
Qy 3017 TTGGCTCTGGAATGCCAGACTACAACTCTTTGATGACATTTGATTCGAAAGAGCC 3076
Db 3023 TGACTGCAAGGGCTTCTGAACTACATGATCAATATACAGTATCTTAAGGACTCTC 3082
Qy 3077 TAGCTTACATTAAGTGAAGAGAGGCTTTGGAGTATTTCAATGAACAAATGATGATG 3136
Db 3083 TTGCATTTAGGAAAGTGAAGAAAGACACTCAAAAGATTTAAGCAAAATTTGATGAGG 3142
Qy 3137 CACATCATGTGGCTGGACAAAGAAATGATTTGATCTTCCACACAAT 3186
Db 3143 CGCTCAGGAAAGCTGACTTAAGTAACTGATGGCCCAACAGATT 3192

RESULT 9
AAS14366
ID AAS14366 standard; cDNA; 3213 BP.
XX
XX AAS14366;
AC
XX
XX
DT 12-MAR-2002 (first entry)
XX
XX cDNA encoding human p110beta isoform of PI3-kinase.
DE
XX
XX Human; phosphatidylinositol 3-kinase; PI3K; p110beta isoform;
KW LASP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;
KW autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
KW Type I diabetes mellitus; cytostatic; immunosuppressive; ss.
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT CDS 1..3213
FT /tag=a
FT /product="p110beta isoform of PI3-kinase"
XX
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PN WO200185986-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 10-MAY-2001; 2001WO-US15065.
XX
XX PR 10-MAY-2000; 2000US-203346P.
XX
XX PA (ICOS-) ICOS CORP.
XX
XX PI Sadhu C.
XX
XX DR WPI, 2002-075252/10.
XX
XX DR P-PSDB; AAU09688.
XX
XX PT Identifying a modulator of p110delta polypeptide binding to SH3
XX PT domain-containing polypeptides e.g. LASP-1, comprising allowing the
XX PT binding partners to interact in the presence and absence of a test
XX PT compound.
XX
XX PS Example 1; Page 63-68; 85pp; English.
XX
XX CC The present invention relates to identifying a modulator of the
XX CC phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to
XX CC the catalytic subunit via a SH3 domain-containing polypeptide such as
XX CC LASP-1. Also described are methods of assaying the specific binding
XX CC affinity of the PI3-kinase binding partner. Such modulators are useful
XX CC for the treatment of diseases characterised by the undesirable or
XX CC excessive activity of PI3Kdelta. For example the modulators can be used
XX CC for inhibiting the growth or proliferation of cancer cells
XX CC (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,
XX CC Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid
XX CC arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),
XX CC autoimmune diseases (e.g. systemic lupus erythematosus), inflammatory
XX CC bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
XX CC dermatoses (e.g. contact dermatitis; central or peripheral nervous
XX CC system inflammatory disorders (e.g. meningitis), bacterial pneumonia,
XX CC and Type I diabetes mellitus. The present sequence encodes for human
XX CC p110beta isoform of PI3K.
XX
XX SQ Sequence 3213 BP; 979 A; 612 C; 704 G; 918 T; 0 other;

Query Match 13.5%; Score 460.8; DB 24; Length 3213;
Best Local Similarity 50.4%; Pred. No. 1.8e-110;
Matches 1597; Conservative 0; Mismatches 1467; Indels 106; Gaps 15;

Qy 58 ATCCATAGGGAATGTTTACTACCAATGAGATGATGATGATGCTTGCCTCGTAG 117
Db 88 ATACCTGTGGAATTCCTTTTGGCCACTGGGATTTATATTCAGTTGGAGTACCTGGGA 147
Qy 118 GCTACATTAGTAACTATAAGCATGAACTATTTAAGAAGCAAGAAATACCTCTCAT 177
Db 148 GCTACCATTTCTTATATTAAGCAGATGTTAAGAAAGCAATTCACAAATTACCAATGTTTC 207
Qy 178 CAATCTTTCAAGATGAATCTTTTCAATTTTCTGAAGTTTACCCAAAGACAGAAAGG 237
Db 208 AACCTCTTATGATGATTTGACTCTCTATATGTTGATGTGATGATCAACATGCTGTATAT 267
Qy 238 GAAAGAAATTTTGAAGAAACAGAGACTTTGTGATCTTGGCTTTTCAACCATTTTTA 297
Db 268 GAGGAGCTTGAAGATGAAGAAACAGAACTGTGTGTGATCAACCTTTTCTTCAATTTCTC 327
Qy 298 AAAGTAATTTGAACCGTAGGCAACCGTGAAGAAAGATCCCAATCGAAGAAATTTGTTT 357
Db 328 AAATTATGTACAGAAAGTTGTGATCCCAAGGAAAA--ATTAGACTCAAAAATTTGAATC 384
Qy 358 GCTATGGCATGCCAGTGTGCGAATTTGATATGTTAAAGATCTGAAGTACAGACTTC 417
Db 385 CTTATAGAAAAAGGCTCGATGAATTTGATTCCTTGAAGATTCGAAGTAAATGAATTT 444
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QY 478 CATAGTAGCAATGATGTCTATCCGCACTGTAGAACTCTTACCCAGAGCTGCGCAAG 537  
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## RESULT 10

AAL37431/C  
ID AAL37431 standard; DNA: 4074 BP.

XX AAL37431;

DT 08-JAN-2002 (first entry)

DE Human musculoskeletal system related polynucleotide SEQ ID NO 3796.

XX Cytostatic; immunosuppressive; nocotropic; neuroprotective; antiviral;  
XX anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anticancer;  
XX antiviral; anticonvulsant; antibacterial; antifungal; antiparasitic;  
XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
XX neurological disease; infection; human; secreted protein;  
XX musculoskeletal system; ds.

OS Homo sapiens.

XX WO200155367-A1.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01338.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

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XX PR 17-MAR-2000; 2000US-0190076.

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PR 22-AUG-2000; 2000US-0227182.  
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PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.
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KM	gastrointestinal disorder; Crohn's disease; duodenal ulcer; ds.	
XX	Homo sapiens.	
OS	WO200155206-A1.	
PN	02-AUG-2001.	
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PF	17-JAN-2001; 2001WO-US01353.	
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		PR 08-DEC-2000; 2000US-0251869.
		PR 08-DEC-2000; 2000US-0251989.
		PR 11-DEC-2000; 2000US-0251990.
		PR 05-JAN-2001; 2001US-0255678.

```
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM,
XX WPI: 2001-45717/49.
XX
XX Isolated pancreatic cancer polypeptide for treating, preventing and/or
XX prognosing disorders related to the pancreas including pancreatic
XX cancers and also for testing and detection e.g. diagnosis -
XX
XX Disclosure: SEQ ID NO 608; 537pp; English.
XX
XX The invention relates to an isolated polypeptide comprising an amino
XX acid sequence at least 90% identical to 188 amino acid sequences fully
XX defined in the specification and encoded by 188 cDNA clones fully
XX defined in the specification. The invention also relates to a fragment
XX having biological activity, a domain, an epitope, full length protein,
XX variant, allelic variant or a species homologue of the fully defined
XX sequence. The polynucleotide and polypeptide are useful for treating,
XX preventing and/or prognosing disorders related to the pancreas including
XX pancreatic cancer, pancreatitis, diabetes, endocrine disorders such as
XX acromegaly or hyperthyroidism, and gastrointestinal disorders such as
XX Crohn's disease and duodenal ulcers. The present sequence encodes a
XX pancreatic cancer-related polypeptide of the invention.
XX
XX Sequence 4074 BP; 1382 A; 640 C; 647 G; 1405 T; 0 other;
XX
XX Query Match 13.2%; Score 452; DB 22; Length 4074;
XX Best Local Similarity 98.6%; Pred. No. 4,1e-108;
XX Matches 477; Conservative 0; Mismatches 5; Indels 2; Gaps 2;
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XX 2931 TGAGAGGTTTCGAGAGTGTGTACAGGCTTATCTAGCTATTTCGACAGATGCCATCT 2990
XX 659 TTATAGTTTCGAGAGTGTGTACAGGCTTATCTAGCTATTTCGACAGATGCCATCT 718
XX 2991 CTTCAATTAATCTTTTCTCAATGATGCTTGGCTGTGGAATGCCAATCAATCTTTTGA 3050
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XX 3349 ATATATATTAATTAATGTAAGCAAGCAAGGGTTTGATGACATTAATGATGATG 3408
XX 1079 ATATATATTAATTAATGTAAGCAAGCAAGGGTTTGATGACATTAATGATGATG 1138
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XX
XX RESULT 12
XX ABA07290
XX ID ABA07290 standard; DNA; 4074 BP.
XX
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AC ABA07290;
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XX 14-JAN-2002 (first entry)
XX
XX Human pancreatic cancer related genomic DNA, SEQ ID NO: 609.
XX
XX Human: cytostatic; antidiabetic; antiinflammatory; gastric; osteopathic;
XX antihormone; antitumor; thyroid-active; gene therapy; antisense therapy;
XX pancreatic cancer antigen inhibitor; pancreatic cancer; pancreatitis;
XX diabetes; endocrine disorder; acromegaly; hyperthyroidism;
XX gastrointestinal disorder; Crohn's disease; duodenal ulcer; ds.
XX
XX Homo sapiens.
XX
XX WO200155206-A1.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01353.
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XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
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XX 12-SEP-2000; 2000US-0231968.
XX 14-SEP-2000; 2000US-0232397.
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DB 1138 AAAA 1141  
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ID AAK89934 standard; DNA; 4074 BP.  
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AC AAK89934;  
XX 05-NOV-2001 (first entry)  
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XX Human digestive system antigen sequence SEQ ID NO: 3510.  
DE  
XX Human: digestive system antigen; gene therapy; cancer; appendicitis;  
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;  
KW digestive system disorder; Meckel's diverticulum; ds.  
XX Homo sapiens.  
OS  
XX WO200155314-A2.  
PN  
XX 02-AUG-2001.  
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XX  
XX 17-JAN-2001; 2001WO-US01324.  
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PR 08-DEC-2000; 2000US-0251989.  
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PR 11-DEC-2000; 2000US-0254097.  
PR 05-JUN-2001; 2001US-0259678.  
XX  
XX

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-502630/55.

PT Polynucleotides encoding digestive system antigens, useful for  
PT diagnosing, treating, preventing and/or prognosing disorders of the  
PT digestive system, particularly cancer and cancer metastases -  
XX

PS Disclosure; SEQ ID NO 3510; 986bp; English.

CC The present invention provides the protein and coding sequences of a  
CC number of human digestive system antigens. These can be used in the  
CC diagnosis, treatment and prevention of digestive system disorders,  
CC including cancer, Meckel's diverticulum, bacterial or parasitic  
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or  
CC ulcerative colitis. The present sequence is a genomic DNA fragment  
CC encoding a digestive system antigen of the invention.  
XX

SQ Sequence 4074 BP; 1382 A; 640 C; 647 G; 1405 T; 0 other;

Query Match 13.2%; Score 452; DB 22; Length 4074;  
Best Local Similarity 98.6%; Pred. No. 4.1e-108;

Matches 477; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

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QY 2991 CTTGATTAATCTTTTCTCAATGATGCTTGCTCGAATGCCAGAACTCAATCTTTTGA 3050  
DB 719 CTTGATTAATCTTTTCTCAATGATGCTTGCTCGAATGCCAGAACTCAATCTTTTGA 778  
QY 3051 TGACATTCGATACATTCGAAAGCCTTAGCTTAGTAAACTGACAGAGGCTTTTGA 3110  
DB 779 TGACATTCGATACATTCGAAAGCCTTAGCTTAGTAAACTGACAGAGGCTTTTGA 838  
QY 3111 GATATTCATGAACCAATGATGATGATGATGATGATGATGATGATGATGATGATG 3170  
DB 839 GATATTCATGAACCAATGATGATGATGATGATGATGATGATGATGATGATGATG 898  
QY 3171 GATCTTCACACAAATTAACAGCATGATGAACTG-AAAGATTAATGAGAAATGAAG 3229  
DB 899 GATCTTCACACAAATTAACAGCATGATGAACTGAAAGATTAATGAGAAATGAAG 958  
QY 3230 CTCACCTCTGACACCTACCTGCTGTTAATCTTCAGCAGGCAAGCCGATTCAT 3289  
DB 959 CTCACCTCTGATTCACACCTGCTGTTAATCTTCAGCAGGCAAGCCGATTCAT 1018  
QY 3290 AGGAATTCGACATTCGATGACAGATTCG-ATTACAGCAAGCAAGAAATTAATCT 3348  
DB 1019 AGGAATTCGACATTCGATGACAGATTCG-ATTACAGCAAGCAAGAAATTAATCT 1078

QY 3349 ATATTAATTAATTAATGTAACGCAACGAGGTTGATGCACTTAAGTACTTCTTC 3408  
DB 1079 ATATTAATTAATTAATGTAACGCAACGAGGTTGATGCACTTAAGTACTTCTTC 1138  
QY 3409 AAAA 3412  
DB 1139 AAAA 1142

RESULT 14

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ID AAK89935 standard; DNA; 4074 BP.

AAK89935;

05-NOV-2001 (first entry)

DE Human digestive system antigen genomic sequence SEQ ID NO: 3511.

KW Human; digestive system antigen; gene therapy; cancer; appendicitis;  
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;  
KW digestive system disorder; Meckel's diverticulum; ds.

XX Homo sapiens.

XX WO200155314-A2.

XX 02-AUG-2001.

PD 17-JUN-2001; 2001WO-US01324.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

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PR 05-JAN-2001; 2001US-0259676.  
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PA (HUMA-) HUMAN GENOME SCI INC.  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX MPI; 2001-502630/55.  
DR  
XX  
PT Polynucleotides encoding digestive system antigens, useful for  
PT diagnosing, treating, preventing and/or prognosing disorders of the  
PT digestive system, particularly cancer and cancer metastases -  
XX  
PS Disclosure; SEQ ID NO 3511; 986bp; English.  
XX  
CC The present invention provides the protein and coding sequences of a  
CC number of human digestive system antigens. These can be used in the  
CC diagnosis, treatment and prevention of digestive system disorders,  
CC including cancer, Meckel's diverticulum, bacterial or parasitic  
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or  
CC ulcerative colitis. The present sequence is a genomic DNA fragment  
CC encoding a digestive system antigen of the invention.  
XX  
SQ Sequence 4074 BP; 1382 A; 641 C; 645 G; 1405 T; 1 other;  
Query Match 13.2%; Score 452; DB 22; Length 4074;  
Best Local Similarity 98.6%; Pred. No. 4, 1e-108;  
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DB 778 TGACATGATGATCATTCCGAAAGACCCCTAGCCCTTAATATAAATGAGCAAGAGCTTTGA 837  
QY 3111 GTATTTCAATGAACAAATGAATGATGACATCATGCTGGCTGGACACAAATGATGATG 3170  
DB 838 GTATTTCAATGAACAAATGAATGATGACATCATGCTGGCTGGACACAAATGATGATG 897  
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 AC ABX60419;  
 XX  
 DT 26-FEB-2003 (first entry)  
 XX  
 DE cDNA encoding novel human musculoskeletal system antigen #2763.  
 XX  
 KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;  
 KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;  
 KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;  
 KW post-operative tissue repair; limb regeneration; neuronal growth;  
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
 KW AIDS-related complex; chondrocyte growth; bone regeneration;  
 KW periodontal regeneration; tissue transport; bone graft; skin aging;  
 KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;  
 KW cell growth; organ transplant; cell differentiation; body height;  
 KW weight; hair colour; eye colour; skin; percentage of adipose tissue;  
 KW pigmentation; cosmetic surgery; metabolism; biorthym; cardiac rhythm;  
 KW depression; tendency for violence; pain; reproductive capability;  
 KW hormone level; endocrine level; appetite; libido; memory; stress;  
 KW storage capability; fat content; lipid content; protein content;  
 KW carbohydrate content; vitamin content; cofactor content;  
 KW nutritional component.  
 XX  
 OS Homo sapiens.  
 OS  
 PN US2002147140-A1.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764877.  
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 PR 31-JAN-2000; 2000US-179065P.  
 PR 04-FEB-2000; 2000US-180628P.  
 PR 28-JUN-2000; 2000US-214886P.  
 PR 07-JUL-2000; 2000US-216647P.  
 PR 07-JUL-2000; 2000US-216880P.  
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 PR 01-NOV-2000; 2000US-244617P.  
 PR 17-NOV-2000; 2000US-249299P.  
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 PR 08-DEC-2000; 2000US-251869P.  
 XX  
 XX (ROSE/) ROSEN C A.  
 PA (RUBEN/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 PI Rosen CA, Ruben SM, Barash SC;  
 DR WPI; 2003-128199/12.  
 XX  
 PT Isolated nucleic acid molecules encoding musculoskeletal system  
 XX associated polypeptides, useful for detecting disorders, e.g. cancer -  
 PS disclosure; SEQ ID NO 3796; 321pp; English.  
 XX  
 CC The invention describes an isolated nucleic acid molecule comprising a  
 CC sequence encoding musculoskeletal system associated polypeptides useful  
 CC for detecting disorders, e.g. cancer or cancer metastases, in animals  
 CC or humans. The nucleic acid stimulates re-vascularisation of ischaemic  
 CC tissues associated with conditions such as thrombosis, arteriosclerosis,  
 CC and other cardiovascular conditions; treats wounds due to injuries,  
 CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis  
 CC and limb regeneration; stimulates neuronal growth; can treat and prevent  
 CC neuronal damage occurring in certain disorders or neurodegenerative  
 CC conditions, such as, Alzheimer's disease, Parkinson's disease, and  
 CC AIDS-related complex; stimulates chondrocyte growth, thus they can be  
 CC used to enhance bone and periodontal regeneration and aid in tissue  
 CC transports or bone grafts; prevents skin aging due to sunburn by  
 CC stimulating keratinocyte growth; prevents hair loss, since FGF family  
 CC members activate hair-forming cells and promotes melanocyte growth;  
 CC stimulates growth and differentiation of hematopoietic cells and bone  
 CC marrow cells when used in combination with other cytokines; maintains  
 CC organs before transplantation or for supporting cell culture of primary  
 CC tissues; induces tissue of mesodermal origin to differentiate in early  
 CC embryos; increases or decreases the differentiation or proliferation of  
 CC embryonic stem cells; besides, haematopoietic lineage; modulates  
 CC mammalian characteristics, such as, body height, weight, hair colour, eye  
 CC colour, skin, percentage of adipose tissue, pigmentation, site, and shape  
 CC (e.g., cosmetic surgery); modulates mammalian metabolism; changes  
 CC mammal's metal state or physical state by influencing biorthym; changes  
 CC cardiac rhythms, depression, tendency for violence, tolerance for pain,  
 CC reproductive capabilities, hormonal or endocrine levels, appetite,  
 CC libido, memory, or stress; increases or decreases storage capabilities,  
 CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors  
 CC or other nutritional components. This sequence encodes a novel human  
 CC musculoskeletal system antigen.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?DocID=20020147140.

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XX Sequence 4074 BP; 1405 A; 645 C; 641 G; 1382 T; 1 other;
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Best Local Similarity 98.6%; Pred. No. 4,1e-108;
Matches 477; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 04:09:02 ; Search time 8208.59 Seconds

(without alignments)  
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Perfect score: 3412

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Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

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14: gb\_vl:\*

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16: em\_fun:\*

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18: em\_in:\*

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22: em\_ov:\*

23: em\_pac:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_hg\_hum:\*

31: em\_hg\_inv:\*

32: em\_hg\_other:\*

33: em\_hg\_mus:\*

34: em\_hg\_pln:\*

35: em\_hg\_rtd:\*

36: em\_hg\_mam:\*

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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#### ALIGNMENTS

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DEFINITION Sequence 32 from patent US 5824492.

ACCESSION AR048985

VERSION AR048985.1 GI:6005024

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3412)

AUTHORS Hiles,I.D., Fry,M.J., Dhand,R., Waterfield,M.D., Parker,P.J.,

TITLE Otsu,M., Panayotou,G., Volinia,S. and Gout,I.

JOURNAL Polypeptides having kinase activity, their preparation and use

Patent: US 5824492-A 32 20-OCT-1998;

Pred. No. is the number of results predicted by chance to have a

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 Source 1..3412 /organism="unknown"  
 BASE COUNT 1129 a 616 c 706 g 961 t  
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 SOURCE  
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 Unclassified.  
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 Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J.,  
 Oseu, M., Panayotou, G., Volinia, S., and Gou, I.  
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VERSION AR164679.1
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UNCLASIFIED.
REFERENCE 1 (bases 1 to 3412)
AUTHORS Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J.,
Otsu, M., Panayotou, G., Volinia, S. and Gout, I.
TITLE Polypeptides having kinase activity, their preparation and use
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FEATURES	source
LOCUS	A75939
DEFINITION	Sequence 39 from Patent WO9321328.
ACCESSION	A75939
VERSION	A75939.1 GI:6088143
KEYWORDS	
SOURCE	unidentified unclassified. unclassified.
ORGANISM	
REFERENCE	1 (bases 1 to 3412)
AUTHORS	Hiles, I.D. and F.Y.M.J.
TITLE	POLYPEPTIDES HAVING KINASE ACTIVITY, THEIR PREPARATION AND USE
JOURNAL	PATENT. NO 9321328-A 39 28-OCT-1993; LUDWIG INST CANCER RES (GB); HILES IAN D (GB) Location/Qualifiers 1..3412

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AX327651

LOCUS AX327651 3424 bp DNA linear PAT 07-JAN-2002  
DEFINITION Sequence 5 from Patent WO0185986.  
ACCESSION AX327651  
VERSION AX327651.1 GI:18097981  
KEYWORDS  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE 1  
AUTHORS Sathu, C.  
TITLE Phosphatidy1 inositol 3-kinase delta binding partner  
JOURNAL Patent: WO 0185986-A 5 15-NOV-2001;  
ICOS CORPORATION (US)

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DEFINITION  
ACCESSION Z29090



VERSION 229090.1 GI:472990  
KEYWORDS phosphatidylinositol 3-kinase.  
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ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1068)  
AUTHORS Volinia,S., Hiles,I., Ormondroyd,E., Nizetic,D., Antonacci,R.,  
Mammalia, Eubheria; Primates; Catarrhini; Hominoidea; Homo.  
TITLE Molecular cloning, cDNA sequence, and chromosomal localization of  
the human phosphatidylinositol 3-kinase p110 alpha (PIK3CA) gene  
JOURNAL Genomics 24 (3), 472-477 (1994)  
MEDLINE 95229146  
PUBMED 7713498  
REFERENCE 2 (bases 1 to 3424)  
AUTHORS Volinia,S.  
TITLE Direct Submission  
JOURNAL Submitted (16-DEC-1993) Stefano Volinia, Receptor Studies, Ludwig  
Institute for Cancer Research, 91 Riding House Street, London, W1P  
8BT, UK  
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BASE COUNT 1134 a 618 c 709 g 963 t  
ORIGIN  
Query Match 99.9%; Score 3407.2; DB 9; Length 3424;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3409; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCTCCAGACATCATCAGTGAACCTGTGGGCATCCACTTATGCCCCCAAGAATC 60  
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QY 1201 CGACTTTGCTTTTCATTTGCTCTGTTAAAGCCGAAAGGGTGTCTAAAGAGAAACATGT 1260  
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RESULT 7  
AR048986 3240 bp DNA linear PAT 29-SEP-1999  
LOCUS AR048986 3240 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 34 from patent US 5824492.

ACCESSION AR048986  
VERSION AR048986.1 GI:6005025  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 3240)  
AUTHORS Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J.,  
Otsu, M., Panayotou, G., Volinia, S. and Gout, I.  
TITLE Polypeptides having kinase activity, their preparation and use  
JOURNAL Patent: US 5824492-A 34 20-OCT-1998;  
FEATURES  
source location/Qualifiers  
1..3240 /organism="unknown"  
BASE COUNT 1057 a 582 c 682 g 919 t  
ORIGIN  
Query Match 94.9%; Score 3236.8; DB 6; Length 3240;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3238; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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DB 61 CTAGTGAATGTTTACTACCAATGAAATGATGACTTTAGAAATGCTCCGTGAGCT 120  
QY 121 ACATTAGTACTATTAAGCATGACTATTTAAAGACAGAAATACCTCTCATCAA 180  
DB 121 ACATTAGTACTATTAAGCATGACTATTTAAAGACAGAAATACCTCTCATCAA 180  
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DB 181 CTCTTCAAGATGAAATCTTCTACATTTTCGTAAGTACCAGAGCAGAAAGGGA 240  
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QY 301 GTAATGAACCGATAGGCAACCGTGAAGAAAGATCTCAATCGAAGAAATGGTTTGT 360  
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DB 1741 GCCCAGATGATTTGCTTGTAAAGATTTGGCTTCAATCAACCTGAACAGGCTATGGA 1800  
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Dp	1861	AAATTTTAAAGATGACAAACTTCTCAGATTTTAATTACGCTAGTACAGGTCCCTAAA	1920
Qy	1921	TATGAACAATATTTGGATPACTGTGCTTGAGATTTTACTGAGAAAGCATGACTAAT	1980
Dp	1921	TATGAACAATATTTGGATPACTGTGCTTGAGATTTTACTGAGAAAGCATGCTAAT	1980
Qy	1981	CAAGAGATTTGGCACTTTTCTCTTTGGCATTTAAATCGAGATGCACAATPAAACACTT	2040
Dp	1981	CAAGAGATTTGGCACTTTTCTCTTTGGCATTTAAATCGAGATGCACAATPAAACACTT	2040
Qy	2041	AGCCAGAGTTTGGCTGCTGTTTGGAGTCTTAATGTGCTGATGAGGATGTATTTGAAG	2100
Dp	2041	AGCCAGAGTTTGGCTGCTGTTTGGAGTCTTAATGTGCTGATGAGGATGTATTTGAAG	2100
Qy	2101	CACCTGAATAGGCAAGTCGAGGCAATGGAAGAGCTCAATTACTTAACATTCCTCAA	2160
Dp	2101	CACCTGAATAGGCAAGTCGAGGCAATGGAAGAGCTCAATTACTTAACATTCCTCAA	2160
Qy	2161	CAGAGAGAAAGATGAAACAACAAGGTACAGAGAAAGTTTATGTTGACCAATGAGG	2220
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Qy	2221	CGACCAGATTTTCATGATGAGCTTACAGGGCTTGCTGTCTCCCTPAAACCTGCTCATCA	2280
Dp	2221	CGACCAGATTTTCATGATGAGCTTACAGGGCTTGCTGTCTCTCTPAAACCTGCTCATCA	2280
Qy	2281	CTAGAAACCTCAGGCTTAAAGAGTGTGCAATTATGCTTTCGCAAAAAGGCCACTGTGG	2340
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Qy	2341	TTGATTTGGGAGAACCCAGACATCATGTCAAGTTTACTGTTTCAGAACATGAGATCATC	2400
Dp	2341	TTGATTTGGGAGAACCCAGACATCATGTCAAGTTTACTGTTTCAGAACATGAGATCATC	2400
Qy	2401	TTTAAAAATGGGGATGATTTTACGGCAAGATATGCTPAACTTAACTTATGCTGATTATG	2460
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Qy	2461	GAAATATCTGGCAAAATCAAGGCTTGATCTTCGAAATTTACCTTAATGATGTCTGTCA	2520
Dp	2461	GAAATATCTGGCAAAATCAAGGCTTGATCTTCGAAATTTACCTTAATGATGTCTGTCA	2520
Qy	2521	ATCGGTGACTGTGTGGGACTTATTTGAGGTGTGGCAAAATTCACACTAATTATCAAAAT	2580
Dp	2521	ATCGGTGACTGTGTGGGACTTATTTGAGGTGTGGCAAAATTCACACTAATTATCAAAAT	2580
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Dp	2581	CAGTGCAAAAGCGGCTTGAAAGGTGCATGAGTTCAACACCCACACATCAATCAATGG	2640
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Qy	2701	TGTGCTGATACCTGTGTAGTACTTCAATTTTGGAAATTTGGAGATTCGTCAATATGTAAC	2760
Dp	2701	TGTGCTGATACCTGTGTAGTACTTCAATTTTGGAAATTTGGAGATTCGTCAATATGTAAC	2760
Qy	2761	ATCATGTGGAAGACGATGACAACGTGTTTCATATAGTTTTTGGACACTTTTITGGATCAC	2820
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Dp	2821	AAGAAAGAAAAAATTTGGTTATPAAACGAGAACGTGTGCCATTTGTTTGAACACAGATTTT	2880
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Dp	2881	TTAAATAGTATTTAGTAAAGAGCCCAAGATGCAAAAGACAAAGAAATTTGAGAGTTT	2940
Qy	2941	CAGAGATGTGTTCAAAGGCTTATCTAGCTAATTCAGACAGTCGCAATCTTCTCATTAAT	3000

Dp	2941	CAGAGGATGTGTTCAAAGCGTTATCTVAGTATTGTGACAGCATGGCAATCTCTCATAAAT	3000
Qy	3001	CTTTTCTCAATGATGCTTGCGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCA	3066
Dp	3001	CTTTTCTCAATGATGCTTGCGCTCTGGAATGCCAGAACTACAATCTTTTGATGACATTGCA	3066
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Dp	3061	TACATTGGAAGACCCTTAGCCCTTGAGTAATAACTGAGCAAGGCGCTTGGAGTATTTCATG	3120
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<b>RESULT 8</b>			
LOCUS	AR064287	3240 bp	DNA linear PAT 29-SEP-1999
DEFINITION	Sequence 34 from patent US 5846824.		
ACCESSION	AR064287		
VERSION	AR064287.1 GI:593595		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	Hiles,I.D., Fry,M.J., Dhand,R., Waterfield,M.D., Parker,P.J., Otsu,M., Panayotou,G., Volinia,S. and Gout,T. Polypeptides having kinase activity, their preparation and use Patent: US 5846824-A 34 08-DBC-1998; Location/Qualifiers 1..3240 /organism="unknown"		
TITLE	JOURNAL FEATURES		
BASE COUNT	1057 a 582 c 682 g 919 t		
ORIGIN			
Query Match	94.9%; Score 3236.8; DB 6; Length 3240;		
Best Local Similarity	99.9%; Pred. No. 0;		
Matches 3238; Conservative	0; Mismatches 2; Indels 0; Gaps 0;		
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LOCUS ARI64680  
DEFINITION Sequence 34 from patent US 6274327.  
ACCESSION ARI64680  
VERSION ARI64680.1 GI:16237790  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 3240)  
AUTHORS Hiles,I.D., Fry,M.J., Dhand,R., Waterfield,M.D., Parker,P.J.,  
Otsu,M., Panayotou,G., Volinia,S. and Gout,I.  
TITLE Polypeptides having kinase activity, their preparation and use  
JOURNAL Patent: US 6274327-A 34 14-AUG-2001;  
FEATURES  
source 1..3240  
BASE COUNT 1057 a 582 c 682 g 919 t  
ORIGIN  
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complete cds.  
ACCESSION U79143  
VERSION U79143.1 GI:1763625  
KEYWORDS



SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
AUTHORS 1 (bases 1 to 3207)  
Stidivant, S.M., Ahern, J., Conroy, R.R., Barnett, S.F., Ledger, L.M.,  
Cliff, A. and Heimbrook, D.C.  
TITLE Cloning and mutagenesis of the p110 alpha subunit of human  
phosphoinositide 3'-hydroxylase  
JOURNAL Bioorg. Med. Chem. 5 (1), 65-74 (1997)  
MEDLINE 97196568  
PUBMED 9043658  
REFERENCE 2 (bases 1 to 3207)  
Stidivant, S.M., Ahern, J., Conroy, R.R., Barnett, S.F., Ledger, L.M.,  
Cliff, A. and Heimbrook, D.C.  
TITLE Direct Substitution  
JOURNAL Submitted (21-NOV-1996) Cancer Research, Merck Research Labs,  
Summerville, Pike, West Point, PA 19486, USA  
FEATURES  
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VERSION M93252.1 GI:163519  
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Hiles, I.D., Otsu, M., Volinia, S., Fry, M.J., Gout, I., Dhan, R., Panayotou, G., Ruiz-Larrea, F., Thompson, A.S., Totty, N.F., Hsuan, J.J., Courtneidge, S.A., Parker, P.J. and Waterfield, M.D. Phosphatidylinositol 3-kinase: structure and expression of the 110 kD catalytic subunit  
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Db 2341 TTGAATTTGGAGAACCCAGACATCATGTCAAGTATCTGTTTACAGAAATGAGATCATC 2400  
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QY 2461 GAAAAATCTGCAAAATCAAGTCTTGAATCTTGAATGTTAACCCTTATGTTGCTGTCA 2520  
Db 2461 GAAAAATCTGCAAAATCAAGTCTTGAATCTTGAATGTTAACCCTTATGTTGCTGTCA 2520  
QY 2521 ATCGGTGATCTGTGTGGGCTTATTTGAGTGTGCGAAATTTCTCACATTAATGCAATT 2580  
Db 2521 ATCGGTGATCTGTGTGGGCTTATTTGAGTGTGCGAAATTTCTCACATTAATGCAATT 2580  
QY 2581 CAGTCAAAAGGCGCTTGAAGGTGCACTGAGATTTCAACAGCAACACTCATCAGAGG 2640  
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QY 2641 CTCAAAAGCAAGAACAAAGGAAATATATGATGAGCAGCATTTGATTTTACAGCTTCA 2700  
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QY 2821 AAGAGAAAAAATTTGGTTATATAAGAGACGTGTGCCATTTGGTTTGACACAGATTTTC 2880  
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QY 2941 CAGGAGATGTGTACAGAGCTTATCTAGCTATTTCGACAGATGCCAATCTCTTCAATAAT 3000  
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QY 3001 CTTTTCATCATATATGCTTGGCTCTGGAATGCCAATACTTATTTGATGACATTTGCA 3060  
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DB 3121 AAACAAATGATGATGACATCATGCTGGCTGGACAAACAAATGGAATTGATCTTCCAC 3180  
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## RESULT 15

AR064288 3207 bp DNA linear PAT 29-SEP-1999  
LOCUS AR064288  
DEFINITION Sequence 35 from patent US 5846824.  
ACCESSION AR064288  
VERSION AR064288.1 GI:5993596  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3207)  
AUTHORS Hiles,I.D., Fry,M.J., Dhand,R., Waterfield,M.E., Parker,P.J.,  
Olsen,M., Panayotou,G., Volinia,S. and Gout,I.  
TITLE Polypeptides having kinase activity, their preparation and use  
JOURNAL Patent: US 5846824-A 35 08-DEC-1998;  
FEATURES Location/Qualifiers  
source 1..3207  
/organism="unknown"

BASE COUNT 1028 a 581 c 680 g 918 t  
ORIGIN

Query Match 88.2%; Score 3008.6; DB 6; Length 3207;  
Best Local Similarity 96.1%; Pred. No. 0;  
Matches 3083; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 1 ATGCTCCAAAGCAATCATCAGTGAATCTGTGGGATCCACTTGATGCCCAAGAAATC 60  
DB 1 ATGCTCCAAAGCAATCATCAGTGAATCTGTGGGATCCACTTGATGCCCAAGAAATC 60  
QY 61 CTAGTGAATGTTTACTACCAATGGAATGATGATGATCTTTAGATGCTCCGTGAGCT 120  
DB 61 CTAGTGAATGTTTACTACCAATGGAATGATGATGATCTTTAGATGCTCCGTGAGCT 120  
QY 121 ACATTAAGTACTATTAAGCATGAACTATTAAAGAACAAATAATACCTCTCCATCA 180  
DB 121 ACATTAAGTACTATTAAGCATGAACTATTAAAGAACAAATAATACCTCTCCATCA 180  
QY 181 CTTCTTCAAGATGAATCTTTCAATTTTCTGTAAGTGTACCCAGAGACAGAAAGGGA 240  
DB 181 CTTCTTCAAGATGAATCTTTCAATTTTCTGTAAGTGTACCCAGAGAGAAAGGGA 240  
QY 241 GAATTTTGTGATGAAGAAAGAGAGACTTTGTGATCTTGGCTTTTGAACCATTTTAAA 300  
DB 241 GAATTTTGTGATGAAGAAAGAGAGACTTTGTGATCTTGGCTTTTGAACCATTTTAAA 300

QY 301 GTAATTGAACCAATGAGCAACCGTGAGAAAAAGATCTCAATCGAGAAATGGTTTGT 360  
DB 301 GTAATTGAACCAATGAGCAACCGTGAGAAAAAGATCTCAATCGAGAAATGGTTTGT 360  
QY 361 ATGGCATGCCAGTGTGGAAATTTGATATGTTAAAGATCTGAAATGACAGACTTCCGA 420  
DB 361 ATGGCATGCCAGTGTGGAAATTTGATATGTTAAAGATCTGAAATGACAGACTTCCGA 420  
QY 421 AGAAATATTTCTTAATGTTTGTAAAGACCTGTGATCTTAAAGGATCTTAATCACTCAT 480  
DB 421 AGAAATATTTCTTAATGTTTGTAAAGACCTGTGATCTTAAAGGATCTTAATCACTCAT 480  
QY 481 AGTAGAGCAATGATATGCTATCCGACATGATGATCTTACACAGAGCTGCCAAAGAC 540  
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QY 601 AATATGACAAGCAGAGATATCTGTAATTAACCATGACTGTGTCAGAACAGATA 660  
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DB 661 ATTGCTGAAGCAATCAGAAAAAACTAGAAATGTTGCTATCATCTGAACAAATTTAAA 720  
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DB 721 CTCTGTGTTTGAATATCAGGCGCAATGATTTAAAGTGTGATGATGATGATATC 780  
QY 781 TTCTGAGAAAAATATCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 840  
DB 781 TTCTGAGAAAAATATCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 840  
QY 841 AGGATGCCCAATTTGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 900  
DB 841 AGGATGCCCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 900  
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QY 961 GAAATATCTACAAAAATCCCTTGGGTATTAATTAAGACATCAGATGATGATGATGAT 1020  
DB 961 GAAATATCTACAAAAATCCCTTGGGTATTAATTAAGACATCAGATGATGATGATGAT 1020  
QY 1021 GCAACCTAGTGAATCTTAATATTTGAGACATGATGATGATGATGATGATGATGATG 1080  
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DB 1081 TACATGAGAGAGAAACCTTATGATGATGATGATGATGATGATGATGATGATGATG 1140  
QY 1141 CCCAGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200  
DB 1141 CCCAGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200  
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DB 1201 CGACTTGGCTTTCATTTGCTGTGTAAGGCGAAAGGCTGTAAGAGAGAACTGT 1260  
QY 1261 CCATTGGCATGGGAAATATAACTTGTGATTAACAGACACTCTAGATCTGGAATA 1320  
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DB 1321 ATGCTTTGATCTTTGGCAGTACCTGATGATGATGATGATGATGATGATGATGATG 1380

QY 1381 GTTACTGATCAATCCAAATTAAGAACTCCATGCTTAGAGTTGAGTTGATGCTGTTTC 1440  
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 QY 1441 AGCAGTGTGGTAAAGTTCCAGATATGTCAGTATGTAAGAGCATGCAATTTGCTGTA 1500  
 DB 1441 AGCAGTGTGGTAAAGTTCCAGATATGTCAGTATGTAAGAGCATGCAATTTGCTGTA 1500  
 QY 1501 TCCCGAAGACAGAGATTAGCTATTTCCACGACGAGCTGAGTAAACAGACTAGTAGAC 1560  
 DB 1501 TCCCGAAGACAGAGATTAGCTATTTCCACGACGAGCTGAGTAAACAGACTAGTAGAC 1560  
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 DB 1561 AATGAATTAAGAGAAATGATTAAGAAACAGCTCCAGCAATTTGTACACAGATCTCTC 1620  
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 DB 1621 TCTGAATCACTGAGAGAGAAAGATTTTCTATGAGTCAAGACACTATGTAAC 1680  
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 QY 1741 GCCCAGATGATGCTTGTGTAAGAGATGGCTTCATCAACCTGACAGGCTATGGA 1800  
 DB 1741 GCTCAGATGATGCTTGTGTAAGAGATGGCTTCATCAACCTGACAGGCTATGGA 1800  
 QY 1801 CTCTGAGCTGTAATTAACCAAGATCTATGAGTGAAGTTTGTGCTGCTGCTGCTGGA 1860  
 DB 1801 CTCTGAGCTGTAATTAACCAAGATCTATGAGTGAAGTTTGTGCTGCTGCTGCTGGA 1860  
 QY 1861 AATATTTTAAACAGATGACAACTTTCTCAGTATTTAATTCAGCTAGTACAGGCTTAA 1920  
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 QY 2161 CAGAGAGAGAGATGAACACAAAAGGTACAGATGAAGTTTAACTTGAGCAAAATGAG 2220  
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DB 2461 GAAAAATATCTGCAAAAATCAAGGCTTGAATCTTGAAATGTTACTTATGAGATGCTGCTCA 2520  
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 QY 2641 CTCAAAGACAAAGCAAGGAGAAATATATGATGAGCCATTTGACCTGTTTACAGTTCA 2700  
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 DB 3001 CTTTCTCATATGCTTGTGCTGTGGAATGCCAATCTTAATCTTTTATGATGATGCA 3060  
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 DB 3061 TACATTTGAAAGACCTTACCTTATAGTAAATCTGAGCAAGAGCTTTGGAGTATTTCA 3120  
 QY 3121 AAACAATGAATGATGACATCATGCTGTGGAACAAAGAAATGATTTGATCTTCCAC 3180  
 DB 3121 AAACAATGAATGATGACATCATGCTGTGGAACAAAGAAATGATTTGATGATCTTCCAC 3180  
 QY 3181 ACAATTTAAACGATGATGATGCACTGA 3207  
 DB 3181 ACAATTTAAACGATGATGATGCACTGA 3207

Search completed: November 7, 2003, 10:43:54  
 Job time : 8225.09 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 05:29:07 ; Search time 4255.49 Seconds  
(without alignments)  
18316.216 Million cell updates/sec

Title: us-09-325-095-35

Perfect score: 3207  
Sequence: 1 ATGCTTCACAGACCATCATC.....AGCAGCATGCTTGAACTGA 3207

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estbda:\*  
2: em\_estbhum:\*  
3: em\_estlin:\*  
4: em\_estlmu:\*  
5: em\_estloy:\*  
6: em\_estlpl:\*  
7: em\_estlro:\*  
8: em\_estlc:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_estc:\*  
12: gb\_estc3:\*  
13: gb\_estc4:\*  
14: gb\_estc5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_man:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gssl:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2343	73.1	3866	11	AK051885 Mus muscu
2	748.4	23.3	872	13	BQ228953 AGENCOURT
3	697.8	21.8	750	9	AL706270 DKFZP6860
4	688.6	21.5	1063	12	BM470620 AGENCOURT

5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45																																																																																																																																																															
671.4	20.9	834	13	BX437220	669.2	20.9	883	13	BU167122	651.4	20.3	854	14	CB723732	650.6	20.3	809	14	CB246283	622.8	19.4	785	14	CD349473	614.2	19.2	759	14	CB520825	612.2	19.1	733	12	BM986382	605	18.9	833	12	BM986382	599.2	18.7	844	9	AU129890	599	18.7	844	10	BG391265	578.2	18.0	666	14	CD351100	574.2	17.9	1051	12	BG974639	559.4	17.4	627	2	HSM084196	552.8	17.2	730	13	BU481912	550	17.1	706	9	AU134684	523.2	16.3	759	12	BG867168	514.4	16.0	636	9	AV693521	508.6	15.9	548	9	AU280420	507	15.8	798	10	BG436153	500.6	15.6	663	10	BB657738	500.4	15.6	864	10	BF242935	494.4	15.4	685	10	AW914263	485.2	15.1	767	14	CB964053	481.6	15.0	600	12	BG806901	478.8	14.9	614	13	BU478467	477	14.9	613	12	BI249391	475.8	14.8	841	14	CA791375	474.2	14.8	836	10	BF691754	473.8	14.8	887	14	CA986999	472.8	14.7	827	13	BX437219	468.6	14.6	533	10	BE279196	468.2	14.6	918	10	BF784374	464.4	14.5	848	13	BU306943	463.4	14.4	531	9	AW209721	462.8	14.4	601	10	BE379970	452.8	14.1	505	2	HSM096925	445.8	13.9	563	13	BO570031	445.6	13.9	784	14	CA511243	443.6	13.6	609	13	BU396606	434.6	12.8	789	13	BU852815

## ALIGNMENTS

RESULT 1  
AK051885  
LOCUS  
DEFINITION Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length  
3-kinase, catalytic, alpha polypeptide, full insert sequence.  
ACCESSION AK051885  
VERSION AK051885.1 GI:26094824  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE  
1 Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
JOURNAL MEDLINE 20495374  
PUBMED 11042159

REFERENCE AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsuna, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, K., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaihiagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
TITLE	4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, K., Hara, A., Fukunishi, Y., Konno, H., Maachi, D., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kanukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Mateno, Y., Nikaïdo, I., Pesole, G., Tomita, M., Quekkehush, D., Schriml, L. M., Staudl, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Buit, C., Fletcher, C., Fujita, M., Gariboldi, M., Gestblom, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Mochizuki, J., Washima, J., Mazzarelli, J., Mombere, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wyshaw-Borja, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohlski, S. and Hayashizaki, Y. Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
TITLE	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	6 (bases 1 to 3866) Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-resgsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]
COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse cDNAs. Please visit our web site for further details. URL: http://fantom.gsc.riken.go.jp/ URL: http://genome.gsc.riken.go.jp/ location/Qualifiers
FEATURES	

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	ORIGIN	
	Query Match	73.1%; Score 2343; DB 11; Length 3866;
	Best Local Similarity	88.6%; Pred. No. 0;
	Matches 2538; Conservative	0; Mismatches 325; Indels 0; Gaps 0;
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QY	465	TCTTAATTCCTCATATGATGAGCAATGATATGTTATCTTCGCAATGTAGATTTACC 524
DB	153	TCTCACTCGCTCATATGAGCAATGATATGTTATCTTCGCAATGTAGATTTACC 212
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832  
833  
834  
835  
836  
837  
838  
839  
840  
84

BASE COUNT	227 a	147 c	165 g	208 t	3 others
------------	-------	-------	-------	-------	----------





QY 1478 AAGAGATGCAATTTGGTCTGATCCCGAGAGAGATTTAGTATTCCTCCATGCAGAGC 1537  
 DB 607 AAGAGATGCAATTTGGTCTGATCCCGAGAGAGATTTAGTATTCCTCCATGCAGAGC 666  
 QY 1538 TGAGTACAGACTAGCTAGAGACAAATGATTAAGAGAAATGATTAAGAAAGACCTCCAG 1597  
 DB 667 TGAGTACAGACTAGCTAGAGACAAATGATTAAGAGAAATGATTAAGAAAGACCTCCAG 726  
 QY 1598 CAATTTGACAGAGATCTCTATCTGAAA--TCACTGAGCA-AGAGAAAGATTTCTGT 1654  
 DB 727 CAATTTGACAGAGATCTCTCTGAAAATCACTGAGCAGAGAGAAAGATTTCTAT 786  
 QY 1655 GG-AGCCACAGACACTATT 1672  
 DB 787 GGAAGTCACAGACCTATT 805  
 RESULT 5  
 BX437220 834 bp mRNA linear EST 15-MAY-2003  
 LOCUS BX437220 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP005YF10  
 DEFINITION 5-PRIME, mRNA sequence.  
 ACCESSION BX437220  
 VERSION BX437220.1 GI:30781556  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE Li, W.B., Gruber, C., Jessup, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 1992.f For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0CAP005YF10&cluster=1992.f. Contact :  
 Feng Liang Email : fliang@life-tech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CS0CAP005YF10.  
 FEATURES  
 source location/Qualifiers  
 1. 834  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="CS0CAP005YF10"  
 /issue\_type="THYMUS"  
 /clone\_id="Homo sapiens THYMUS"  
 /note="Vector: PCWVS/PORT 6; 1st strand cDNA was primed  
 with a NotI-oligo(dT) primer. Five prime end enriched,  
 double-strand cDNA was digested with Not I and cloned into  
 the Not I and EcoRV sites of the PCWVS/PORT 6 vector.  
 Library was not normalized."  
 BASE COUNT 256 a 152 c 184 g 241 t 1 others  
 ORIGIN  
 Query Match 20.9%; Score 671.4; DB 13; Length 834;  
 Best Local Similarity 94.8%; Pred. No. 1.8e-150;  
 Matches 693; Conservative 1; Mismatches 37; Indels 0; Gaps 0;  
 QY 1742 CTGAGATGATCTCTGTTAAAGATGGCTCCATCAAGCTGAACAGGCTATGAGC 1801  
 DB 104 CACAGAGATGATCTCTGTTAAAGATGGCTCCATCAAGCTGAACAGGCTATGAGC 163  
 QY 1802 TTCTGAGCTCAATTAACCAAGATCTATGTTCCAGGTTTGTCTGTTGGTCTTGA 1861  
 DB 164 TTCTGAGCTCAATTAACCAAGATCTATGTTCCAGGTTTGTCTGTTGGTCTTGA 223

QY 1862 AATATTTAAGATGACAAACTTCTCAGTACTTAATCAGTAGTACAGTACTTAAT 1921  
 DB 224 AATATTTAAGATGACAAACTTCTCAGTACTTAATCAGTAGTACAGTACTTAAT 283  
 QY 1922 ATGAACAGATTTGGATTAACCTGCTTGGATTTTAACTCAAAAAGCGTTAACT 1981  
 DB 284 ATGAACAGATTTGGATTAACCTGCTTGGATTTTAACTCAAAAAGCGTTAACT 343  
 QY 1982 AAAGATCGGTCACTTTTCTTTGGCATTTAAATTCGAGATGACATTAAGAGTTA 2041  
 DB 344 AAAGATCGGTCACTTTTCTTTGGCATTTAAATTCGAGATGACATTAAGAGTTA 403  
 QY 2042 GTCAAGATTTGGCGCTTTTGGAGTCTTATTCGCGTCAATGAGATGATCTGA 2101  
 DB 404 GCCAGAGTTTGGCGCTTTTGGAGTCTTATTCGCGTCAATGAGATGATCTGA 463  
 QY 2102 ACCTTAATAGGCAAGTGGAGCTATGAAAAGCTCAATTAAGTACTGACATTTCA 2161  
 DB 464 ACCTTAATAGGCAAGTGGAGCTATGAAAAGCTCAATTAAGTACTGACATTTCA 523  
 QY 2162 AAGAGAAAGAGATGAACCAAAAGCTACAGATGAAGTTTATGTTGAGCAATG 2221  
 DB 524 AAGAGAAAGAGATGAACCAAAAGCTACAGATGAAGTTTATGTTGAGCAATG 583  
 QY 2222 GACCAATTTCAATGAGATGCTCTCAGGCTTTCTCTCTCTCTCTCTCTCTCT 2281  
 DB 584 GACCAATTTCAATGAGATGCTCTCAGGCTTTCTCTCTCTCTCTCTCTCTCTCT 643  
 QY 2282 TGGGAATTCACAGCTTGAAGATGTCGATTAATGTTCTTCTGCAAAAAGCCACT 2341  
 DB 644 TAGGAACCTCAGGCTTGAAGATGTCGATTAATGTTCTTCTGCAAAAAGCCACT 703  
 QY 2342 TGAATTTGGAGAACCCAGACATCATGTCAGATTAATCTCTGCAAAAAGATCAT 2401  
 DB 704 TGAATTTGGAGAACCCAGACATCATGTCAGATTAATCTCTGCAAAAAGATCAT 763  
 QY 2402 TTAATAATGGGATGATTTACGGCAGATGATGTCACCTTCAGATTATTCGATTA 2461  
 DB 764 TTAATAATGGGATGATTTACGGCAGATGATGTCACCTTCAGATTATTCGATTA 823  
 QY 2462 AAAATATCTGG 2472  
 DB 824 AAAATATCTGG 834

RESULT 6  
 BU167122 883 bp mRNA linear EST 04-SEP-2002  
 LOCUS AGENCOURT\_7958965 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6163390  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BU167122  
 VERSION BU167122.1 GI:22681087  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE NIH-MGC http://mgs.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 AUTHORS Unpublished  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cga@bbs-r@mail.nih.gov  
 Tissue Procurement: ATCC/DCID/DTF  
 DNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNL at:  
 http://image.llnl.gov  
 plate: LLM13518 row: m column: 23  
 High quality sequence stop: 555.  
 Location/Qualifiers

FEATURES



source 1. .883  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
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 /lab\_host="DH10B (phage-resistant)"  
 /clone\_1b="NIH\_MGC\_72"  
 /note="Organ: skin; Vector: PCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: oligo dT.  
 Average insert size 2 kb. Library constructed by Life  
 Technologies."

BASE COUNT 272 a 161 c 189 g 261 t

Query Match 20.3%; Score 669.2; DB 13; Length 883;  
 Best Local Similarity 92.3%; Pred. No. 6.2e-150; Indels 2; Gaps 1;  
 Matches 716; Conservative 0; Mismatches 58;

682 AAAAGTGAAGTATGTTGCTATCATCTGAACAATAAAGCTGTTTGAATATCAG 741  
 1 ATAAGTGAAGTATGTTGCTATCATCTGAACAATAAAGCTGTTTGAATATCAG 60

742 GCGAAGTATATTTTAAAGCTGTGATGATGATGATGATGATGATGATGATGAT 801  
 61 GCGAAGTATATTTTAAAGCTGTGATGATGATGATGATGATGATGATGATGAT 120

802 AGTCAGAT 861  
 121 AGTCAGAT 180

862 ATGGCTAAAGAAAGCTTATATCTCACTGCAATGAGCTGTTTACATGCCATCAT 921  
 181 ATGGCTAAAGAAAGCTTATATCTCACTGCAATGAGCTGTTTACATGCCATCAT 240

922 TCCAGAGCATCTCCACAGCTACGCCATATATGATGAGAAACATCTACAAATCCCTT 981  
 241 TCCAGAGCATCTCCACAGCTACGCCATATATGATGAGAAACATCTACAAATCCCTT 300

982 TGGGTTATATAATGTGCACTCAGATATAAATCTTTGTGCACTCAGATATAAAT 1041  
 301 TGGGTTATATAATGTGCACTCAGATATAAATCTTTGTGCACTCAGATATAAAT 360

1042 ATTCGACATTTGACAAAGATTTATGTTCGAACAGATATACCATGGAGAGAACCTTTA 1101  
 361 ATTCGACATTTGACAAAGATTTATGTTCGAACAGATATACCATGGAGAGAACCTTTA 420

1102 TGTGATATATGTGAACACTCAAGAGTACCTTTGCCAATCCAGGTGGAATGAGCTTG 1161  
 421 TGTGATATATGTGAACACTCAAGAGTACCTTTGCCAATCCAGGTGGAATGAGCTTG 480

1162 AATTAGAT 1221  
 481 AATTAGAT 540

1222 TGTGTTAAAGGCCGAAGGCTGCTAAAGAGAAACATGTCATTTGGCTGAGAAATAT 1281  
 541 TGTGTTAAAGGCCGAAGGCTGCTAAAGAGAAACATGTCATTTGGCTGAGAAATAT 600

1282 AACTGTTTGAATTAACAGACTAGTATCTGAAAAATGACTTTGAATCTTTGGCCA 1341  
 601 AACTGTTTGAATTAACAGACTAGTATCTGAAAAATGACTTTGAATCTTTGGCCA 660

1342 GTAACCTAGGATTAAGATTTGCTGAAGCC--TATGGTGTATCTGATCAAAATCCAA 1399  
 661 GTAACCTAGGATTAAGATTTGCTGAAGCCCTATTTGGTGTATCTGATCAAAATCC 720

1400 ATTAAGAACTCATGTTTGAAGTGAAGTTGACTGTTCAAGCAAGTGTGTAAG 1455  
 721 ATTAAGAACTCATGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 776

CB723732  
 LOCUS 854 bp mRNA linear EST 10-APR-2003  
 DEFINITION UI-M-FYO-cez-b-21-0-UI-r1 NIH BMAP\_FYO Mus musculus CDNA clone  
 IMAGE: 6844054 5', mRNA sequence.

ACCESSION CB723732  
 VERSION CB723732.1 GI:29780874  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euleleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 854)  
 NIH-MGC http://mgi.mc.nhl.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished

AUTHORS Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: Dr. Jim Lin, University of Iowa  
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at  
 http://genome.uiowa.edu/distribution/mousefl.html  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)

COMMENT Seq primer: pyx-5.  
 Location/Qualifiers  
 1. 854  
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 /mol\_type="mRNA"  
 /strain="C57BL/6"  
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 /clone="IMAGE: 6844054"  
 /tissue\_type="whole brain"  
 /dev\_stage="embryo 13.5,14.5,16.5,17.5,pcp"  
 /lab\_host="DH10B (T1 phage resistant)"  
 /clone\_1b="NIH BMAP FYO"  
 /note="Organ: Brain; Vector: pyx-Asc; Site 1: EcoR I;  
 Site 2: Not I; The library was constructed according  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. Denatured RNA was size fractionated on a 1% agarose  
 gel. First strand cDNA synthesis was primed with oligo-dT  
 primer containing a Not I site. Double strand cDNA was  
 size selected according to mRNA size fraction. Ligated  
 with EcoR I adaptor, digested with NotI and then cloned  
 directionally into pyx-Asc vector. The library tag  
 sequence located between the Not I site and the polyA tail  
 is AGGAGACAG. This library was created for the University  
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
 Developing Mouse Nervous System', supported by National  
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
 program coordinator."

BASE COUNT 262 a 180 c 189 g 219 t 4 others

Query Match 20.3%; Score 651.4; DB 14; Length 854;  
 Best Local Similarity 87.9%; Pred. No. 1.2e-145;  
 Matches 742; Conservative 0; Mismatches 99; Indels 3; Gaps 3;

67 GAATGTTTACTCAAAATGGATGATGATGATGATGATGATGATGATGATGATGAT 125  
 2 GAATGTTTACTCCCAATGATGATGATGATGATGATGATGATGATGATGATGAT 61

126 AATTAGCAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 185  
 62 CGTACCAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 121

186 TCAAGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 245  
 122 GCAAGATGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 181

246 TTTGATGAACAGACATTTGATGATGATGATGATGATGATGATGATGATGATGAT 305

Db 182 TTTTGATGAACAAGACGACTTGTGACCTTCGGCTTTTTCACCTTTTAAAGTAT 241

Qy 306 TGACCAAGTACGACACCGTGAAGAAAAGATCCCAATCGAAGATTGGTTTCTATCG 365

Db 242 TGAACCAAGTACGACACCGTGAAGAAAAGATCCCAATCGAAGATTGGTTTCTATCG 301

Qy 366 CATGCCAGTGTGATTCGATATGTTAAAGATCCAGAGTACAGACTTCCGAGAAA 425

Db 302 CATGCCAGTGTGATTCGATATGTTAAAGATCCAGAGTACAGACTTCCGAGAAA 361

Qy 426 TATTCATATGTTTGAAGAGCTGTGATCTTAGGGATCTTAATCACTCATAGTAG 485

Db 362 CATTCGATATGTTTGAAGAGCTGTGACCTTCGGGATCTCAACTCGCTCATAGTAG 421

Qy 486 AGCAATATGTTTATCTCTCCAAATCTGAATCTTCCAGAACTGCGCAAGACATATA 545

Db 422 AGCAATATGTTTATCTCTCCAAATCTGAATCTTCCAGAACTGCGCAAGACATATA 481

Qy 546 TAAATTAATGGAATTAAGGCAATATATAGTATGTTGGTAAATAGTTTCTCCAAATA 605

Db 482 CAACAAGTATGATTAAGGCAATATATAGTATGTTGGTAAATAGTTTCTCCAAATA 541

Qy 606 TGAACAAAGAGATATCTCTGAAGAAATCAACCATGACTGTGTCCAGAACAGTAAATGC 665

Db 542 CGACAAAGAGATATCTCTGAAGAAATCAACCATGACTGTGTCCAGAACAGTAAATGC 601

Qy 666 TGAACCAATCGAGAAAAAAATCTCAAGATCTCTCATCTGAACCAACTAAACTCTG 725

Db 602 TGAAGCATCGAGAAAAAAATCTCAAGATCTCTCATCTGAACCAACTAAACTCTG 661

Qy 726 TGTTTGAATATCGAGCAAGTATATTTTAAAGTGTGTGATGATGATACTTCTCT 785

Db 662 TGTCTTAAGATATCGAGCAAGTATATTTTAAAGTGTGTGATGATGATACTTCTCT 721

Qy 786 AGAAAAATATCTCTGAGTCAATATATATTAAGAAAGCTGTATATAGCTTGGAGAGAT 845

Db 722 GAAAAAGTACCTCTGAGTCAATATATTAAGAAAGCTGTATATAGCTTGGAGAGAT 781

Qy 846 GCCCAATTTGATGCTGATGCTTAAGAAAGCTCTATCTCAACGCGCAATGATGTTT 905

Db 782 GNCCTACTTGATGCTGATGCTTAAGAAAGCTCTATCTCAACGCGCAATGATGTTT 839

Qy 906 TACA 909

Db 840 CACA 843

RESULT 8  
CB246283 809 bp mRNA linear EST 12-FEB-2003  
LOCUS UI-M-POD-cdv-f-18-0-UI.r1 NIH\_BMAP\_F00 Mus musculus cDNA clone  
DEFINITION IMAGE: 6834931 5', mRNA sequence.  
ACCESSION CB246283  
VERSION CB246283.1 GI:28367927  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 809)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
<http://image.lnl.gov>  
This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)  
Seq primer: pYX-5.  
Location/Qualifiers  
FEATURES  
source  
1..809  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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/db\_xref="taxon:10090"  
/clone="IMAGE: 6834931"  
/tissue\_type="whole brain"  
/dev\_stage="embryo 12.5dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH BMAP F00"  
/note="Togian: Brain: Vector: pYX-Asc: Site 1: Ecor I;  
Site 2: Not I; The library was constructed according  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction. Ligated  
with Ecor I adaptor, digested with NotI and then cloned  
directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is TGAGAGAGCC. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the  
Developing Mouse Nervous System", supported by National  
Institute of Mental Health (NIMH), Hemm Chin, Ph.D.,  
program coordinator."

BASE COUNT 248 a 173 c 179 g 206 t 3 others

ORIGIN  
Query Match 20.3%; Score 650.6; DB 14; Length 809;  
Best Local Similarity 88.5%; Pred. No. 1.8e-145;  
Matches 715; Conservative 0; Mismatches 92; Indels 1; Gaps 1;

Qy 177 TCAACTCTTCAAGATGATATCTTCTTACATTTTCTGAAGTGTATACCAAGACAGAAAG 236

Db 1 TCACTCTCTGACAGACAGAACTTTTACATTTTGTAGTGTATACCAAGACAGAAAG 60

Qy 237 GGAAGAAATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 296

Db 61 GGAAGAAATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120

Qy 297 AAAAGTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 356

Db 121 AAAAGTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180

Qy 357 TGCTATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCAT 416

Db 181 TGCTATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCATGCGCAT 240

Qy 417 CCGAAGAAATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 476

Db 241 TCGAAGAAATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300

Qy 477 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 536

Db 301 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360

Qy 537 GCACAT 596

Db 361 GCACAT 420

Qy 597 TCCAAAT 656

Db 421 TCCAAAT 480

Qy 657 AGTAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 716

Db 481 AGTAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540

Qy 717 AAAGCTGCTGTTTGAATATCAGGCGCAAGTATATTTTAAAGTGTGTGATGATGATGA 776

Db 541 GAAACTCTGTCTTAGAATATCAGGCAAGTATATTCTGAAAGTGTGTGCTGTGACGA 600

QY 777 ATACTCTTCAAGAAAATATCTCTAGTCAGTATAGTATATAGAAAGCTGTATATGCT 836

Db 601 ATACTCTTCAAGAAAATATCTCTAGTCAGTATAGTATATAGAAAGCTGTATATGCT 660

QY 837 TGGAGAGATGCCAATTTGATGCTGATGCTAAAGAAAGCTCTATTTCTCACTGGCAAT 896

Db 661 GGGGAGAGATGCCAATTTGATGCTGATGCTAAAGAAAG-CTATATCTCTAGCTGCCGAT 719

QY 897 GAGCTGTTTACATGCGCATATTTCCAGAGCGCATCTCCAGCGCATATATAGAA 956

Db 720 TGTATGTTACCATGCGCATATCTCAAGCGCATCTCCAGCGCATATATAGAA 779

QY 957 TGGAGAAACATCTACAAATCCCTTTG 984

Db 780 TGGAGAGACATCTACGAAATCTCTG 807

RESULT 9  
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LOCUS UI-M-FY0-c-fg-j-12-0-UI.r1 NIH\_BMAP\_FY0 Mus musculus cDNA clone  
DEFINITION IMAGE: 6854605 5', mRNA sequence.  
ACCESSION CD349473.1 GI:31140988  
VERSION CD349473.1  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 785)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-rc@mail.nih.gov](mailto:cgabbs-rc@mail.nih.gov)  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mouse1.html>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)  
Seq primer: pYX-5.  
Location/Qualifiers  
1. 785  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE: 6854605"  
/tissue\_type="whole brain"  
/dev\_stage="embryo 13.5,14.5,16.5,17.5dpf"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH BMAP\_FY0"  
/note="Organ: Brain; Vector: pYX-Agc; Site 1: Ecor I;  
Site 2: Not I; The library was constructed according  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction. Ligated  
with Ecor I adaptor, digested with NotI and then cloned  
directionally into pYX-Agc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is AGCGAGACAG. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,  
program coordinator." 169 c 172 g 203 t 3 others

BASE COUNT 238 a

ORIGIN

Query Match 19.4%; Score 622.8; DB 14; Length 785;  
Best Local Similarity 88.3%; Pred. No. 8.9e-139;  
Matches 686; Conservative 0; Mismatches 90; Indels 1; Gaps 1;

QY 241 GAAATTTTGGATGAAACAAGACGATTTGTGACCTTGGCTTTTCAACCTTTTAAAA 300

Db 1 GAAATTTTGGATGAAACAAGACGATTTGTGACCTTGGCTTTTCAACCTTTTAAAA 60

QY 301 GTAATTAACCAATAGGCAACCGCTGAAGAAATCTCAATGAGAAATTTGTTTGT 360

Db 61 GTTATTAACCAATAGGCAACCGCTGAAGAAATCTCAATGAGAAATTTGTTTGT 120

QY 361 ATCGCATGCCATGCTGTGTAATTCGATATGTTAAAGATCCAGAAAGTACAGACTTCGA 420

Db 121 ATTGGCATGCCATGCTGTGTAATTCGATATGTTAAAGATCCAGAAAGTACAGACTTCGA 180

QY 421 AGAATATTTCTCAATGTTGTGTAAGAAAGCTGTGATCTTAAGGATCTTAATTCACCTCAT 480

Db 181 AGAATATTTCTCAATGTTGTGTAAGAAAGCTGTGATCTTAAGGATCTTAATTCACCTCAT 240

QY 481 AGTAGAGCAATGATGTTTATCTCTCCAAATGTGAATCTTACCAAGACTGCGCAAGCAC 540

Db 241 AGCAGAGCAATGATGTTTATCTCTCCAAATGTGAATGTGCTCCAGAACTGCCAAAGCAC 300

QY 541 ATATATATTAATTTGATTAAGGCAAAATTAATGATGTTGGTAAATAGTTTCTCCA 600

Db 301 ATCTACAAACAGTTAATTAAGGCAAAATTAATGATGTTGGTAAATAGTTTCTCCA 360

QY 601 AATTAATGACAAACAGAAATTAATCTGAAATTAACCATGACTGTGTGCCAGAAAGTA 660

Db 361 AATTAATGACAAACAGAAATTAATCTGAAATTAACCATGACTGTGTGCCAGAAAGTA 420

QY 661 ATTGCTGAAGCAATCGAGAAAAAACTCGAAGTATGTTGCTATCACTGAACAATTA 720

Db 421 ATTGCTGAAGCAATCGAGAAAAAACTCGAAGTATGTTGCTATCACTGAACAATTA 480

QY 721 CTCTGATTTTGAATATACAGGGCAAGTATTTTAAAGTGTGTGATGATGTAATAC 780

Db 481 CTCTGATTTTGAATATACAGGGCAAGTATTTTAAAGTGTGTGATGATGTAATAC 540

QY 781 TTCTTGAAGAAATATCTCTGAGTCAATTAATTAAGAAAGCTGTAATGCTTGGG 840

Db 541 TTCTTGAAGAAATATCTCTGAGTCAATTAATTAAGAAAGCTGTAATGCTTGGG 600

QY 841 AGGATGCCAATTTGATGCTGATGCTTAAGAAAGCTCTTATTTCACTGCAATGAC 900

Db 601 AGGATG-CCAATTTGATGCTGATGCTTAAGAAAGCTCTTATTTCACTGCAATGAC 659

QY 901 TGTTTTCAATGCGCATATTTCCAGACCATCTCCAGCGCTACGCGCATATAGATGA 960

Db 660 AGCTTACCAATGCGCATATTTCCAGACCATCTCCAGCGCTACGCGCATATAGATGA 719

QY 961 GAAACATCTACAAATCCCTTTGGGTTAATTAAGTCACTGCAATTAATTTCTT 1017

Db 720 GAGACATCTACGAAATCTCTGGGCTAATTAAGTCACTGCAATTAATTTCTT 776

RESULT 10  
CB520825 759 bp mRNA linear EST 28-MAR-2003  
LOCUS UI-M-GH0-cel-r-01-0-UI.r1 NIH\_BMAP\_GH0 Mus musculus cDNA clone  
DEFINITION IMAGE: 6841250 5', mRNA sequence.  
ACCESSION CB520825.1 GI:29354180  
VERSION CB520825.1  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 759)  
NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
http://genome.uiowa.edu/distribution/mouse1.html  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES  
Seq primer: PYX-5.  
Location/Qualifiers

1..759  
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/mol\_type="mRNA"  
/strain="CS7BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:6841250"  
/tissue\_type="whole brain"  
/dev\_stage="1, 5, and 15 days newborn"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH\_BMAP\_GHO"  
/note="Organ: Brain; Vector: pYX-Asc; Site\_1: EcoR 1; Site\_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGTGAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

BASE COUNT 232 a 161 c 168 g 197 t 1 others

ORIGIN

Query Match 19.2%; Score 614.2; DB 14; Length 759;  
Best local Similarity 88.8%; Pred. No. 1e-136;  
Matches 675; Conservative 0; Mismatches 84; Indels 1; Gaps 1;

QY 1397 CAAATTAAGAACTCCATGTTTGAAGCTTGGAGTTGACCTGTTCCAGCAGTGTGTAAGT 1456  
1 CAAATTAAGAACTCCATGTTTGAAGCTTGGAGTTGACCTGTTCCAGCAGTGTGTAAGT 60

QY 1457 TTCGAGATTCCTGAGTGAAGGATGCAATGCTGTATCCCGTAAGCAGAT 1516  
61 TTCGAGATTCCTGAGTGAAGGATGCAATGCTGTATCCCGTAAGCAGAT 120

QY 1517 TTAGTATTCCTGAGTGAAGGATGCAATGCTGTATCCCGTAAGCAGAT 1576  
121 TCAGTATTCCTGAGTGAAGGATGCAATGCTGTATCCCGTAAGCAGAT 180

QY 1577 ATGATTAAGAACTCCATGTTTGAAGCTTGGAGTTGACCTGTTCCAGCAGTGTGTAAGT 1636  
181 ATGATTAAGAACTCCATGTTTGAAGCTTGGAGTTGACCTGTTCCAGCAGTGTGTAAGT 240

QY 1637 AAGAGAAAGATTTTCTGAGTGAAGGATGCAATGCTGTATCCCGTAAGCAGAT 1696  
241 AAGAGAAAGATTTTCTGAGTGAAGGATGCAATGCTGTATCCCGTAAGCAGAT 300

QY 1697 CCAATTTGCTTCTGCTGTTAATGAAGTCTGAGTGAAGTGAAGTGAAGTGAAGT 1756  
301 CCAATTTGCTTCTGCTGTTAATGAAGTCTGAGTGAAGTGAAGTGAAGTGAAGT 360

QY 1757 TGTATAAAGATTTGGCTTCAATCAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGT 1816  
361 TGTATAAAGATTTGGCTTCAATCAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGT 420

QY 1817 ACCAGATTCCTAATGTTGAGGTTTGGCTTGGGCTTAGAAAAATTTAACAGATG 1876  
Db 421 ATCCAGATTCCTAATGTTGAGGTTTGGCTTGGGCTTAGAAAAATTTAACAGATG 480  
QY 1877 ACAACCTTCTAGTACCTAATTCAGTACAGTACCTAATTAATTAAGACGATTTGG 1936  
Db 481 ACAACCTTCTAGTACCTAATTCAGTACAGTACCTAATTAATTAAGACGATTTGG 540  
QY 1937 ATACCTGCTTGTGAGATTTTACTCAAAAAGCGTTAATCTAATCAAGATCGGCACT 1996  
Db 541 ATACCTGCTTGTGAGATTTTACTCAAAAAGCGTTAATCTAATCAAGATCGGCACT 600  
QY 1997 TTTTCTTTTGGCATTAAATCTGAGATGACATTAACAGTACTGACAGTTGGCC 2056  
Db 601 TTTTCTTTTGGCATTAAATCTGAGATGACATTAACAGTACTGACAGTTGGCC 660  
QY 2057 TGGCTTTGAGTCTTATTTGGCTGATGTTGAGTGTATCTGAAGCACTTAATAGCAAG 2116  
Db 661 TGGCTTTGAGTCTTATTTGGCTGATGTTGAGTGTATCTGAAGCACTTAATAGCAAG 719  
QY 2117 TTGAGGCTATGAAAGCTCATTAACTTGACTGACATTC 2156  
Db 720 TTGAGGCTATGAAAGCTCATTAACTTGACTGACATTC 759

RESULT 11  
Bg497751  
LOCUS 753 bp mRNA linear EST 27-MAR-2001  
DEFINITION 602543009F1 NIH\_MGC\_60 Homo sapiens cDNA clone IMAGE:4665482 5', mRNA sequence.

ACCESSION Bg497751 GI:13459268  
VERSION Bg497751.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 753)  
NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: DCTD/DTF  
CDNA Library Preparation: CLONETECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.lln.gov  
Plate: L10M1471 row: a column: 03  
High quality sequence stop: 649.

FEATURES  
source

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4665482"  
/tissue\_type="adenocarcinoma"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_60"  
/note="Organ: prostate; Vector: pBNR-LIB (Clontech); Site\_1: SfiI (ggcgctcgcc); Site\_2: SfiI (ggcgctcgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGCGCGCGCATG-3' and 3' adaptor sequence: 5'-CACGGCATTAAGGCG-3' (30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC

BASE COUNT 241 a 136 c 176 g 200 t

Library "

Query Match 19.1% Score 612.2; DB 10; Length 753;  
Best Local Similarity 90.9%; Pred. No. 3.1e-136;  
Matches 666; Conservative 0; Mismatches 63; Indels 6; Gaps 3;

2080 GCATGTTGGATGTAATCTGAAGCAGCTTAATAGGCAAGTTGAGGCTATGAGAAAGCTATT 2139  
1 GCATGTTGGATGTAATCTGAAGCAGCTTAATAGGCAAGTTGAGGCTATGAGAAAGCTATT 60

2140 AACTTGCTGACATCTTCCAAACAGAGAAAGAGATGAAACAAACAAAGTTACAGATGAG 2199  
61 AACTTGCTGACATCTTCCAAACAGAGAAAGAGATGAAACAAACAAAGTTACAGATGAG 120

2200 TTTTGTAGTGAAGCAATGCGGCGCAGATTTTCAATGATGCTCTCCAGGGCTTCTCTCT 2259  
121 TTTTGTAGTGAAGCAATGCGGCGCAGATTTTCAATGATGCTCTCAAGGGCTTCTCTCT 180

2260 CCTTAAACCTGCTCATGCTGAGGAAATCTCAGGCTTGAAGAGTGTGCAATTTATGCT 2319  
181 CCTTAAACCTGCTCATGCTGAGGAAATCTCAGGCTTGAAGAGTGTGCAATTTATGCT 240

2320 TCTGCAAAAAGGCCACTGTGTTGAATTTGGAGAACCCAGACATCATGTCAGAAATTA 2379  
241 TCTGCAAAAAGGCCACTGTGTTGAATTTGGAGAACCCAGACATCATGTCAGAAATTA 300

2380 TTTTCAAGCAATGAGATCATCTTAAATAGGGAGATGATTTACGGCAAGATATGCTAAC 2439  
301 TTTTCAAGCAATGAGATCATCTTAAATAGGGAGATGATTTACGGCAAGATATGCTAAC 360

2440 CTTTCAAGTATTCGATTTATGAAATATCTGCAAAATCATAGGCTTGTATCTTCAATG 2499  
361 CTTTCAAGTATTCGATTTATGAAATATCTGCAAAATCATAGGCTTGTATCTTCAATG 420

2500 TTAACCTTATGAGATGCTGCTCAATGCTGATGCTGTGTGGACTTATTCAGAGTGTGAGA 2559  
421 TTAACCTTATGAGATGCTGCTCAATGCTGATGCTGTGTGGACTTATTCAGAGTGTGAGA 480

2560 TCTCACACTTAATGAGATTCAGTGTGAAGAGGCTTGAAGAGTGTGACCTGCACTTTAAC 2619  
481 TCTCACACTTAATGAGATTCAGTGTGAAGAGGCTTGAAGAGTGTGACCTGCACTTTAAC 540

2620 AGCCACACACTCCATCAGTGGCTCAAGACAGAAACAGAGGGGAAATATATGATGCGGCC 2679  
541 AGCCACACACTCCATCAGTGGCTCAAGACAGAAACAGAGGGGAAATATATGATGCGGCC 600

2680 ATCGATTTGTTTACAGGATCATGCTGATGATTTGTTGCACTTCATTT--TGGGAA 2737  
601 ATCGATTTGTTTACAGGATCATGCTGATGATTTGTTGCACTTCATTTGCGGGAAAT 660

2738 TTGGAATGCTGCATAG--TAATATCATGTTTAAAGATATGAGACACTGTTTATATA 2796  
661 TTGGAATGCTGCATAG--TAATATCATGTTTAAAGATATGAGACACTGTTTATATA 720

2797 GATTTTGAACCTTTTGGATCAACAAGAGAAAA 2831  
721 GATTTG---ACATTTGATTCACAGAGAAAA 752

RESULT 12  
BM986382 833 bp mRNA linear EST 25-MAR-2002  
LOCUS BM986382  
DEFINITION EST511169 Rat gene index, normalized rat, norvegicus Rattus  
subunit alpha, mRNA sequence.  
ACCESSION BM986382  
VERSION BM986382.1 GI:19705771  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 833)  
AUTHORS Malek,R.L., Cho,J., Lee,Y., Karamycheva,S., Parvizi,B., Pertea,G.,  
Sultana,R., Tsai,J., White,J., Quakenbush,J. and Lee,N.H.  
TITLE Generation of ESTs from a rat multiple tissue survey  
JOURNAL Unpublished  
COMMENT Other ESTs: EST445877 EST345567  
Contact: Lee, NH  
The Institute for Genomic Research  
9712, Medical Center Drive, Rockville, MD 20850, USA  
Tel: (301)-838-3529  
Fax: (301)-838-0208  
Email: nhlee@tigr.org  
This clone is available through the ATCC, contact the ATCC  
tel#703-365-2700 for further information  
Seq primer: M13 reverse.

FEATURES  
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Location/Qualifiers  
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/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="RG1AC69"  
/tissue\_type="mixed tissue"  
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/note="Vector: pT73pac; Site 1: EcoRI; Site 2: NotI;  
Combination of untreated and NGF-treated p12 cell  
libraries, and Benco Soares normalized libraries of ovary,  
brain, kidney, liver, placenta, lung, embryo, skeletal  
muscle, spleen, heart"

BASE COUNT 225 a 196 c 224 g 188 t

Query Match 18.9% Score 605; DB 12; Length 833;  
Best Local Similarity 86.9%; Pred. No. 1.8e-134;  
Matches 665; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

2044 CAGAGTTTGGCTGCTTTGAGATGCTTATGCGGATGAGATGATGATGAGAAC 2103  
69 CAGAGTTTGGCTGCTTTGAGATGCTTATGCGGATGAGATGATGATGAGAAC 128

2104 CTTAATAGCAATGAGGCTATGAAAGCTGATTAACTGATGATGATCTCAACAA 2163  
129 CTTAATAGCAATGAGGCTATGAAAGCTGATTAACTGATGATGATGATCTCAACAA 188

2164 GAGAAAGAGTAAACACAAAGAGTACAGATGAAGTTTAACTGAGCAAAATGCGGCA 2223  
189 GAGAAAGAGTAAACACAAAGAGTACAGATGAAGTTTAACTGAGCAAAATGCGGCA 248

2224 CCAGATTTATGAGATGCTCTCCAGGGCTTCTGTCTCTCTAAACCTGCTATCAGCT 2283  
249 CCAGATTTATGAGATGCTCTCCAGGGCTTCTGTCTCTCTAAACCTGCTATCAGCT 308

2284 GGAATCTCAGGCTTGAAGAGTGTCCGAATTAATCTTTCGAAAAAGGCACTGTGTT 2343  
309 GGAATCTCAGGCTTGAAGAGTGTCCGAATTAATCTTTCGAAAAAGGCACTGTGTT 368

2344 AATTGGGAAGCCAGACATCATGCAATTAATCTTTTACAGAAACATGATCATCTT 2403  
369 AATTGGGAAGCCAGACATCATGCAATTAATCTTTTACAGAAACATGATCATCTT 428

2404 AAAAATGGGAGATTTAGGCAAGATATGCTAACCTTCAATTTTGGATTATGAA 2463  
429 AAAAATGGGAGATTTAGGCAAGATATGCTAACCTTCAATTTTGGATTATGAA 488

2464 AATATCTGCAAAATCAAGCTCTTGAATCTTGAATGTTAATGATGATGCTGCAATC 2523  
489 AATATCTGCAAAATCAAGCTCTTGAATCTTGAATGTTAATGATGATGCTGCAATC 548

2524 GGTGATGTTGTGGACTTATCGAGTGTGAGAAATTTCAACATTAATGAGATTGAG 2583  
549 GGTGATGTTGTGGACTTATCGAGTGTGAGAAATTTCAACATTAATGAGATTGAG 608

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QY      2584 TGTAAAGAGCGCTGAAAGGTGCACTGACATTAAACAGCCACACACTCCATCAGTGGCTC 2643
DB      609 TCGAAAGAGAGCGCTGAAAGGGGACCTGACATTCAACAGCCACAGCTGACAGTGGCTC 668
QY      2644 AAGACACAGACAGAGGGGAAATATATGATGCGCCCTGCATTTGTTTAAACAGATATGT 2703
DB      669 AAGACACAGACAGAGGGGCGGATATATGACGACCCATTACCTGTTCTCGTCTG 728
QY      2704 GCTGGATATGTTGTGTCACCTTCATTTTGGAAATGGAGATGTCACATAGTAATATC 2763
DB      729 GCTGGGACTGCGGGACACCTTTATCTTGGAAATGGAGACCGGACACAGAACATC 788
QY      2764 ATGTTAAGATGATGACACACTGTTTCATATAGATTTTGGACAC 2808
DB      789 ATGTGAAGATGACGACAGCTGTTTCATATAGATTTTGGGAC 833

RESULT 13
LOCUS   AU129890              753 bp    mRNA    linear    EST 01-AUG-2002
DEFINITION AU129890 NT2RP2 Homo sapiens cDNA clone NT2RP206455 5', mRNA
sequence.
ACCESSION AU129890
VERSION   AU129890.1 GI:10990244
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 753)
AUTHORS   Oca,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
          Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
          Isogai,T.
          HRI human cDNA project
          Unpublished
          Contact: Takao Isogai
          Genomics Laboratory
          Helix Research Institute
          1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
          Tel: 81-438-52-3975
          Fax: 81-438-52-3986
          Email: genomics@hri.co.jp
          HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
          Research Institute; cDNA library construction; Department of
          Virology, Institute of Medical Science, University of Tokyo, and
          Helix Research Institute.
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    /cell_line="NT2"
    /clone_1ib="NT2RP2"
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BASE COUNT 232 a 133 c 160 g 219 t 9 others
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Query Match 18.7%; Score 599.2; DB 9; Length 753;
Best Local Similarity 96.2%; Pred. No. 4.2e-133;
Matches 654; Conservative 0; Mismatches 22; Indels 4; Gaps 4;
QY      762 GTGTGATGTGTAATTAATCTCTTCTAGAAAATATCTCTGAGTCATATAGATATAG 821
DB      1 GTGTGATGTGTAATTAATCTCTTCTAGAAAATATCTCTGAGTCATATAGATATAG 60
QY      822 AAGCTTATTAATGCTTGGAGGATGCCAATTGATGCGTAAAGAAAGCCTCTA 881
DB      61 AAGCTTATTAATGCTTGGAGGATGCCAATTGATGCGTAAAGAAAGCCTCTTA 120
QY      882 TTCTCAACTGCACATGAGACTGTTTACAATGCCATCATATTCGACAGCATCTCCACAG 941

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DB      121 TTCTCAACTGCCAATGAGATGTTTACAATGCCATCTTATTCAGACCATTCACAGC 180
QY      942 TACGCCATATATGATGAGAAACATCTACAAATCCCTTGGGTTATTAATAGGCACT 1001
DB      181 TACACCATATATGAAATGAGAAACATCTACAAATCCCTTGGGTTATTAATAGGCACT 240
QY      1002 CAGAAATAAATCTTTTGGCAACCPATGATGAATGAATATTTGACAGATTGACAAAGAT 1061
DB      241 CAGAAATAAATCTTTTGGCAACCTACGATGAATGAATATTTGACAGATTGATGAAT 300
QY      1062 TTATGTTCAACAGTATCTTACCATGAGAGAGAACCTTATGATATATGATAATGTAACCTCA 1121
DB      301 CTATGTTCAACAGTATCTTACCATGAGAGAGAACCTTATGATATATGATAATGTAACCTCA 360
QY      1122 AAGAGTACCTTGTTCATATCCAGGTGATGAATATGTCGTAATATGATATATATACATTC 1181
DB      361 AAGAGTACCTTGTTCATATCCAGGTGATGAATATGTCGTAATATGATATATATACATTC 420
QY      1182 TGATCTTCTCGTCTGCTGCTGACCTTGCTTCATTTGTTCTGTTAAAGCCGAAGG 1241
DB      421 TGATCTTCTCGTCTGCTGCTGACCTTGCTTCATTTGTTCTGTTAAAGCCGAAGG 480
QY      1242 TGCCTAAAGAGACACCTGTCATTTGCTGGGAGAAATATTAACCTTGTGATTACACAGA 1301
DB      481 TGCCTAAAGAGACACCTGTCATTTGCTGGGAGAAATATTAACCTTGTGATTACACAGA 540
QY      1302 TACTCTAGTATCTGAAAAAATGCTTTGAAATCTTTGGCCAGTACCTCATGCACT-AGAAG 1360
DB      541 CACTCTAGTATCTGAAAAAATGCTTTGAAATCTTTGGCCAGTACCTCATGCACT-AGAAG 600
QY      1361 ATTTCCTGAACCTT-ATTGCTGTATCTGATCAATCAAA-TAAAGAAATCCATGTTT 1418
DB      601 ATTTCCTGAACCTT-ATTGCTGTATCTGATCAATCAAA-TAAAGAAATCCATGTTT 660
QY      1419 AGAG-TTGAGTTTGACTGG 1437
DB      661 AAGTTTGAGTTTGACTGG 680

RESULT 14
LOCUS   BG391265              844 bp    mRNA    linear    EST 12-MAR-2001
DEFINITION BG391265 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4536816 5',
sequence.
ACCESSION BG391265
VERSION   BG391265.1 GI:13284713
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 844)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished
          Contact: Robert Strussberg, Ph.D.
          Email: cga@bsi-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNLN at:
          http://image.llnl.gov
          Plate: LLM10460 row: p column: 01
          High quality sequence stop: 721.
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: This is a NIH MGC Library."
BASE COUNT      286 a      149 c      177 g      232 t
ORIGIN
Query Match      18.7%; Score 599; DB 10; Length 844;
Best Local Similarity 95.8%; Pred. No. 5e-133;
Matches 658; Conservative 0; Mismatches 25; Indels 4; Gaps 4;
QY 445 GAAGCTGTGATCTTAGGATCTTAATTCACCTCATAGTAGAGCAATGATTTATCT 504
DB 1 GAAGCTGTGATCTTAGGATCTTAATTCACCTCATAGTAGAGCAATGATTTATCT 60
QY 505 CCAATGTAGATCTTCCAGCAAGATGCGCAAGACATATATTAATTTGATTAAGG 564
DB 61 CCAATGTAGATCTTCCAGCAAGATGCGCAAGACATATATTAATTTGATTAAGG 120
QY 565 CAAATATATGATGATTTGGGTAAATGTTCTTCCAATATATGCAAAACAGAAATATCT 624
DB 121 CAAATATATGATGATTTGGGTAAATGTTCTTCCAATATATGCAAGCAAGATATATCT 180
QY 625 CTGAATATCAACCATGATGTCGCGCAAGCAAGTAAATTTGCTGAAGCAATGAGAAAA 684
DB 181 CTGAATATCAACCATGATGTCGCGCAAGCAAGTAAATTTGCTGAAGCAATGAGAAAA 240
QY 685 ACTGGAAGTATGTTGCTATCATCTGAACTGAACTGCTGTTTGAATATCAGGCG 744
DB 241 ACTGGAAGTATGTTGCTATCATCTGAACTGAACTGCTGTTTGAATATCAGGCG 300
QY 745 AAGTATATTTTAAAGCTGTGATGATGATGATATCTTCTGAAAAATATCTCTGAGT 804
DB 301 AAGTATATTTTAAAGCTGTGATGATGATGATGATATCTTCTGAAAAATATCTCTGAGT 360
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DB 361 CAGTATATGATATATGAAGCTGATATGATGATGATGATGATGATGATGATGATGATG 420
QY 865 GCTAAGAAAAAGCTCTATATTCATGCACTGCAATGCACTGTTTACATGCAATATCTCC 924
DB 421 G-TAAAGAAAGCTTATATTCATGCACTGCAATGCACTGTTTACATGCAATATCTCC 479
QY 925 AGACGCTATTCACAGCTAGCCATATATGATGATGATGATGATGATGATGATGATGATG 984
DB 480 AGACGCTATTCACAGCTAGCCATATATGATGATGATGATGATGATGATGATGATGATG 538
QY 985 GTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1044
DB 539 GTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 597
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DB 598 CGAGACATTCAGACAGATTTATGTTGCAACAGGATCTTACATGAGAGAGAACCTTTATGT 656
QY 1105 GATTAATGTGAACACTCAAGAGTACT 1131
DB 657 GACAATGTGAACACTCAAGAGTACTT 683

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RESULT 15
CD351100      696 bp      mRNA      linear      EST 29-MAY-2003
LOCUS         CD351100
DEFINITION    UI-M-FY0-c-fc-b-19-0-UI.r1 NIH BMAP_FY0 Mus musculus cDNA clone
IMAGE: 6852116 5', mRNA sequence.
ACCESSION     CD351100
VERSION       CD351100.1 GI:31142675
KEYWORDS      EST.
SOURCE        Mus musculus (house mouse)

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ORGANISM      Mus musculus
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS      1 (bases 1 to 696)
TITLE        NIH-MGC http://mgc.nci.nih.gov/
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished
Contact: Robert Straubeberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pyx-5.
FEATURES      source
Location/Qualifiers
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/lab_host="DH10B (T1 phage resistant)"
/clone_id="NIH_BMAP_FY0"
/notes="Organ: Brain; Vector: pyx-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the poly tail
is AGGAGAGCAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the
Developing Mouse Nervous System", supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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DB 61 TTCACCTTTTAAAGTATGAACAGTAGAGCAACCGTGAAGAAAGATCCTCAATC 120
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DB 181 AAGTACAGGACTTCCGAGAAATATTCATATGTTTGAAGAAAGCTGTGATCTTAAGG 240
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13	159.8	5.0	1248	12	US-10-027-632-21396	Sequence 21396, A
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; Publication No. US20030182669A1
; GENERAL INFORMATION:
; APPLICANT: Rockman, Howard A.
; APPLICANT: Naga Prasad, Sathyamangla V.
; APPLICANT: Laporte, Stephane A.
; APPLICANT: Barak, Larry S.
; APPLICANT: Caron, Marc G.
; TITLE OR INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCRs
; FILE REFERENCE: 033072-064
; CURRENT APPLICATION NUMBER: US/10/101,235A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3207
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; Publication No. US20030165831A1			
; GENERAL INFORMATION:			
; APPLICANT: Lee, John			
; APPLICANT: Thompson, Pamela			
; APPLICANT: Lillie, James			
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR			
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND			
; FILE REFERENCE: MRI-006B			
; CURRENT APPLICATION NUMBER: US/09/814,353			
; CURRENT FILING DATE: 2001-03-21			
; PRIOR APPLICATION NUMBER: US 60/191,031			

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Best Local Similarity		49.9%; Pred. No.	9.5e-102;	
Matches 1559; Conservative		0; Mismatches 1460;	Indels 106; Gaps 15;	
Oy	58	ATCCTAGTAGAATTTTACTACCAAAATGGGATAGTACCTTAGATAGTCCTCGTAG	117	
Db	426	ATACCCTGTGAATTCCTTTTGCCCACTGGGATTATATCCAGTTGGAGTACCTGGGAA	485	
Oy	118	GCTACGTTAATACGATTAAGCATGAATATTTAAAGAACAAGAAATACCTTCAT	177	
Db	486	GCTACCAATTTCTTATTAATTAACAGATGTATGGAAGCAAAGTTCAATTAACCAATGTC	545	
Oy	178	CAACTTCCTCAAGTGAATCTTCTTACTCTTTTGTGTAAGTGTACCAGAAAGCAGAAG	237	
Db	546	AACCTCTTATGATGATTTGACTCTCTAATGTTTTGCATGTGTGAATCAACTGCTGTAT	605	
Oy	238	GAAATATTTTGTGATAAACAGACGACTTTGTACCTTCGGCTTTTCAACCTTTTAA	297	
Db	606	GAGAGCTTGAAGTGAACACAGAAAGCTGTGATGTACACCTTTCTTCCAGTCTC	665	
Oy	298	AAAGTAAATGACCAAGTGGCAACCGTGAGAAAAGATCTCAATCGAAAAATGGTTTT	357	
Db	666	AAATTAGTGAACMAAGTTGTGACCCAGGGGAAAA---ATTAGACTCAAAAATGGAGTC	722	
Oy	358	GCTATGCCATGCGAGTGTGATTTGATATGTTAAAGATCCAGAAAGTACAGACTTC	417	
Db	723	CTTATAGAAAAGGTCTGCATGAATTTGATTTCTTGAAGGATCTGAAAGTAAATTAATTT	782	
Oy	418	CGAAGAAATATTCATATGTTGTGAAGAGAGCTGTGATCTTAGGATCTTAATTAACCT	477	
Db	783	CGAAGAAAAATGCCCAATTCAGCA-----GMAAAAAATCCTGTGCA	824	
Oy	478	CATAGTAGAGCAATGTATGTTTATCTCCAATGTAGATTTTCAACCAAGTGCCAAG	537	
Db	825	CTTATGGGATTTGTTGGATGAGACTGTGTAAMCAACATATCCACCAAGACATGAAACA	884	
Oy	538	CACATATATATTAATGTGATAAAGGCAATAATAGTGGATTTGGGTATATTTCT	597	
Db	885	TCCATCCCTGAAAACTTAGAAGTAAACCTTATGGGGAAGCTATCTGTAGCTGTAT	944	
Oy	598	CCAAATATATGCAACAAGATATCTTGAAAAATCAACATGACTGTGTCAGAACAA	657	
Db	945	TTTGA AAAAATGCGCGAGCGTGTTAGCTTCAATGTCTCCTAATATGAATCTATCAAA	1004	
Oy	658	GTAATTCGTAAAGAAATCAGAAAAAACTCGAAGTATGTTGATATCATCTGAACAATA	717	
Db	1005	GTTAAATGATTTGGCAATC---CAAAAACGTTTGACTATTCATGGAAGGAAGATGAATTT	1061	
Oy	718	AAACTGTGTGTTTAGAATATCAGGGCAAGTATATTTTAAAGTGTGTGATGTATGA	777	

Db 1062 AGCCCCATG-----ATTATGTTGCAAGTCAGCGGAGATGAA 1103  
Qy 778 TACTCTAGAAAAATTCCTCTGAGTCAGTATAAGTATATAGAGCTGTATATGCTT 837  
Db 1104 TATGTTTTGGTGTATCATCCATTAATTCAGTTCCAGATATATCCGAACCTGTGTATGAAAC 1163  
Qy 838 GGGAGATGCGCAATTTGATGCT-----GATGCTAAAGAAAGCTCATCTCACTGAC 892  
Db 1164 AGAGCCCTGCCCCATTTTATATCTGTGAAATCTGCAAGATCAAGAAATATATGAAACA 1223  
Qy 893 CAATGACTGTTTATCAATGCGCATCATATTCAGACGATCTCCAGACGTATGCCATATA 952  
Db 1224 GAATATGATGGCATAGAGGCGCATTAATGAAATTCATCTAATCTTCCCTTCATTA 1283  
Qy 953 TGAATGAGAAACATCTACAAATATCCCTTGGTTATTAATGTCACCTGAAATATAAA 1012  
Db 1284 CCACCAAGAAAMACAGATATTTCTCATGTTGGGAAATMAACAACCTTTCCAAAT 1343  
Qy 1013 TTCTTTGTGCAACTATGTGAAATGTAATATTTGAGACATGACAGATTTATGTTGAA 1072  
Db 1344 GTCTTGTTAGGAAATTAACCTTAACACAGAGAAAC-TGTAAAGTTTATGTCAGG 1401  
Qy 1073 CAGGTATCTACATGAGAGAACCTTATGTGATTAATGTGACACTCAAGAGTACTT 1132  
Db 1402 CTGGCTTTTTCATGTAAGTCTGAGCTCTGTGTTAAACCATGTAAGCTCAGAGGTATCAG 1461  
Qy 1133 GTTCCA--ATCCAGGTGGAATGATGCTGAATTAAGATATATACCTTCTGATCTC 1189  
Db 1462 GGAATAATGATCATATTTGGAAATGACCACTGGAATTTGATTAATATTTGTACACTAC 1521  
Qy 1190 CTGCTGCTGCTGACCTTTCCTTCATTT-----GTTCTGTAAAGGCCGAAAGGCTC 1244  
Db 1522 CAGAAATGCTCGATATATGTTTCTGTTTATGCAAGTTTGGATTAAGTAAAGCAAGA 1581  
Qy 1245 TAAAGAGAACACTGTCAT-----TGCCCTGGGAAATATAAATCTGTTG 1291  
Db 1582 AATCAAGAAACATTAATCCCTCTAAATATACAGACCATCAGAAAGCTGAAAGTGC 1641  
Qy 1292 ATTACACAGATACCTAGTATCTGGAATAATGCGCTTGAATCTTTGGCAGTACTCTG 1351  
Db 1642 ATTATCTGTAGCGTGGGTAATAGATGTTTGTGACTTTAAAGAACATTTGAGAACTG 1701  
Qy 1352 GACTAGAAAGATTTGGTGAACCTATTTGTTACTGATCAATATCCAAATTAAGAACTC 1411  
Db 1702 GAGACATATATTAACAGCTGCTCTTCAATTTCTGATGAACCTGAGAAATATGTAATC 1761  
Qy 1412 CATGTTAGAGTTGGAGTTTGAATGCTGTTACAGAGTGTGTAAGATTTCCAGATATGTCAG 1471  
Db 1762 CAATGGGAACCTGTTCAAAACAATCCATATATCGAAATGCAACAGCTTGTGATGTTAAT 1821  
Qy 1472 TGATTTGAAGACATGCAATGCTGTATCCCGTGAAGCAGATTTAGTTATCCCATG 1531  
Db 1822 TTCCAGAGAAATTAATAAACACCTTATTTATACCCCTCGATTAAGATTTATGAAAGG 1881  
Qy 1532 CAGAGCTAGTAACAGACTAGCTAGAGACATGAAATTAAGAAATATATAAGAACAGC 1591  
Db 1882 CAGCTGAAATGCAAGCAAGTATAGTCTAATGCTCAAGTCAGCTGAAAAAAGTTTC 1941  
Qy 1592 TCC-----GAGCAATTTGTACACGAGATCCTCTATCTGAAATCACTGACAAAGA 1642  
Db 1942 TTCCGTATTTGAAAGAAATCTTTGACAGGAAATCCCTGTCTCACTGTGTGAAATGAAA 2001  
Qy 1643 AAGATTTTCTGTGAGCAACAGAC--ACTATGTGTAACTATCCCGAAATTTCTAACCA 1699  
Db 2002 TGGATCTTATTTGGACTTTGGCAACAGACTGCGGAGATTTTCCACAAATCACTGCCAA 2061  
Qy 1700 AATGCTCTGTGCTGTAAATGGAACCTAGAGATGAGTAGCTAGATGTACTGCTTGG 1759  
Db 2062 AATTATCTGTCTGATCAATGAAATTAATTTGAGAGATGTGCTAGCTTACAGGCGCTGC 2121  
Qy 1760 TAAAGATTTGGCCTCAATCAAGCTGAAACAGGCTATGAGGCTTCTGCACTGCAATTAAC 1819  
Db 2122 TTGAGATTTGGCTTAACTGCCCCCGGAGGCGCTAGAGCTTGTGATTTCAACTATC 2181

Qy 1820 CAGATCCTATGTTGAGGTTTGGTGTGCTGTAGAAAAATATTTAACAGATGACA 1879  
Db 2182 CAGACAGATACGTTCCAGAAATATGCTGTAGGCTGCTC---GCCACAGATGAGATGAAAG 2238  
Qy 1880 AACTTCTCAGTACCTAATTCAGCTAGTACAGGTACTAAATATATGAAACGATATTGGATA 1939  
Db 2239 AACTTCTCAGTATCTTTTACACTGCTGCAAGTGTAAATATATGAGCCCTTTCTTGATTT 2298  
Qy 1940 AACTGCTTGTGAATTTTACTCAAAAAGCGTTAACTAATCAAGATGCGTCACTTT 1999  
Db 2299 GTGCCCCCTCTAATTTCTAATTAAGAAAGACACTGTGTATTCGAGAGATAGGCAAGTTTC 2358  
Qy 2000 TCTTTGCAATTTAAATCTGAGATGACACAAATAAACAGTTAGTCAAGCTTGGCTGC 2059  
Db 2359 TATTTTGGCATCTTAGTTCAGAAAGTGCACATTCCTGCTGTCTAGTACAAATTTGTGTCA 2418  
Qy 2060 TTTTGAAGTCTTATGCGGTGCAATGTGGAGTATCTGAAGCACTTAATAGCAAGTTG 2119  
Db 2419 TCCTTGAAGCATCTGCGGGGAAAGTGGGCAATGAAGTCTTTCTAAGCAGGTTG 2478  
Qy 2120 AGGCTATGAAAAAGCTCATTAATCTGACATCTTCTCAAAACAAGAAAGAAAGATGAAA 2179  
Db 2479 AAGCACTCAATTAAGTTAAACCTTAAATATGTTAAATCAAACTGAATGCCGTGAATTA 2538  
Qy 2180 CACAAAAGTACAGATGAAGTTTATGTTAGCAAAATGCGGCAACAGATTTGATGATG 2239  
Db 2539 ACAGAGCAAAAGGAAGAGGCCATGATACCTGTTTAAACAGAGTCTTACCGGGAAG 2598  
Qy 2240 CTCTCCAGGCTTCTGTCTCTCTTAACCTGCTCATGCTGGGAAATCTCAGGCTTG 2299  
Db 2599 CCTCTCTGACCTGCAAGTCAACCTCGAACCAGTGTATCTCTCAGAACTGATGTTG 2658  
Qy 2300 AAGAGTCCGAATTAATCTCTGCAAAAAGGCACTGTGTTGAATTTGGAGAACCCAG 2359  
Db 2659 AAAAGTCAAAATCAATGATTTCAAAATGAAGCTTTGTGCTGTATACAAATACAGG 2718  
Qy 2360 ACATCATGTCAATATCTCTTTCAGAACATGAGATCATCTTTAAATAATGGGATGAT 2419  
Db 2719 TATTTGGTGAAGATTCAGT-----TGAGATGATTTTAAATAATGTGATGAT 2766  
Qy 2420 TAGGCAAGATATGCTAACCTCTCAGATTAATGTCATTAATGAAATATCTGGCAAAATC 2479  
Db 2767 TAGACAGATATGTTGACACTCCAAATGTTGGCTGTGATGAGATTTACTCTGGAATAAG 2826  
Qy 2480 AAGGCTTGAATCTTTCGAATGTTAATGATGATGCTGTGTAATGCGTGAATGCTGGAC 2539  
Db 2827 CTGTTTGGATCTTCGAGATGTGCTTATGCTGTGTTAGCAACAGAGATGCTCTGGCC 2886  
Qy 2540 TTATCGAGTGTGAGAAATTTCTCACACTTAATATGACAGATTTCAAGTGAAGGAGC---C 2596  
Db 2887 TCAITGAAGTTGTGACACCTCTGAACAATGTGTCATTCAGCTGAACAGTATGCAATG 2946  
Qy 2597 TGAAGGTGCACTGCAAGTTTAACAGCCACACTCATCATGATGCTCAAAAGCAAGACA 2656  
Db 2947 TGCGTGTGACAGCAAGCTTCAACAAAGATGCCCTTGAAGCTGAGCTTAAAGATTAACA 3006  
Qy 2657 AAGGGGAAATATATGATGCGGCCATCATTTGTTTAACAGATCATATGCTGATATGTTG 2716  
Db 3007 CTGGGATGACCTGAGACCGAACATTAAGAAATTTAATCATGCTGTGCTGCTGCTACGTG 3066  
Qy 2717 TTGCACTTCATTTTGGGAATTTGAGATGCTCAATATGATATATCATGTTTAAAGATG 2776  
Db 3067 TAGCTTTATATGCTCTTGGATTTGTATGACAGACATATGACACATATGCTCAAAAAA 3126  
Qy 2777 ATGACAACATGTTTCAATATAGATTTTGAACAATTTTGGATCACAAGAAAGAAAAATTTG 2836  
Db 3127 CTGGCAGCTCTTCCACATTTGACATTTTGAACAATTTTGAATTTCAATCTAAGTTTG 3186  
Qy 2837 GTTATTAACGAGAGCGGTGCTGTTGTTTGAACAAGATTTCTTAAATAGTGAATTAAGTA 2896  
Db 3187 GCATTAAGAGGACGAGTGTCTTTTATCTTACCTATGATTTGATCATCATGTCAATCAAC 3246

QY 2897 AAGAGCCCAAGAAATGCAAAAGCAAGAAATTTGAGAGTTTCAAGAGATGCTTACA 2956  
DB 3247 AAGG-----AAAAACAGAAATAACAGAAAAGTTTGGCCGGTTCGCCAGTGTTGAGG 3300  
QY 2957 AGGCTATCTAGCATTTGGGAGCATGCCATCTCTCATTAATCTTTTCTCATGTGC 3016  
DB 3301 ATGCATATCTGATTTTTCAGACGCATGGAAATCTCTTCATCAGCTCTTTGGCGTGATGT 3360  
QY 3017 TTGGCTCTGAAATGCCAGAACTGCAATCTTTTGATGATTTGATATGATTCGAAAGACC 3076  
DB 3361 TGACGTGAGGGCTTCCGAACTCAGATCAGTCAAAAGATATACGATATTAAGGACTCTC 3420  
QY 3077 TACCTTAGTAAATACTGAGCAAGAGGCTTTGAGTATTTTCATGAAACAAATGATGATG 3136  
DB 3421 TTGCATTAGGAAAGAGTAAAGAAAGCACTCAAAACAGTTTAAGCAAAAATTGATGAGG 3480  
QY 3137 CACAC 3141  
DB 3481 CGCTC 3485

## RESULT 3

US-09-352-2439  
; Sequence 2439, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathiasan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511.006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 2439  
; LENGTH: 412  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; OTHER INFORMATION: Clone ID: 11-LIB3058-019-Q1-C11  
US-09-352-2439

Query Match 12.7%; Score 408.8; DB 10; Length 412;  
Best Local Similarity 99.5%; Pred. No. 1.5e-97;  
Matches 410; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1354 CTAGAAATTTGCTGAACCTTATGTTGTTACTGATCAATCAATAAAGAACTTCA 1413  
DB 1 CTAGAAATTTGCTGAACCTTATGTTGTTACTGATCAATCAATAAAGAACTTCA 60  
QY 1414 TGTTTAGAGTTGGAGTTTGACTGCTTCAGAGTGTGTAAAGTTTCCAGTATGTCAGT 1473  
DB 61 TGTTTAGAGTTGGAGTTTGACTGCTTCAGAGTGTGTAAAGTTTCCAGTATGTCAGT 120  
QY 1474 ATTGAAGACATGCCAATGTTGTTATCCCGTGAAGCAGATTTAGTTATCCCATGCA 1533  
DB 121 ATTGAAGACATGCCAATGTTGTTATCCCGTGAAGCAGATTTAGTTATCCCATGCA 180  
QY 1534 GGACTGATPAACAGACTAGTGAAGCAATGAATTAAGAGAAAATGATAAGAAACAGCTC 1593  
DB 181 GGACTGATPAACAGACTAGTGAAGCAATGAATTAAGAGAAAATGATAAGAAACAGCTC 240  
QY 1594 CGAGCAATTTGTAACAGAGATCCTATATGAAATCACTGAGCAAGAAAGATTTTTCG 1653  
DB 241 CGAGCAATTTGTAACAGAGATCCTATATGAAATCACTGAGCAAGAAAGATTTTTCG 300  
QY 1654 TGGAGCCACAGACACTATTTGTGTAATATCCCGAATTTCTACCAATTTGCTTGTCT 1713  
DB 301 TGGAGCCACAGACACTATTTGTGTAATATCCCGAATTTCTACCAATTTGCTTGTCT 360  
QY 1714 GTTAAATGAACTTGAAGATGAAGTCTCAGATGTAAGTCTGTTGTTAAAG 1765  
DB 1714 GTTAAATGAACTTGAAGATGAAGTCTCAGATGTAAGTCTGTTGTTAAAG 1765

DB 361 GTTAAATGAACTTGAAGATGAAGTCTCAGATGTAAGTCTGTTGTTAAAG 412

## RESULT 4

US-10-162-160-2  
; Sequence 2, Application US/10162160  
; Publication No. US20030099627A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Hasebroeck, Bart  
; APPLICANT: Waterfield, Michael D.  
; TITLE OF INVENTION: No. US20030099627A1e1 Lipid Kinase  
; FILE REFERENCE: 2332-1-002  
; CURRENT APPLICATION NUMBER: US/10/162,160  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US/09/194,640  
; PRIOR FILING DATE: 1998-12-01  
; PRIOR APPLICATION NUMBER: 9611460.8  
; PRIOR FILING DATE: 1996-06-01  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 3387  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-162-160-2

Query Match 10.5%; Score 336.2; DB 14; Length 3387;  
Best Local Similarity 53.5%; Pred. No. 9.7e-78;  
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;

QY 1682 TCCCCCAAAATTCACCCAAATGCTTCTGTCTGTAAATGAACTCAGATGATGATAG 1741  
DB 1625 TCCCGAGGCGCTAGCCCGGCTGCTGTGTACCAAGTGAACAAAGCATGAGAGATGTG 1684  
QY 1742 CTCAGATGATGCTGCTTGTGTAAGAAATGTCCTCAATCAAGCCTGAACGCTATGAGC 1801  
DB 1685 CCCAGATGCTCTACCTGCTGTGTCTGCTGCGCGGAGCTGCCCGTCTGAGGCGCTGAGC 1744  
QY 1802 TTCTGAGCTGCAATTCACCAATTCCTATGTTGAGAGTTTGTGTGCTTGTGCTTGA 1861  
DB 1745 TGTCTAAGCTTCAAGCTTCCCGGATTCGACGTAGGCTCTTCGCAATCAAGTCCGCTG 1804  
QY 1862 AATATTAAACAGATGCAAACTTTCTCAGTACTTAATCAGTAGTACAGTACTAAAT 1921  
DB 1805 AAC--TGACGACAGATGAGCTGTTCCAGTACTCTGCAAGCTGTGACAGGCTTCAAGT 1861  
QY 1922 ATGAACGATATTGATTAACCTGCTTGTGAGATTTTCTCAAAAAGGCTTAATATC 1981  
DB 1862 ACAGATCTTCACTGAGCTGCAAGCTGACCAAAATTCCTGTGACCGGCGCTGGCAAC 1921  
QY 1982 AAAGATGCTCACTTTTCTTTTGGCATTTAATCTGAGATGCAATTAACAGTTA 2041  
DB 1922 GCAAGATCGGCCACTTCTTTCTGCACTCCGCTCCAGATGACAGTGCCTGCTG 1981  
QY 2042 GTGAGAGTTTGGGCTTTTGGAGTCTTATTTGCCGTCATGAGTATCTGAAC 2101  
DB 1982 CCTGCGCTTCGCTCATCTGAGGCTTACTGAGGCGGACAGACCAACCATGATGAG 2041  
QY 2102 ACCTTAATAGGCAAGTGAAGCTATGAAAGCTCAATTAATCTGACTGACATTTCTCAAC 2161  
DB 2042 TGTCTGATGAAGCAGGGGGAACACTGAGCAAACTGAAGCCCTGATGATGATCTGTAAC 2101  
QY 2162 AAGAGAAAGATGAAACACAAAGGTACAGATGAATTTTATGTTAGCAATTCGCGC 2221  
DB 2102 TGAAGTCTCAGAAAGACCCCAAGCCCAAGCAAGAGCTGATGACATTTGCAATGCGC 2161  
QY 2222 GACCAAGATTCATGATGCTCTCCAGGCTTTCTGCTCTCTAAACCTGCTCATACG 2281  
DB 2162 AAGAGGCTTCACTTAAGGCGCTCTCCACCTGACCTGACCTCCCACTGACCAACCTTGC 2221  
QY 2282 TGGAAATCTCAGGCTTGAAGAGTGTGAATATGCTTTCTGCAAAAAGGCCACTGTGT 2341  
DB 2222 TGGCTGAAGTGTGCTGAGCAGTGCACCTTATGAGCTCCAAATGAAGCCCTGTGGA 2281

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OY 2342 TGAATTGGGAGAACCCAGACATCATCTCAGAAATTACTCTTTCAGAACATGAGATCATCT 2401
DB 2282 TCATGTACAGCAACGAGAG-----GCAGGACGCGCGGACCGTGGGATATCT 2332
OY 2402 TTTAAAAATGGGGATGATTTACCGGCAAGATATGCTAAACCTTCAGATTAATTCGATTATG 2461
DB 2333 TTAAGAACGGGATGACCTCCGCGAGACATGCTGACCCGCGAGATGATCAGACTCATG 2392
OY 2462 AAAATATCTGGCAAAATCAAGGCTTGTANTTGAATGTTAACTTATGATGATCTCTCA 2521
DB 2393 ACCTCTGTGGAAGCAGAGAGGCTGCACTGAGATGACCCCTATGCTGCTCCCA 2452
OY 2522 TCGGTGATCTGTGGGACTTATGAGGTGTGAGAAATTCCTACATATATAGATTC 2581
DB 2453 CCGGGGACCCGACAGGCTCATGAGGTGTACTCCGTTCAGACACATGCCAACTCC 2512
OY 2582 A---GTGTAAAGAGGCGCTGAAAGGTGACCTGAGTTTAAACGACACACTCCATAGT 2638
DB 2513 AACTCAACAAAGAGACATGACGACCCACAGCCGCTTCACAGAGATGCCCTGCTCACT 2572
OY 2639 GGCTCAAGACAAAGACAAAGGCGGAAATATATGATGCGGCCATGATTTGTTTACAGAT 2698
DB 2573 GGCTGAAGTCCAGAACCCCGGGAGGCGCTGATGAGCATGAGAGATTCACTCTCT 2632
OY 2699 CATGTGCTGATATGTTGTTGCCACTTCACTTTGGGAATTTGGAGATCGTACAAATAGTA 2758
DB 2633 CCGTGTGCTGATTTGTGTGCGCCATATGCTGCGGATTTGGAGATGCGACAGCCACA 2692
OY 2759 ATATCATGTTAAAGATGATGAGCAACTGTTCAATATGATTTTGAACACTTTTGGATC 2818
DB 2693 ACATCATGATCCGAGAGATGGGACGCTGTTCCATTTGATTTTGGCCACTTTCGGGGA 2752
OY 2819 ACAAGAGAAAAATTTGGTTATTAACGAGCGCGTGGCTGTTTGTGACACAAGATT 2878
DB 2753 ATTTCAAGACCAAGTTTGAATCAACCGGAGCGTGTCCCATTTCACTCTACCTACGACT 2812
OY 2879 TCTTAATAGATTAATGTAAGAGAGCCCAAGATGACAAAGACAAAGAAATTTGAGAGT 2938
DB 2813 TTGTTCATGTATTCAGCAGG-----GAAGACTAATTAATGAGAAATTTGACGCT 2866
OY 2939 TTTCAAGAAATGTTTACAGGCTTATCTAGCTATTCGCGAGCATCCCATCTCTTCAATTA 2998
DB 2867 TCCGGGGCTACTGTAAAGGCTCTACACCATCTCGGGCCAGGGGCTCTCTCTCTCC 2926
OY 2999 ATCTTTCTCAATGATGCTTGGCTGTGAAATGCAAGAACTGCAATCTTTTGAATATG 3058
DB 2927 ACCTCTTTGCTGATGAGGCGGCGGAGGCTGCTGAGCTCAGCTGCTCCAAAGACATCC 2986
OY 3059 CATACATTCGAAGACCTTACCTTAAATTAAGTGAAGAGAGGCTTTGAGTATTTCA 3118
DB 2987 ACTATCTCAAGACTCCCTGGGCACTGGGGAAAAACAGAGAGAGGACCTGAAGCACTTCC 3046
OY 3119 TGAACAAATGAATGATGACACCAATGCTGTCGACCAAAATGATTTGATCTTCC 3178
DB 3047 GAGTGAAGTTTAAAGAACCTTCTGAGAGCTGGAAGAACAAAGTGAAGTGGCTGGCCC 3106
OY 3179 ACA 3181
DB 3107 ACA 3109
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RESULT 5
US-10-337-192-1
; Sequence 1, Application US/10337192
; Publication No. US20030195211A1
; GENERAL INFORMATION:
; APPLICANT: SABOH, Chanchal et al.
; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
; FILE REFERENCE: 2786/39033
; CURRENT APPLICATION NUMBER: US/10/337,192
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: 60/199,655
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; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/238,057
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 1
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Human p110delta complete cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(3327)
; US-10-337-192-1

Query Match 10.5%; Score 336.2; DB 12; Length 5220;
Best Local Similarity 53.5%; Pred. No. 1,3e-77;
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;

OY 1682 TCCCGAAATTTCTACCCAAATTTGCTTCTGTTTAAATGGAATCTTATGATGAGTAG 1741
DB 1820 TCCCGAGGCGCTAGCGCGGCTGCTGCTGTCTACCAAGTGAACAAAGATGAGATGTGG 1879
OY 1742 CTGAGATGTAAGTCTGTTGTAAGATTTGGCTTCCATCAAGCCTGAACAGGCTATGAGC 1801
DB 1880 CCGAGATGCTTCTACCTGCTGTGTCTGCTGCGCGGAGCTGCCGCTGAGCGCTGAGC 1939
OY 1802 TTCTGAGCTGCAATTAACCCAGATCTATAGTTGTGAGAGTTTGTCTTCCGTGTTGAAA 1861
DB 1940 TGTAGACTTCACTTCCCGATTTGCGACGTAAGCTCTTGGCATCAAGTCCCTGGGA 1999
OY 1862 AATATTTAAAGATGACAACTTTCTCAGTACCTAATTCAGTACTAGTACAGTAAAT 1921
DB 2000 AAC---TGAGGACGATGAGACTGTTCCAGTACTGCTGAGCTGTGTGCAAGTCTCAAGT 2056
OY 1922 ATGAACGATATTGGATTAACCTCTGTGTGATTTTACTCAAAAAAGCTTAACTAATC 1981
DB 2057 ACGAGTCTTACCTGAGCTGAGGTGACCAAAATTCCTGAGACCGGGCCCTGGCCAAAC 2116
OY 1982 AAAGATCGGTCACTTTTCTTTTGGCATTTAAATTTGAGATGACAAATTAAGACGTTA 2041
DB 2117 GCAAGATCGGCACTTCTTTTTCGACCTCCGCTCGAGATGACAGTCCGCTGGTGG 2176
OY 2042 GTCAAGAGTTTGGCTGCTCTTTTGGAGTCTATTGCGGTGATGAGGATGATCTGAAGC 2101
DB 2177 CCGTCCGCTGCGCTCAATCTGAGGCTTACTGAGGCGACAGACCCACCACTGAAGG 2236
OY 2102 ACCTTAATAGGCAAGTGGAGCTATGAAAGCTCATTAATCTGACTGACATTTCAAC 2161
DB 2237 TGTGATGAAGCAGGGGGAACACATGAGCAAACTGAAGGCCCTGAATGACTTGTCAAGC 2296
OY 2162 AAGAGAAAGATGAACACAAAGATGAGAAATTTTATGTTGAGCAAAATGGCGC 2221
DB 2297 TGAGCTTCAAGAACCCCAAGCCCAAGACCCAGAACAGAGATGATGACTTGTGATGGC 2356
OY 2222 GACCAAGTTTCAATGATGATCTCCAGGCTTTCTGCTCTCTAAACCTCTCATACG 2281
DB 2357 AAGAGGCTTACCTTAAGGCTCTTCCACCTGCACTGCCACTGCAACCCAGACCTGCG 2416
OY 2282 TGGAAATCTCAGGCTTGAAGGTGTCGAATTAATGTTCTTTCGAAAAAGCCACTGTGCT 2341
DB 2417 TGGCTGAAGTCTGCTGAGAGCAGTGCACCTTATGAGCTCCAAAGATGAAGCCCTGTGGA 2476
OY 2342 TGAATTTGGAGAACCCAGACATCATGTCAAAATTAATCTTTCAAGAAATGAGATCATCT 2401
DB 2477 TCATGTACAGCAACGAGAG-----GCAGGACGCGCGGCGGAGCTGGGCACTATCT 2527
OY 2402 TTTAAAAATGGGATGATTTACGGCAAGATATGCTAAACCTTCAGATTAATTCGATTAATG 2461
DB 2528 TTAAGAACGGGATGACCTCCGCGAGACATGCTGACCTGCAAGATGATCCAGCTCATATG 2587
OY 2462 AAAATATCTGGCAAAATCAAGGCTTGTATCTTGAATGTTTAACTTATGATGATCTCTCA 2521
DB 2588 ACCTCTGTGGAAGCAGAGGCGCTGAGCTTGAAGATGACCCCTATGCTGCTCTCCCA 2647
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QY 2522 TCGGTGACTGTGTGGACTTATGAGGTGTGGAATTTCTCACTATATGACAGATTG 2581
DB 2648 CCGGGGACCGCACAGGCTTCATTTAGGTGTACTCCGTTGACAGACCATGCCAATCC 2707
QY 2582 A---GTGTAAGAGGCGCTGAAAGGTGCACTGCAAGTTTACACACACTGCATCAGT 2638
DB 2708 AACTCAACAAGACCAACATGGCAGCCACCGCCCTTCAACAGAGATGCTCTCAACT 2767
QY 2639 GGCTCAAGACAAACAAGGGGGAAATATATGATGCGGCTCATGATTTGTTACAGAT 2698
DB 2768 GGCTGAAGTCCAGAACCCGGGGAGGCCCTGATGAGCATTTAGAGATTACCTCT 2827
QY 2699 CATGTCTGATATGTGTGTGCCACTTCAATTTGGGAATGGAGATCGTCAAAATAGTA 2758
DB 2828 CCGTGTCTGATATTTGTGTGGCCACATATGTGTGGCATTTGGCATGGCAGAGACA 2887
QY 2759 ATATCATGTGTTAAGATGATGACAACTGTTTATATATGTTTGGACACTTTTGGATC 2818
DB 2888 AACTCATGATCCGAGAGAGTGGCAGCTGTTCACATTTGATTTGGCACTTTCTGGGGA 2947
QY 2819 ACAGAAGAGAAAAATTTGGTTATTAACGAGAGCGCGTCCGTTTGTGACACAGATT 2878
DB 2948 ATTCAAGACCAAGTTTGAATACCGGAGCGGTGCCATTCACTCACTATGACT 3007
QY 2879 TCTTAATAGTATTAAGTAAAGAGCCCAAGATGACAAAGACAGAAATTTGAGAGT 2938
DB 3008 TTGTCCATGTGATTCAGCAGGG-----GAAAGCTAATAATAGTGAATTTGAACGGT 3061
QY 2939 TTCAGAGATGTGTTCAAGAGCTTATCTAGCTATTTGGCAGCATGCCAATCTTTATTA 2998
DB 3062 TCCGGGGCTACTGTGAAAGGGCCCTACACCATCTGGGGGCGCCAGGCTTCTCTCTCC 3121
QY 2999 ATCTTTTCTCAATGATGCTGTGCTGTGAATGCCAGACTGCAATCTTTTGAATATTTG 3058
DB 3122 ACTCTTTCCTCGATGCGGGGCGGAGGCTGCTGCTAGCTCTCCAAAGACATCC 3181
QY 3059 CATACATTCGAAAGACCTTAGCTTTAGATTAACCTGAGCAGAGGCTTTGGATATTTCA 3118
DB 3182 AGTATCTCAAGACCTCCCTGGCAGCTGGGGAACAGAGGAGGAGCATGAAAGCACTTCC 3241
QY 3119 TGAACAATGATATGACACACATGTGGCTGGACAAACAAATGATTTGATCTTCC 3178
DB 3242 GAGTGAAGTTTAAAGAGCCCTCCGTGAGAGCTGGAACCAAAAGTAACTGGCTGGCC 3301
QY 3179 ACA 3181
DB 3302 ACA 3304

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RESULT 6
US-10-027-591-1
; Sequence 1, Application US/10027591
; Publication No. US20020161014A1
; GENERAL INFORMATION:
; APPLICANT: SMDHU, Chanchai et al.
; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
; FILE REFERENCE: 27866/36170C
; CURRENT APPLICATION NUMBER: US/10/027,591
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/841,341
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/199,655
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/238,057
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 5220
; TYPE: DNA
; ORGANISM: Human p10delta complete cDNA
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (196)...(3327)
US-10-027-591-1
Query Match 10.5%; Score 336.2; DB 13; Length 5220;
Best Local Similarity 53.5%; Pred. No. 1,3e-77;
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;
QY 1682 TCCCGGAAATTCACCAAAATGCTTCTGCTGTTTAAATGGAACCTTAGAGATGAAGTATG 1741
DB 1820 TCCCGAGGCGCTAGCCGCGCTGTCTGTGTACCAAGTGAACAAACATGAGATGTGG 1879
QY 1742 CTCAGATGACTGCTTGTGTAAGATTTGGCTTCAATCAAGCTGAACAGGCTATGAGC 1801
DB 1880 CCAAGATGCTTCACTGCTGTGTCTGTGCGGAGCTGCCGCTCGAAGCCCTTGAGC 1939
QY 1802 TTCTGACTGCAATTAACCAAGATCCTATGCTTGAGAGTTTGTGTGCTTGAAGA 1861
DB 1940 TGTGACTTCAAGCTTCCCGAATGCGCAGTAGGCTCTTCCCATCAAGTGGCTGCGA 1999
QY 1862 AATATTAAACAGATGACAACTTCTCACTACTTAATGAGTAGTACAGTAACTAAAT 1921
DB 2000 AAC---TGACGACGATGAGCTGTTCAGTACTGTGAGCTGTGTGACAGGTGCTCAAGT 2056
QY 1922 ATGAACAGTATTTGGATAACCTGCTTGTGAGATTTTAACTCAAAAAAGGTTAACTAATC 1981
DB 2057 ACGAGTCTCACTGAGCTGCGAGCTGACCAAAATTCGTGTGACCGGGCCCTGGCAAC 2116
QY 1982 AAGGATCGGTCACTTTTCTTTGGCATTTAAATCTGAGATGACAAATTAACAGTTA 2041
DB 2117 GCAGATCGGCCCATCTCTTTCTGTGCACTCCGCTCCGAGATGACGTCGCGGTGG 2176
QY 2042 GTCAGAGTTTGGCTGCTTTTGGAGTCTTATTCGCGTCAATGAGATGTATCTGAAC 2101
DB 2177 CCTGGCTTGGCCCTCATCTCTGAGGCTTACTGTGAGGGGCGACCCACCAATGAAG 2236
QY 2102 ACCTTAATAGGCAATGTTGAGGCTATGAGAAACCTCAATTACTGATGACTTCTCAAC 2161
DB 2237 TGCTATGAGAGAGGGGAGACACTGAGCAACTGAGGCCCTGATATGACTTGTCAAC 2296
QY 2162 AAGAGAGAGATGAACACAAAAGTACAGATGAAGTTTATGTTGACAAATGCGGC 2221
DB 2297 TGAGCTCTCAGAAAGACCCCAAGCCCAAGACCAAGAGGTATGACCTGTGATGCGGC 2356
QY 2222 GACCAATTTTCAATGATGCTCTCCAGGCTTCTGTCTCTTAACCTGCTCATCAGC 2281
DB 2357 AGGAGGCTTACCTTAAGGCGCTCTCCACCTGCACTGCCCATCGAACCCACACCTTGC 2416
QY 2282 TGGAAATCTCAGGCTTGAAGAGTGTGCAATATGATCTTTCGAAAAGGCCACTGTGGT 2341
DB 2417 TGGCTGAAGTCTGCTGTGAGAGCTGACACTTATGATGATCCAAAGTGAAGCCCTGTGGA 2476
QY 2342 TGAATTTGGAGAACCCAGACATCATGTCAATTAATCTTTTCAGAAACATGATCATCT 2401
DB 2477 TCATGTACAGCAACGAGAG-----GCAGGACAGGGGGCGGCGTGGGCATCATCT 2527
QY 2402 TTAATAATGAGGATATTTAGCGCAAGATGTCTTAACCTTCAAGTTATTTGCAATTAAG 2461
DB 2528 TTAACAAAGGGGATACCTCCGGCAGACATGCTGACCTGTGAGATGATCCAGCTCATGG 2587
QY 2462 AAAATATCTGCGCAAAATCAAGGCTTGTGATCTTCAATGATGATGATGATGATGATGAT 2521
DB 2588 AGCTCTGTGAGAGAGAGAGGGGCTGAGACTGAGAGATTAACCTCTATAGGCTGTCCCA 2647
QY 2522 TCGGTGACTGTGTGGACTTATGAGGTGTGAGAAATTTCTCACACTATTAATGACAGATTG 2581
DB 2648 CCGGGGACCGCACAGGCTTCATTTAGGTGTACTCCGTTGACAGACCATGCCAATCC 2707
QY 2582 A---GTGTAAGAGGCGCTGAAAGGTGCACTGCAAGTTTACACACACTGCATCAGT 2638
DB 2708 AACTCAACAAGACCAACATGGCAGCCACCGCCCTTCAACAGAGATGCTCTCAACT 2767
QY 2639 GGCTCAAGACAAACAAGGGGGAAATATATGATGCGGCTCATGATTTGTTACAGAT 2698

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3317 TTAAGTCGTGTCCTTCTTCAAGTTCAATGCTGTCCCTTAAAGTCACAAATGTAATG 3376  
2357 CAGACATCATGTGCAATTACTCTTTTCAGAAACATGATCATCTTAAATGGGATG 2416  
3377 CTGACCCCTGGGAGAGAA-----ATTATGTCAGTTTAAAGTTGGAG 3424  
2417 ATTACGGCAATATGCTAACCTTCAGATTAATTCGATTAATGAAATATCTGGCAA 2476  
3425 ATCTTGGGCAAGATTCCTTACATTAAGATTAATGATTAAGATCTGGCTTA 3484  
2477 ATCAAGCTCTTATCTTCAATGATTAATGATTAATGATTAATGATTAATGATTA 2536  
3485 AAGAGGACTAGATCTGAGATGTAATTTCAATCTCTCAACTGGAGAGATGAG 3544  
2537 GACTTATCGAGGTGCTGAGAAATTCACACTAATTAAGAGATTAAGAGAGCC 2596  
3545 GCATGGTGGAGCTGCTTCTGCTCCGATACCTCAGGAAATCCAGTGAATATGAG 3604  
2597 TGAAGGTGACCTGACGTTTAAAGCAGCAGCAGCTCAGTCTGCTCAAGAGAGACA 2656  
3605 TGACAGATCTCTTAAAGATTAACCACTTGAGAGTGGCTAAG--AAATACATCCCT 3661  
2657 AGGGGAAATATATGATGCGGCTGATTTTGAACGATCATGCTGATATTGTG 2716  
3662 CTGAAGAAGATATGAAGAGCTTCAAGAACTTATCTATCTGCTGATGATGCTG 3721  
2717 TTGCACTCTTATTTTGGGAATGAGATGCTCAATATGATATATGATGTTAAGATG 2776  
3722 TAGCAGCTATGTTTGGATGCTGATGATGACAAATGACAAATATATGCTTGAAGCA 3781  
2777 ATGCAACTGTTTCAATATGATTTTGGACACTTTTGGATCAGAGAGAGAAATTTG 2836  
3782 CGGACACATCTTCACTTGAATTTTGGAGATTTTGGAGATGACAGATGTTGGCA 3841  
2837 GTTATTAACGAGACGCGCTGCTGTTTGGACAAAGATTTCTTAATGATGATGA 2896  
3842 GCTTCAAAAGGATCGGCTCTTTTGTGCTGACCTGATATGCAATGCTATATG 3901  
2897 AAGAGCCCAAGATGCAAAAGACAGAAATTTGAGAGTTTCAAGAGATGTTACA 2956  
3902 GGGGG-----AAAGCCACATCTGTTTCACTTGTGTTGAGACCTGCTGTC 3952  
2957 AGGCTTATCTAGCTATTCGGGAGCATGCAATCTCTTCAATTAATCTTTTCAATGATG 3016  
3953 AGGCTTCACTGATTAAGAAAGAGAGACAACTTTTCTTAACCTCTTCACTGATGA 4012  
3017 TTGCTCTGGAATGCAAGCTGCAATCTTTGATGATTAATGATTAATGAAAGACC 3076  
4013 TTCTTCAAGGTTTACAGAACTTCAAGATTTCAAGATTTGAAATGATGAGATGAC 4072  
3077 TAGCTTATGATTAATCTGAGCAAGGCTTTGAGATTTTCAAGAAATGATGATG 3136  
4073 TTCAACCCCAATCTGAGAGAGAGCT--ACAATTTCTTAACTGAGCTTATTAAT 4129  
3137 CACACATGCTGCTGAGCAACAAATGATGATTTTCAACAAATTAAGAGAGATG 3196  
4130 CAAGTTTGGAGAGATGCTGCAAAAGTTTAACTTCTTCAATTAACAACTTCTGAGCTTC 4189

RESULT 10  
US-09-917-800A-477  
Sequence 477, Application US/09917800A

GENERAL INFORMATION:  
APPLICANT: Mendick, Donna  
APPLICANT: Porter, Mark  
APPLICANT: Johnson, Kory  
APPLICANT: Castle, Arthur

APPLICANT: Blashoff, Michael  
APPLICANT: Gene Logic, Inc.  
TITLE OF INVENTION: Molecular Toxicology Modeling  
FILE REFERENCE: 44921-5038-US  
CURRENT APPLICATION NUMBER: US/09/917,800A  
CURRENT FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: US 60/222,040  
PRIOR FILING DATE: 2000-07-31  
PRIOR APPLICATION NUMBER: US 60/222,880  
PRIOR FILING DATE: 2000-11-02  
PRIOR APPLICATION NUMBER: US 60/290,029  
PRIOR FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: US 60/290,645  
PRIOR FILING DATE: 2001-05-15  
PRIOR APPLICATION NUMBER: US 60/292,336  
PRIOR FILING DATE: 2001-05-22  
PRIOR APPLICATION NUMBER: US 60/295,798  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: US 60/297,457  
PRIOR FILING DATE: 2001-06-13  
PRIOR APPLICATION NUMBER: US 60/298,884  
PRIOR FILING DATE: 2001-06-19  
PRIOR APPLICATION NUMBER: US 60/303,459  
NUMBER OF SEQ ID NOS: 1740  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 477  
LENGTH: 5990  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
OTHER INFORMATION: Genbank Accession No. US20020119462A1 AB009636  
US-09-917-800A-477

Query Match 5.7%; Score 183; DB 10; Length 5990;  
Best Local Similarity 48.5%; Pred. No. 5.1e-37;  
Matches 677; Conservative 0; Mismatches 685; Indels 33; Gaps 5;

1737 AGTAGCTCAGATGACTGCTTGGTAAAGATTTGGCTTCAATCAAGCTGAAAGGCTAT 1796  
2405 AGTTCCGAATGATGATCCGCTTGTGAGAGGTGACATTTCCATCCGTTGAGAGCTCT 2464  
1797 GAGACTCTGAGACGCAATTAACCAATCTATGATGCTGAGATTTGCTGCTGCTT 1856  
2465 TGCCCTTTGACTTCCAGGTTTCCAGACCAAGACATTCGTAAGTTCCGCTTAAAGCTT 2524  
1857 AGAAAAATATTTAACAAGATGACAACTTTCTCACTTAATTAATCACTTAATCACTTA 1916  
2525 AGACAATCTTGAACGATG--AGCTGATGATGCTCCACAGCTAGTTCAAGGCTGT 2581  
1917 AAAATATGACAGATTTGATTAACCTGCTTGTGATATTTTACTCAAAAAAGGCTTAAC 1976  
2582 CAAGTTTGAAGTGTGATCGAAAGTCTTGTGGAATCTCTGCTTCAATGATCTTGA 2641  
1977 TTAATCAAGATGCTGATCTTTTCTTTGCAATTAATCTGATGACAAATTAAC 2036  
2642 AAGCATCGAGTGTGATCCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2701  
2037 AGTAGTCAGAGTGTGCTGCTTGTGAGTCTTATGCTGCTGCTGCTGCTGCTGCTGCTG 2096  
2702 CTTTAAAGCTGTATCCAGAGCTTTTGGCGCTCTCAGTCTGTGAGAGAGAGGCTT 2761  
2097 GAAGCACCCTTAATAGGCAAGTTGAGGCTATGAGAAAGCTCACTTAATGATGATGATCT 2156  
2762 GATGAGAGCTTTCAGAAAGAGAGCAAACTTGTCAAACTCC-----TGGGTGATTTGG 2815  
2157 CAACAAAGAGAGAGATGAGAAACAAAGGTAAGTATTAAGTTTGAAGCAAT 2216  
2816 AGAAAAATGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2875  
2217 GCGGCAACAGATTTCAATGATGCTCTCCAGAGCTTTTGTCTCTCTTAAACCTGCTCA 2276  
2876 CAGCTTAAGATTTCTTAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 2935

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QY 2277 TCAGCTGGGAAATCTCAGGCTTGAAAGTGTGCAATTAATGTTCTTCTGCAAAAAGGCCACT 2336
DB 2936 GTGCGTAAAAGAAATGATCGGGATGATGTTCAATTTTCAATCTAATGCTTGCCACTT 2995
QY 2337 GTGGTTGAATTTGGAGAAACCAAGCATCATGTCAAGAAATCTCTTCAAGAAATGAGAT 2396
DB 2996 GAAGATCACTT-----TCATCAATGCTTAATCCAAATGG3CAAAAATATACAGTGT 3043
QY 2397 CATCTTAAATAATGGGATGATTTACGGCAAGATATCTAATCCCTTGAGATTATTCGCAAT 2456
DB 3044 TATTTTAAAGCCGGCCACATCTTCGGCAGATATCTGTTTGTGAGATTATTCAGT 3103
QY 2457 TATGAAAATATCTGCGAAAATCAAGGCTTGATCTTTCGAATGTTTACCTTATGAGATCT 2516
DB 3104 GATGSAACAAGTGTGCTTCAAGAGGCTTCGATATCAATATGATTCATTTATGAGATCTCT 3163
QY 2517 GTCAATCGGTGATCTGTGGGACTTATCGAGGTGTGAAGAAATTTTCACTATATATGCA 2576
DB 3164 AGCCACAGAAAGGCTCAAGGATTCATAGAGATGTCCTGATGCTTGAACGCTTGCCAA 3223
QY 2577 GATTAGTGTAAAGAGGCTGAAAGGTGCACTGCAATTTAACAAGCACAACCTCCATCA 2636
DB 3224 GATTCATCTGCACTCTGGGCTGATAGGACCCCTGAAAGAAACACATCA--AGAAGTG 3280
QY 2637 GTGGCTCAAGACAAAGAAAGAGGGGAAATATATGATGCGGCCATCGATTGTGTTACAGC 2696
DB 3281 GTTCAGTCAGACAAACCACTTAAAGAAATATAGAAAGGCCCTGAGGAACCTTTTGA 3340
QY 2697 ATCATGTGCTGATATTTGTTGTCACCTTCAATTTTGGAAATGGAGATGTCACAAATAG 2756
DB 3341 CTCTTGCTGCTGGCTGTGTGTGTGATTCATCTTGGGAGTGTGTACCGACATATATGA 3400
QY 2757 TAATATCATGTTAAAGATGATGAGACAACGTTTCATATATGATTTTGGACATTTTGA 2816
DB 3401 CAATATCATCTGACAAAGTCAAGGCCACATGTTTCATATGACTTTGAAAATTTCTTGGG 3460
QY 2817 TCACAAAGAAATAATTTGGTTATTAACGAGAGCGGCTGCTTGTGTTGACACAAAGA 2876
DB 3461 TCACGCAAAACATTTGGCGGTATTAAGAGGACCGGCGCTTTCATTTTACTTCAGA 3520
QY 2877 TTTCTTATATGATTTATGTAAGAGGCCCAAGAAATGCAAAAGACAAAGAAATTTGAG 2936
DB 3521 GATGAGTACTTATTAACGAGAGGCTG-----GGAAAAACACAGCATTTTCAAGA 3571
QY 2937 GTTTCAGAGATGTTTACAGGCTTATCTAGCTATTCGCGCAGATGCCAATCTTTCAT 2996
DB 3572 CTTCGTGAAGCTCTGCTGACAGGCTTACAAATTTGAGGAGACACAGCACTGCTCCT 3631
QY 2997 AAATCTTTTCTCAATGATGCTTGGCTGTGGAATGCGCAAGTGCATCTTTTATGATAT 3056
DB 3632 GACGCTTCTGAATATATGCTGATGCGGCTTCCGAGCTAGAGGGGATTTGAAGACT 3691
QY 3057 TGCATACATTTGAAAGACCTTACCTTTAGATTAATACTGAGCAAGGCTTTGAGATTTT 3116
DB 3692 GAAATACGTACAGACATCTCCGSCACAAAGACACAGACTTGGAGCCCAAGTCAATTT 3751
QY 3117 CATGAAACAAATGAA 3131
DB 3752 TACCAAGAAATAAA 3766

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; FILE REFERENCE: 033072-064
; CURRENT APPLICATION NUMBER: US/10/101,235A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ. ID NOS: 9
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3237
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-101-235A-5

Query Match      5.2%; Score 167; DB 12; Length 3237;
Best Local Similarity 52.7%; Pred. No. 5.9e-33;
Matches 510; Conservative 0; Mismatches 433; Indels 24; Gaps 6;

QY 1793 CTATGAGCTTTCGAGCTGCAATTAACCAATCTTATGTTTCAGAGTTTGTCTGCT 1852
DB 1877 CAATGACGCTCCGAGCTGCACTTCTCAGATGAATGAAGAGCCATTGACAGTTTCA 1936
QY 1853 GCTTAGAAAATATTTAACAGATGACAACTTCTCAGTACTAATTCAGCTAGTACAGG 1912
DB 1937 AACTGAGAG--GCTTGAGAGAGATGATGTTCTGATTAATCTTACAAATGCTCAGG 1993
QY 1913 TACTAAATATGAACGATTTTGGATTAACCTGCTGTGAGATTTTAACTCAAAAACCGT 1972
DB 1994 CTGTGAAATTTGAACATACATGATAGGCGCTTCCAGATTTTGTGCTGAAGCGTGT 2053
QY 1973 TAACTATCAAGAGATCGGTCATTTTCTTTTGGCATTTAAATCTGAGAT--GCACA 2029
DB 2054 TAAGAAACAAAMAATTTGGTCACTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2113
QY 2030 ATAAACAGTTTACAGAGGTTTGCGCTGCTTGTGAGTCTTATGCGGCGATGAGGGA 2089
DB 2114 CCAGACATATACAGAGAGTTTGTGTATTTCTGAAGCTTATCTGAGGCGCTGTGCA 2173
QY 2090 TGTATGGAACCACTTAATAGGCAATGAGGCTATGAAAAGCTATTAATCTTGA 2149
DB 2174 CAGCCATGCTGACGACCTTATACCAACAAAGTCAAGTAAATGAGATGTTACAAAAGTCA 2233
QY 2150 ACATTTCTCAACAGAGAAAGAGATGAAACAAAGTACAGATGAAATTTTATGTTG 2209
DB 2234 CCCTTATATTAATGCTCTCTGCTGAAAAGTATGACGTCAGTCCCAATATTTTAC 2293
QY 2210 AGCAAAATGCGGACCAAGATTTTCATGATGCT-----CTCCAGGGCTTCTGCTC 2260
DB 2294 AACTTAAACAAAGCTTGAACCTTCAGATTTCTCAATCCCGCAAGCTTTAGGTTT 2353
QY 2261 CTCTAAACCTGCTCATCAGCTGGAATCTCAGGCTTGAAGATGTCGATTAATGCTT 2320
DB 2354 CATATGATCTGAGCTGAAAGCAGAGCGCTGCAATTTGAAAATGTAATGAGTGGCT 2413
QY 2321 CTGCAAAAAGGCACTGTGTGTAATTTGGAGAACCAAGACATCATGTCAAAATTA 2380
DB 2414 CCAGGAAAAAACCATATGAGCTTGAATTAATGTCGATCTTA--CAGCCCTATCA 2470
QY 2381 TTGAGAACATGAGATCATCTTAAATAAGGGATGATTTAGGCAAGATATGCTAACCC 2440
DB 2471 ATGAAACAAATTTGAATTTCTTTAAACATGATGATATCTGCGCCAAAGACATGCTA 2530
QY 2441 TTGAGATTTATGCAATTAAGAAATATCTGCAAAATCAAGGCTTGTGAATCTTGAATGT 2500
DB 2531 TACAGATTTCTAGAAATCATGAGATCTATTTGGAGACTGATCTTTTGAATCTATGCTCC 2590
QY 2501 TACCTTATGAGATGCTGTCAATGCGTGTGCTGTGAGACTTATTCAGAGTGTGAGAAAT 2560
DB 2591 TGCATATATGTTGCAATTTCACTGAGCAAAATAGGAATGATGAGATTTGTAAGAGAG 2650
QY 2561 CTCACACTATATGAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2620
DB 2651 CCAGCAATTTGCAAAATTTGCAAGAGCAGTGGGCAACGGA--GCATTTAAAG 2707
QY 2621 GCCACACTTCATGAGTGTCAAGACAAAGAAC--AAGGGGAAATATATGATGCGG 2677

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;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 213996  
;; LENGTH: 1248  
;; TYPE: DNA  
;; ORGANISM: Human  
US-10-027-632-213996

Query Match 5.0%; Score 159.8; DB 13; Length 1248;  
Best Local Similarity 86.7%; Pred. No. 2.5e-31;  
Matches 176; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 1987 ATCGTCACCTTTCTTTGGCATTAAATCTGAGTGCACATTAACAGTTAGTCAG 2046  
DB 751 ATTTTCTAATTTTGCATGATCTTTTAGATCTGAGATGCACATTAACAGTTAGTCAG 810  
QY 2047 AGGTTGGCCTGCTTTTGGAGTCTTATGCGGTCATGGGATGTATCTGAAGCACCTT 2106  
DB 811 AGGTTGGCCTGCTTTTGGAGTCTTATGCGGTCATGGGATGTATCTGAAGCACCTG 870  
QY 2107 AATAGGCAAGTGTAGGCTATGAAAGCTGATTAAGTGAATCTTCAACAAAGAG 2166  
DB 871 AATAGGCAAGTGTAGGCAAGTGAAGAGCTGATTAAGTGAATCTTCAACAAAGAG 930  
QY 2167 AAGAGGATGAACACAAAAGT 2189  
DB 931 AAGAGGATGAACACAAAAGT 953

RESULT 15  
US-09-878-178-229  
; Sequence 229, Application US/09878178  
; Patent No. US20020177552A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Secrist, Heather  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER  
; FILE REFERENCE: 210121.527  
; CURRENT APPLICATION NUMBER: US/09/878,178  
; CURRENT FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 2237  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 229  
; LENGTH: 167  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-878-178-229

Query Match 4.6%; Score 147.2; DB 10; Length 167;  
Best Local Similarity 98.0%; Pred. No. 1.5e-28;  
Matches 149; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1358 AAGATTGCTGAACCTATATGTTACTGATCAATCAATTAAGAACTCCATGTT 1417  
DB 16 AAGATTGCTGAACCTATATGTTACTGATCAATCAATTAAGAACTCCATGTT 75  
QY 1418 TAGAGTTGAGTTGACTGTTGAGCAGTGTGTTAAAGTTCCAGATATGTCAGTATTG 1477  
DB 76 TAGAGTTGAGTTGACTGTTGAGCAGTGTGTTAAAGTTCCAGATATGTCAGTATTG 135  
QY 1478 AAGAGCATGCGCAATTTGTTCTGTATCCCGTGA 1509  
DB 136 AAGAGCATGCGCAATTTGTTCTGTATCCCGAGAA 167

Search completed: November 7, 2003, 13:39:18  
Job time : 670.362 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 05:38:38 ; Search time 145.839 Seconds  
(Without alignments)  
9706.030 Million cell updates/sec

Title: US-09-325-095-35

Perfect score: 3207  
Sequence: 1 ATGCTTCCAGACCATCATC.....AGCAGCATGCTTGAACCTGA 3207

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 segs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seg length: 0  
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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2: /cgn2\_6/prodata/2/ina/5B\_COMB.seg.\*  
3: /cgn2\_6/prodata/2/ina/6A\_COMB.seg.\*  
4: /cgn2\_6/prodata/2/ina/6B\_COMB.seg.\*  
5: /cgn2\_6/prodata/2/ina/PCUTUS\_COMB.seg.\*  
6: /cgn2\_6/prodata/2/ina/backfile1.seg.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3207	100.0	3207	1	US-08-162-081B-35
2	3207	100.0	3207	2	US-08-780-872-35
3	3207	100.0	3207	3	US-09-085-957-35
4	3011.8	93.9	3240	1	US-08-162-081B-34
5	3011.8	93.9	3240	2	US-08-780-872-34
6	3011.8	93.9	3240	3	US-09-085-957-34
7	3008.6	93.8	3412	1	US-08-162-081B-32
8	3008.6	93.8	3412	2	US-08-780-872-32
9	3008.6	93.8	3412	3	US-09-085-957-32
10	448.2	14.0	3213	4	US-09-392-350-1
11	336.2	10.5	3387	4	US-09-194-640A-2
12	336.2	10.5	3387	4	US-09-357-070-1
13	336.2	10.5	5220	2	US-08-777-405A-1
14	336.2	10.5	5220	2	US-08-977-871A-1
15	336.2	10.5	5220	2	US-08-972-630-3
16	336.2	10.5	5220	2	US-08-972-630-3
17	336.2	10.5	5220	2	US-08-972-630-3
18	288.8	9.0	5162	3	US-08-916-917-13
19	288.8	9.0	5162	3	US-08-916-917-13
20	285	8.9	4134	2	US-08-817-090B-1
21	277.6	8.7	3808	2	US-08-817-090B-1
22	277.6	8.7	3808	2	US-08-916-917-3
23	277.6	8.7	3808	2	US-08-972-631-3
24	277.6	8.7	3808	2	US-08-972-630-3
25	277.6	8.7	3808	2	US-08-972-630-3
26	277.6	8.7	3808	2	US-08-972-630-3
27	224.8	7.0	5285	2	US-08-609-049A-29

28	224.8	7.0	5285	3	US-09-170-996-29	Sequence 29, Appl
29	218.4	6.8	5061	4	US-09-355-160D-1	Sequence 1, Appl
30	146.4	4.6	3504	3	US-08-857-076-47	Sequence 4, Appl
31	111.8	3.5	6831	2	US-08-609-049A-27	Sequence 27, Appl
32	111.8	3.5	6831	3	US-09-170-996-27	Sequence 27, Appl
33	108.6	3.4	333	1	US-08-162-081B-40	Sequence 40, Appl
34	108.6	3.4	333	2	US-08-780-872-40	Sequence 40, Appl
35	108.6	3.4	333	3	US-09-085-957-40	Sequence 40, Appl
36	85.4	2.7	357	4	US-09-765-298A-13	Sequence 13, Appl
37	68.6	2.1	204	4	US-09-016-434-245	Sequence 245, App
38	66	2.1	222	4	US-09-016-434-525	Sequence 525, App
39	62.2	1.9	3063	4	US-09-620-312D-474	Sequence 474, App
40	62.2	1.9	3252	3	US-09-118-442-1	Sequence 1, Appl
41	62.2	1.9	3252	3	US-09-677-064-1	Sequence 1, Appl
42	48	1.5	381	1	US-08-162-081B-38	Sequence 38, Appl
43	48	1.5	381	2	US-08-780-872-38	Sequence 38, Appl
44	48	1.5	381	3	US-09-085-957-38	Sequence 38, Appl
45	45.2	1.4	277	4	US-09-313-294A-6757	Sequence 6757, Ap

#### ALIGNMENTS

RESULT 1  
US-08-162-081B-35  
Sequence 35, Application US/08162081B  
Patent No. 5824492  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph, Otsu, Masayuki; Panayotov, George; Volinla,  
APPLICANT: Stefa, Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
TITLE OR INVENTION: THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felle & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162, 081B  
FILING DATE: February 7, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-162-081B-35  
Query Match 100.0%; Score 3207; DB 1; Length 3207;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGCCCTCCAAAGACCATCATCAGGTGAACTGTGGGGCATCTCATTGATGCCCCCCAAGATC	60
Db	1	ATGCCCTCCAAAGACCATCATCAGGTGAACTGTGGGGCATCTCATTGATGCCCCCCAAGATC	60
QY	61	CTGTGTGAATGTTTACTTACCAATGGGAGATAGTGAAGCTTTGAAATGTCCTCGTAGGCT	120
Db	61	CTGTGTGAATGTTTACTTACCAATGGGAGATAGTGAAGCTTTGAAATGTCCTCGTAGGCT	120
QY	121	ACGTTAATAAGATGAAAGCATGAACTATTTAAAGAACCAAGAAAATACCTCTCCATCA	180
Db	121	ACGTTAATAAGATGAAAGCATGAACTATTTAAAGAACCAAGAAAATACCTCTCCATCA	180
QY	181	CTTCTTCAGATGATCTTCTTAACATTTTCTGTAAGCTTAAACCAAGAACGAAAGGAA	240
Db	181	CTTCTTCAGATGATCTTCTTAACATTTTCTGTAAGCTTAAACCAAGAACGAAAGGAA	240
QY	241	GAATTTTTTGAATGAAACAAGACCTTGTGACCTTGCGCTTTTCAACCTTTTAAAA	300
Db	241	GAATTTTTTGAATGAAACAAGACCTTGTGACCTTGCGCTTTTCAACCTTTTAAAA	300
QY	301	GTAATTGAACACAGTAGGCAACCGTGAAGAAAAGATCTGATCGAGAAATGCTTTGCT	360
Db	301	GTAATTGAACACAGTAGGCAACCGTGAAGAAAAGATCTGATCGAGAAATGCTTTGCT	360
QY	361	ATCGGCATGCCAGTGTGTGAATTCGATATGTTTAAAGATCCGAATTAAGAGACTCCGA	420
Db	361	ATCGGCATGCCAGTGTGTGAATTCGATATGTTTAAAGATCCGAATTAAGAGACTCCGA	420
QY	421	AGAAATATCTCCAAATGTTGTAAAGAGCTGTGATCTTAGGGATCTTAATTCACCTCAT	480
Db	421	AGAAATATCTCCAAATGTTGTAAAGAGCTGTGATCTTAGGGATCTTAATTCACCTCAT	480
QY	481	AGTAGAGCAATGTATGTTTATCTCCAAATGTAGAACTTTCACAGAACTGCCAAGCAC	540
Db	481	AGTAGAGCAATGTATGTTTATCTCCAAATGTAGAACTTTCACAGAACTGCCAAGCAC	540
QY	541	ATATATTAATAATTGGATAAAGGGCAATAATAGTGTGATTTGGGTAATAGTTTCTCCA	600
Db	541	ATATATTAATAATTGGATAAAGGGCAATAATAGTGTGATTTGGGTAATAGTTTCTCCA	600
QY	601	AATATGACAAACAGAACTATCTCTGAAATCAACCATGACTGTGTGCCAAGCAAGTA	660
Db	601	AATATGACAAACAGAACTATCTCTGAAATCAACCATGACTGTGTGCCAAGCAAGTA	660
QY	661	ATTGTGTAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATATCTGAAACAATTA	720
Db	661	ATTGTGTAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATATCTGAAACAATTA	720
QY	721	CTCTGTGTTTGAATATACAGGGCAAGTATTTTAAAGGTGTGGATGTAATAC	780
Db	721	CTCTGTGTTTGAATATACAGGGCAAGTATTTTAAAGGTGTGGATGTAATAC	780
QY	781	TTCCCTGAAGAAAATATCTCTGAGTCAGTATAAGTATATAGAACTGTATTAATGCTTGG	840
Db	781	TTCCCTGAAGAAAATATCTCTGAGTCAGTATAAGTATATAGAACTGTATTAATGCTTGG	840
QY	841	AGGATGCCCAATTTGATGCTGATGCGTAAAGAAACCTCTATTTCCAACTGCCAATGAC	900
Db	841	AGGATGCCCAATTTGATGCTGATGCGTAAAGAAACCTCTATTTCCAACTGCCAATGAC	900
QY	901	TGTTTTTACAATGCCATCATATTCACAGCCATCTCCAGCTGACCCATATATAGATGA	960
Db	901	TGTTTTTACAATGCCATCATATTCACAGCCATCTCCAGCTGACCCATATATAGATGA	960
QY	961	GAAACATCTACAAATATCCCTTTGGGTTATTAATAGTGAAGTGAATTAATTTCTTGT	1020
Db	961	GAAACATCTACAAATATCCCTTTGGGTTATTAATAGTGAAGTGAATTAATTTCTTGT	1020
QY	1021	GCAACCTATGTGAATGAAATATTTGAGACATTTAGCTGAAACAGTATC	1080
Db	1021	GCAACCTATGTGAATGAAATATTTGAGACATTTAGCTGAAACAGTATC	1080
QY	1081	TACCATGAGAGAAACCCCTTAATGTGAATATGTGAACATCCAAAGATACCTTTGCCAAT	1140

Db	1081	TACCATGAGGAGAAACCCCTTATGTGATATGGAACACTCAAAAGTACCTTGTTCCAAAT	1140
Qy	1141	CCAGGTGGAATGAATAGCGTGAATTAACGATATATACATTCCTGATCTTCTGTGTCCT	1200
Db	1141	CCAGGTGGAATGAATAGCGTGAATTAACGATATATACATTCCTGATCTTCTGTGTCCT	1200
Qy	1201	CGACTTGGCCTTCCATTTGTTCTGTGTTAAAGGCCGAAAGGGTGCTTAAAGGAAACACTGT	1260
Db	1201	CGACTTGGCCTTCCATTTGTTCTGTGTTAAAGGCCGAAAGGGTGCTTAAAGGAAACACTGT	1260
Qy	1261	CCATTGGCCTGGGAAATATTAACCTTGTTTACACGATACCTGTATCTGGAAAA	1320
Db	1261	CCATTGGCCTGGGAAATATTAACCTTGTTTACACGATACCTGTATCTGGAAAA	1320
Qy	1321	ATGGCTTGAATCTTTGGCCAGTACCTCAGTGAAGATTTGCTGAACCCCTATTTGCT	1380
Db	1321	ATGGCTTGAATCTTTGGCCAGTACCTCAGTGAAGATTTGCTGAACCCCTATTTGCT	1380
Qy	1381	GTTACTGATCAAAATCCAAATTAAGAACTCCATGTTTAGAGTTGAGTTTGACTGTTC	1440
Db	1381	GTTACTGATCAAAATCCAAATTAAGAACTCCATGTTTAGAGTTGAGTTTGACTGTTC	1440
Qy	1441	AGCAGTGTGTAAAGTTTCCAGATATGTCAAGTATTTGAAGAGATGCCAATTTGCTGTA	1500
Db	1441	AGCAGTGTGTAAAGTTTCCAGATATGTCAAGTATTTGAAGAGATGCCAATTTGCTGTA	1500
Qy	1501	TCCCGTGAAGAGATTAGTTTATCCCATGCAAGACTGAGTAAACAGACTAGCTAGAGAC	1560
Db	1501	TCCCGTGAAGAGATTAGTTTATCCCATGCAAGACTGAGTAAACAGACTAGCTAGAGAC	1560
Qy	1561	AATGAATTTAAGAGAAATGATTAAGAAACAGCTCCGAGCAATTTGTAACAGATTCCTCTA	1620
Db	1561	AATGAATTTAAGAGAAATGATTAAGAAACAGCTCCGAGCAATTTGTAACAGATTCCTCTA	1620
Qy	1621	TCTGAATCAGTGAACAAAGAAAGATTTTCTGTGAGCCACAGACATATTTGTAATCT	1680
Db	1621	TCTGAATCAGTGAACAAAGAAAGATTTTCTGTGAGCCACAGACATATTTGTAATCT	1680
Qy	1681	ATCCCCGAAATTTACCCCAATTTGCTTCTGTGTTAAATGAACTCTAGAGATGAAGTA	1740
Db	1681	ATCCCCGAAATTTACCCCAATTTGCTTCTGTGTTAAATGAACTCTAGAGATGAAGTA	1740
Qy	1741	GCTCAGATGTACTGCTTGTTAAAGAGTTGGCTTCCATCAAGCCTGAACAGGCTATGGAG	1800
Db	1741	GCTCAGATGTACTGCTTGTTAAAGAGTTGGCTTCCATCAAGCCTGAACAGGCTATGGAG	1800
Qy	1801	CTTTCGAGCTGCAATTAACCCAGATTCCTATGTTGAGAGTTTGTGTCGTCGTTAGAA	1860
Db	1801	CTTTCGAGCTGCAATTAACCCAGATTCCTATGTTGAGAGTTTGTGTCGTCGTTAGAA	1860
Qy	1861	AAATATTTTAACGATGACAAACTTCTCAGTACCTAATTCAGTATGACAGTACTAAAA	1920
Db	1861	AAATATTTTAACGATGACAAACTTCTCAGTACCTAATTCAGTATGACAGTACTAAAA	1920
Qy	1921	TATGAACAGTATTTGATACCTGCTTGAGATTTTACTCAAAAAAGCCTTAACTAAT	1980
Db	1921	TATGAACAGTATTTGATACCTGCTTGAGATTTTACTCAAAAAAGCCTTAACTAAT	1980
Qy	1981	CAAGGATCGCTACTTTTCTTTTGGCATTTTAAATCTGAGAGCAAAATTAACAGTT	2040
Db	1981	CAAGGATCGCTACTTTTCTTTTGGCATTTTAAATCTGAGAGCAAAATTAACAGTT	2040
Qy	2041	AGTCAAGGTGGCCCTGCTTTGGAGTCTATTCGCTGATGATGGGATGATCTGAAG	2100
Db	2041	AGTCAAGGTGGCCCTGCTTTGGAGTCTATTCGCTGATGATGGGATGATCTGAAG	2100
Qy	2101	CACCTTAATAGGCAATGAGCTATGAAAAAGTCAATTAACCTGACACATTCCTCAA	2160
Db	2101	CACCTTAATAGGCAATGAGCTATGAAAAAGTCAATTAACCTGACACATTCCTCAA	2160
Qy	2161	CAAGAGAAAGGATGAACACAAAGGTAACAGTGAAGTTTGTAGTGAAGATGGGG	2220



2161 CAAGAGAGAGATGAAACAAAGGATGAGATGAAATTTTGTGACAAATGCGG 2220  
2221 CGACGAGATTTGATGATGCTCTCCAGGGGCTTTCTGTCTCTTAAACCTGCTCATG 2280  
2222 CGACGAGATTTGATGATGCTCTCCAGGGGCTTTCTGTCTCTTAAACCTGCTCATG 2280  
2281 CTGGGAAATCTCAGGCTTGAAAGGTGCTGCAATTAATGCTTTGCAAAAAGGCACTGTG 2340  
2282 CTGGGAAATCTCAGGCTTGAAAGGTGCTGCAATTAATGCTTTGCAAAAAGGCACTGTG 2340  
2341 TTGAATTTGGAGAACCCAGCATCATGTAATTTCTTTTCAAAAATGATGATC 2400  
2342 TTGAATTTGGAGAACCCAGCATCATGTAATTTCTTTTCAAAAATGATGATC 2400  
2401 TTTAAAAATGGGAGATTTTACGCAAGATATGCTAACCTTCAATTTTGCATTATG 2460  
2402 TTTAAAAATGGGAGATTTTACGCAAGATATGCTAACCTTCAATTTTGCATTATG 2460  
2461 GAAATATCTGCGCAAAATCAAGGCTTTGATCTTTCGAATGTTTACCTTATGATGCTGCA 2520  
2462 GAAATATCTGCGCAAAATCAAGGCTTTGATCTTTCGAATGTTTACCTTATGATGCTGCA 2520  
2521 ATCGGAGACTGTGGGACTTATCGAGGTGTGAGAAATTTTCACTAATATGAGAT 2580  
2522 ATCGGAGACTGTGGGACTTATCGAGGTGTGAGAAATTTTCACTAATATGAGAT 2580  
2581 CAGTGTAAAGAGAGGCTGAAAGGTGCTGAGTTTAAAGCCACATCTCATGATG 2640  
2582 CAGTGTAAAGAGAGGCTGAAAGGTGCTGAGTTTAAAGCCACATCTCATGATG 2640  
2583 CAGTGTAAAGAGAGGCTGAAAGGTGCTGAGTTTAAAGCCACATCTCATGATG 2640  
2641 CTCAAAAGACAGAACAGGGGGAAATATATGATGCGGCAATGATTTGTTTACAGATCA 2700  
2642 CTCAAAAGACAGAACAGGGGGAAATATATGATGCGGCAATGATTTGTTTACAGATCA 2700  
2701 TGTGCTGATATGTTGCTGCTCCTCATTTTGGGAATTTGAGATGCTCAATATGAT 2760  
2702 TGTGCTGATATGTTGCTGCTCCTCATTTTGGGAATTTGAGATGCTCAATATGAT 2760  
2761 ATCATGTTTAAAGATGATGACACACTGTTTCAATATGATTTTGAACATTTTGGATC 2820  
2762 ATCATGTTTAAAGATGATGACACACTGTTTCAATATGATTTTGAACATTTTGGATC 2820  
2821 AAGAGAAAAAATTTGTTATATAAGAGAGCGGCTGCGTTGTTTGAACAGATTTT 2880  
2822 AAGAGAAAAAATTTGTTATATAAGAGAGCGGCTGCGTTGTTTGAACAGATTTT 2880  
2881 TTAATGATGATTAATAAGAGAGCGGCTGCGTTGTTTGAACAGATTTT 2940  
2882 TTAATGATGATTAATAAGAGAGCGGCTGCGTTGTTTGAACAGATTTT 2940  
2941 CAGAGATGTTTAAAGGCTTATCTAGCTTATCGGAGAGGCTTCTTCAATAT 3000  
2942 CAGAGATGTTTAAAGGCTTATCTAGCTTATCGGAGAGGCTTCTTCAATAT 3000  
3001 CTTTCTCATGATGCTTGGCTCTGGAATGCCAAGATCTTCAATCTTTTATGATATGCA 3060  
3002 CTTTCTCATGATGCTTGGCTCTGGAATGCCAAGATCTTCAATCTTTTATGATATGCA 3060  
3061 TACATTTGAAAGACCTTACCTTATGATTAATAAGAGAGGCTTGGAGATTTTCAATG 3120  
3062 TACATTTGAAAGACCTTACCTTATGATTAATAAGAGAGGCTTGGAGATTTTCAATG 3120  
3121 AAACAAATGATGATGACACCATGCTGAGCAAAAGAAATGATGATGCTTCCAG 3180  
3122 AAACAAATGATGATGACACCATGCTGAGCAAAAGAAATGATGATGCTTCCAG 3180  
3181 ACAATTTAGCAGATGCTTTGAATGCA 3207  
3182 ACAATTTAGCAGATGCTTTGAATGCA 3207

RESULT 2  
US-08-780-872-35

Sequence 35, Application US/08780872  
Patent No. 5846824  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph, Olu, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefano, Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
TITLE OF INVENTION: THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felle & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/780,872  
FILING DATE: 09-Jan-1997  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/162,081  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pascualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3207 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-780-872-35  
Query Match 100.0%; Score 3207; DB 2; Length 3207;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3207; Mismatches 0; Indels 0; Gaps 0;  
1 ATGCTCCAGACCATCATCAGTGAATCTGCGGAGATCCATTTGATGCCCCAAGATC 60  
1 ATGCTCCAGACCATCATCAGTGAATCTGCGGAGATCCATTTGATGCCCCAAGATC 60  
61 CTAGTAGAATGTTTACTACCAATGGAGATGATGATCTTTAGATGCTCCGTAGAGCT 120  
61 CTAGTAGAATGTTTACTACCAATGGAGATGATGATCTTTAGATGCTCCGTAGAGCT 120  
121 ACGTTAATPACGATTAAGCATTAATTTTAAAGAGAGAAATACCTTCTCATCA 180  
121 ACGTTAATPACGATTAAGCATTAATTTTAAAGAGAGAAATACCTTCTCATCA 180  
181 CTTCTCAAGATGATCTTTTACATTTTGTAGTGTACCAAGAGAGAGAGAGGAA 240  
181 CTTCTCAAGATGATCTTTTACATTTTGTAGTGTACCAAGAGAGAGAGAGGAA 240  
241 GAATTTTGTGAGAAAGAGAGAGCTTTGTGACCTTGGCTTTTCAACCTTTTAA 300  
241 GAATTTTGTGAGAAAGAGAGAGCTTTGTGACCTTGGCTTTTCAACCTTTTAA 300  
301 GTAATTGAACGATGAGCAACCGTGAAGAAAGATCTCAATCGAAGAAATGCTT 360  
301 GTAATTGAACGATGAGCAACCGTGAAGAAAGATCTCAATCGAAGAAATGCTT 360

QY 361 ATCGGATCCAGTGTGTAATTGATATGCTTAAAGATCCAGAGTACAGGACTTCCGA 420  
DB 361 ATCGGATCCAGTGTGTAATTGATATGCTTAAAGATCCAGAGTACAGGACTTCCGA 420  
QY 421 AGAAATATCTCAATGTTGTAAGAAGCTGTGATCTTAAAGGATCTTAATTCACCTCAT 480  
DB 421 AGAAATATCTCAATGTTGTAAGAAGCTGTGATCTTAAAGGATCTTAATTCACCTCAT 480  
QY 481 AGTAGAGCAATGATGTTTATCTCCAAATGTAGAAATCTTACACAGACTGCCAAAGCAC 540  
DB 481 AGTAGAGCAATGATGTTTATCTCCAAATGTAGAAATCTTACACAGACTGCCAAAGCAC 540  
QY 541 ATATATATATATATGATGTAAGGCAAAATAAGTGTGATTTGGTAATAGTTCTCCA 600  
DB 541 ATATATATATATATGATGTAAGGCAAAATAAGTGTGATTTGGTAATAGTTCTCCA 600  
QY 601 AATATATGACAAACAGAGTATCTGAAATCAACCATGACTGTGCGAGAACAGTA 660  
DB 601 AATATATGACAAACAGAGTATCTGAAATCAACCATGACTGTGCGAGAACAGTA 660  
QY 661 ATTGCTGAAGCAATCAGAGAAAAAACTCGAAGTATGTTGCTATCTTGAACAATAAAA 720  
DB 661 ATTGCTGAAGCAATCAGAGAAAAAACTCGAAGTATGTTGCTATCTTGAACAATAAAA 720  
QY 721 CTCTGTGTTTGAATATCAGGGCAAGTATTTTAAAGTGTGATGATGAATAC 780  
DB 721 CTCTGTGTTTGAATATCAGGGCAAGTATTTTAAAGTGTGATGATGAATAC 780  
QY 781 TTCTTCAAAAAATTCCTGAGTCAAGTATATATATAGAAAGCTGATATATGCTTGG 840  
DB 781 TTCTTCAAAAAATTCCTGAGTCAAGTATATATATAGAAAGCTGATATATGCTTGG 840  
QY 841 AGATGCCCAATTTGATGCTGATGCTTAAAGAAAGCTCTATCTCAATGCGCAATGAC 900  
DB 841 AGATGCCCAATTTGATGCTGATGCTTAAAGAAAGCTCTATCTCAATGCGCAATGAC 900  
QY 901 TGTTTTACAAATGCTATATTTCCAGACCATCTTCCAGAGTACGCGCATATATGATGGA 960  
DB 901 TGTTTTACAAATGCTATATTTCCAGACCATCTTCCAGAGTACGCGCATATATGATGGA 960  
QY 961 GAAACATCTACAAAATCCCTTGGGTTATTAATAGTGCACCTGAGATAAAAATCTTTGT 1020  
DB 961 GAAACATCTACAAAATCCCTTGGGTTATTAATAGTGCACCTGAGATAAAAATCTTTGT 1020  
QY 1021 GCACCTATGTAATGTAATATTCGAGACATTGACAAAGTTTATGTTGAAACAGATAC 1080  
DB 1021 GCACCTATGTAATGTAATATTCGAGACATTGACAAAGTTTATGTTGAAACAGATAC 1080  
QY 1081 TACCATGAGAGAAACCTTATGATGTAATGTAAGACATCAAGAGTACCTTGTCCAAAT 1140  
DB 1081 TACCATGAGAGAAACCTTATGATGTAATGTAAGACATCAAGAGTACCTTGTCCAAAT 1140  
QY 1141 CCCAGGTGAATGAATGAGTGAATTCAGATATATCAATCTGATCTTCTGCTGCT 1200  
DB 1141 CCCAGGTGAATGAATGAGTGAATTCAGATATATCAATCTGATCTTCTGCTGCTGCT 1200  
QY 1201 CGACTTGGCTTCAATTTGTTCTGTTAAAGGCGAAAGGTCCTAAAGAGAACCTGT 1260  
DB 1201 CGACTTGGCTTCAATTTGTTCTGTTAAAGGCGAAAGGTCCTAAAGAGAACCTGT 1260  
QY 1261 CCATTTGGCTGGGAAATATAACTTTGTTGATTAACAGATATCTCTAGATGTGAAAA 1320  
DB 1261 CCATTTGGCTGGGAAATATAACTTTGTTGATTAACAGATATCTCTAGATGTGAAAA 1320  
QY 1321 ATGGCTTTGAATCTTTGGCCAGATCTCATGAGACTAGAAATTTGCGAACCTATTTGT 1380  
DB 1321 ATGGCTTTGAATCTTTGGCCAGATCTCATGAGACTAGAAATTTGCGAACCTATTTGT 1380  
QY 1381 GTTACTGATCAATCAATAAAGAAACTCATGTTTGAAGTTGAGTTGACTGCTTC 1440  
DB 1381 GTTACTGATCAATCAATAAAGAAACTCATGTTTGAAGTTGAGTTGACTGCTTC 1440

QY 1441 AGCATGTGTAATGCTTCCAGATATGTCAGATGTTAAAGAGATGCCAATGCTGTGA 1500  
DB 1441 AGCATGTGTAATGCTTCCAGATATGTCAGATGTTAAAGAGATGCCAATGCTGTGA 1500  
QY 1501 TCCCGTAAGCAGATTTAGTATTTCCATGCAAGACTGAGTACAGACTAGTGAAGAC 1560  
DB 1501 TCCCGTAAGCAGATTTAGTATTTCCATGCAAGACTGAGTACAGACTAGTGAAGAC 1560  
QY 1561 AATGAATTAAGAAATGATTAAGAACAGCTCCAGACAAATTTGATACAGAGATCTCTA 1620  
DB 1561 AATGAATTAAGAAATGATTAAGAACAGCTCCAGACAAATTTGATACAGAGATCTCTA 1620  
QY 1621 TCTGAATACCTGAGAGAGAAAGATTTCTGTGAGCCACAGACACTATTTGTAACT 1680  
DB 1621 TCTGAATACCTGAGAGAGAAAGATTTCTGTGAGCCACAGACACTATTTGTAACT 1680  
QY 1681 ATCCCGGAATCTACCCAAATTTGCTTGTGTTAAATGAACTTACAGATGAACTA 1740  
DB 1681 ATCCCGGAATCTACCCAAATTTGCTTGTGTTAAATGAACTTACAGATGAACTA 1740  
QY 1741 GCTCAGATGATCTGCTTGTAAAGATTTGCTCCAAATCAAGCTTGAAGAGCTATGAG 1800  
DB 1741 GCTCAGATGATCTGCTTGTAAAGATTTGCTCCAAATCAAGCTTGAAGAGCTATGAG 1800  
QY 1801 CTCTGAGCTGCAATTAACCAAGATCTATGATTCAGAGTTTGTGCTGCTTGAAG 1860  
DB 1801 CTCTGAGCTGCAATTAACCAAGATCTATGATTCAGAGTTTGTGCTGCTTGAAG 1860  
QY 1861 AATATATTAACAGATGACAAATTTCTCAGTACCTAATTCAGTATGACGATCTAAA 1920  
DB 1861 AATATATTAACAGATGACAAATTTCTCAGTACCTAATTCAGTATGACGATCTAAA 1920  
QY 1921 TATGAACAGTATTTGATTAACCTGCTTGTGATTTTAACTCAAAAAGGTTAACTAAT 1980  
DB 1921 TATGAACAGTATTTGATTAACCTGCTTGTGATTTTAACTCAAAAAGGTTAACTAAT 1980  
QY 1981 CAAGAGTGGTCACTTTCTTTTGGCATTTAAATCTGAGATGCAATTAACAGATT 2040  
DB 1981 CAAGAGTGGTCACTTTCTTTTGGCATTTAAATCTGAGATGCAATTAACAGATT 2040  
QY 2041 AGTGAAGTTTGGCTGCTTGTGATGCTTATGCTGATGCTGATGCTGATGCTGATG 2100  
DB 2041 AGTGAAGTTTGGCTGCTTGTGATGCTTATGCTGATGCTGATGCTGATGCTGATG 2100  
QY 2101 CACCTTAATGAGCAAGTTGAGCTGATGAGAAAGCTCATTAATCTGACGATCTCAAA 2160  
DB 2101 CACCTTAATGAGCAAGTTGAGCTGATGAGAAAGCTCATTAATCTGACGATCTCAAA 2160  
QY 2161 CAAGAGAAAGATGAAACCAAAAGGTACAGATGAAAGTTTATGTTGAGCAATGCGG 2220  
DB 2161 CAAGAGAAAGATGAAACCAAAAGGTACAGATGAAAGTTTATGTTGAGCAATGCGG 2220  
QY 2221 CGACCAATTTCAATGATGCTCTCCAGGCTTTCTGCTCTTAAACCTGCTCATAG 2280  
DB 2221 CGACCAATTTCAATGATGCTCTCCAGGCTTTCTGCTCTTAAACCTGCTCATAG 2280  
QY 2281 CTGGGAAATCTCAGGCTTGAAGAGTGTGCAATTAATGCTTCTGCAAAAAGGCACTGG 2340  
DB 2281 CTGGGAAATCTCAGGCTTGAAGAGTGTGCAATTAATGCTTCTGCAAAAAGGCACTGG 2340  
QY 2341 TTGAATTTGGGAAACCCAGACATCATGTGCAATTAATCTTCTGCAAAAAGGCACTGCATC 2400  
DB 2341 TTGAATTTGGGAAACCCAGACATCATGTGCAATTAATCTTCTGCAAAAAGGCACTGCATC 2400  
QY 2401 TTTAAATATGGGATGATTTTACGCAAGATATGCTTACCTTCAATTTTGCATATG 2460  
DB 2401 TTTAAATATGGGATGATTTTACGCAAGATATGCTTACCTTCAATTTTGCATATG 2460  
QY 2461 GAAATATCTGCAAAATCAAGCTTGTATCTTCAATTTTACCTTATGAGATGCTGCTA 2520  
DB 2461 GAAATATCTGCAAAATCAAGCTTGTATCTTCAATTTTACCTTATGAGATGCTGCTA 2520  
QY 2521 ATCGTGAATGCTGTGGACTTATCGAGGTGTGAGAAATTTCTACACTAATGACATTT 2580

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Db      2521 ATCGGACTGTGTGGACTTATCGAGGTGTGAGAAATTCACACTAATAAGCAGATT 2580
Qy      2581 CAGTGTAAAGAGAGCCCTGAAAGGTGACATGAGATTAAACGACACACTCCATCGATGG 2640
Db      2581 CAGTGTAAAGAGAGCCCTGAAAGGTGACATGAGATTAAACGACACACTCCATCGATGG 2640
Qy      2641 CTCGAAAGACAGAAACAAAGGGGGAATATATATGATGCGGCCATGATTTGTTACACGATCA 2700
Db      2641 CTCGAAAGACAGAAACAAAGGGGGAATATATGATGCGGCCATGATTTGTTACACGATCA 2700
Qy      2701 TGTGCTGGAATATTTGCTTCCACCTTCATTTTGGGAATTTGAGATGTCACATAGTAAT 2760
Db      2701 TGTGCTGGAATATTTGCTTCCACCTTCATTTTGGGAATTTGAGATGTCACATAGTAAT 2760
Qy      2761 ATCATGTGTTAAAGATGATGACAACTGTTCAATATGATTTTGGACACTTTTGGATCC 2820
Db      2761 ATCATGTGTTAAAGATGATGACAACTGTTCAATATGATTTTGGACACTTTTGGATCC 2820
Qy      2821 AAGAAAGAAAAATTTGGTTATTAACGAGAGCGCGCTGCTTTGTTTGAACAGATTTTC 2880
Db      2821 AAGAAAGAAAAATTTGGTTATTAACGAGAGCGCGCTGCTTTGTTTGAACAGATTTTC 2880
Qy      2881 TTAATATGATTTATGTAAGAGAGCCCAAGATGACAAAGACAAAGAAATTTGAGAGTTT 2940
Db      2881 TTAATATGATTTATGTAAGAGAGCCCAAGATGACAAAGACAAAGAAATTTGAGAGTTT 2940
Qy      2941 CAGAGATGTGTTTAAAGGCTTATCTAGCTATTTGGGCGAGCAATCTCTCAATAAT 3000
Db      2941 CAGAGATGTGTTTAAAGGCTTATCTAGCTATTTGGGCGAGCAATCTCTCTCAATAAT 3000
Qy      3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTGCAATCTTTGATGATTTGCA 3060
Db      3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTGCAATCTTTGATGATTTGCA 3060
Qy      3061 TACATTTGCAAAAGACCTTACCTTTAATTAATACTGACAAAGAGCTTTGAGATTTGATG 3120
Db      3061 TACATTTGCAAAAGACCTTACCTTTAATTAATACTGACAAAGAGCTTTGAGATTTGATG 3120
Qy      3121 AAACAAATGATGATGACACACATGCTGGCTGGGACAAAGAAATGATGATTTGATCTTCCAC 3180
Db      3121 AAACAAATGATGATGACACACATGCTGGCTGGGACAAAGAAATGATGATTTGATCTTCCAC 3180
Qy      3181 ACAATTAAGCAGCATGCTTTGAACCTGA 3207
Db      3181 ACAATTAAGCAGCATGCTTTGAACCTGA 3207

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RESULT 3  
US-09-085-957-35  
Sequence 35, Application US/09085957  
Patent No. 6274327

## GENERAL INFORMATION:

APPLICANT: Hiler, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Balai, Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph, Otsu, Masayuki; Panayocou, George; Volinia,  
APPLICANT: Stefano, Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Felife & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York

COUNTRY: USA  
ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/085,957
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/780,872
FILING DATE: 09-JAN-1997
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 3207 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-085-957-35

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Query Match 100.0%; Score 3207; DB 3; Length 3207;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 ATGCTCCAAAGACATCATCTAGTGAATCTGGGGCATCCACTTGATGCCCCCAAGAATC 60
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Db      61 CTAGTAGAATGTTTACTACCAAAATGGAGATGATGATCTTTAGAAATGCTCCGTGAGGCT 120
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Qy      181 CTTCTTCAAGATGATCTTCTTACATTTTGTAGTGTATACCAAGAGCAAGAAAGGAA 240
Db      181 CTTCTTCAAGATGATCTTCTTACATTTTGTAGTGTATACCAAGAGCAAGAAAGGAA 240
Qy      241 GAAATTTTGTATGAAGACAGACCTTGTGACCTTGGCTTTTCAACCTTTTAAAA 300
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Db      301 GTAATTGAACCAATGAGCAACCGTGAAGAAAGATCTCTCAATCGAAGAAATTTGGTCT 360
Qy      361 ATCGGATGCGAGGTGTGGAATTTGATATGTTTAAAGATCCAGAAAGTACGGAATTCGGA 420
Db      361 ATCGGATGCGAGGTGTGGAATTTGATATGTTTAAAGATCCAGAAAGTACGGAATTCGGA 420
Qy      421 AGAAATATTCATATGTTTGTAAAGAGCTGTGATCTTAAAGGATCTTAATTCACCTCAT 480
Db      421 AGAAATATTCATATGTTTGTAAAGAGCTGTGATCTTAAAGGATCTTAATTCACCTCAT 480
Qy      481 AGTAGAGCAATGATATGTTTATCTCCCAATGTAGAAATCTTCAACCAAGATCCCAAGAC 540
Db      481 AGTAGAGCAATGATATGTTTATCTCCCAATGTAGAAATCTTCAACCAAGATCCCAAGAC 540
Qy      541 ATATATATAAATTTGATTAAGGCAATATATGTTGTTTGGGTAATATGTTTCTCCA 600
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Db      601 AATTAATGACAAAGAGATTAATCTGAAATCAACCATGACTGTGTGCCAAGAAAGTA 660

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DB 1141 CCCAGGTGAATGAATGCTGTAATAGCATATATACATTCCTGATCTTCTGCTGCT 1200  
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DB 1201 CGACTTGGCTTTCCATTTGTTCTGTAAGAGCCGAAAGGCTGTAAGAGAACCTGT 1260  
QY 1261 CCATTGGCTGGGAAATATTAATCTGTTGATTAACAGATCTCTGATCTTCTGCTGCT 1320  
DB 1261 CCATTGGCTGGGAAATATTAATCTGTTGATTAACAGATCTCTGATCTTCTGCTGCT 1320  
QY 1321 ATGCTTTGAAATCTTTGGCCAGTACCTCATGACCTAGAACGATTTGCTGATGCT 1380  
DB 1321 ATGCTTTGAAATCTTTGGCCAGTACCTCATGACCTAGAACGATTTGCTGATGCT 1380  
QY 1381 GTTACTGATCAATCCAAATTAAGAACTCCATGTTTGAAGTGGATTTGACTGTTTC 1440  
DB 1381 GTTACTGATCAATCCAAATTAAGAACTCCATGTTTGAAGTGGATTTGACTGTTTC 1440  
QY 1441 AGCAGTGGTAAAGTTTCCAGATATGTCAGTATTAAGAGCATGCTCAATTTGCTGTA 1500  
DB 1441 AGCAGTGGTAAAGTTTCCAGATATGTCAGTATTAAGAGCATGCTCAATTTGCTGTA 1500  
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DB 1501 TCCCGTGAAGCAGATTTAGTATTCCTCATGCGAGCTGATTAAGAGCATGCTCAAT 1560  
QY 1561 AATGAATTAAGAGAAATGATTAAGAAAGCTCCGAGCAATTTGTACAGAGATCTCTTA 1620  
DB 1561 AATGAATTAAGAGAAATGATTAAGAAAGCTCCGAGCAATTTGTACAGAGATCTCTTA 1620  
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DB 1621 TCTGAATTAAGAGAAAGATTTCTGTGAGCCAGACATTAATTTGCTGTA 1680  
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DB 1681 ATCCCGAAATTTACCCAAATTTGCTGCTGTTAAATGGAATCTGAGATGAAGTA 1740  
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DB 1741 GCTCAGATGTAAGTGTGTAAGATTTGGCTCCTCAATCAAGCTGAAAGGCTATGAG 1800  
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DB 1801 CTCTGAGATGCAATTAACCAATCTTATGTTGAGGTTTGGTGTGCTTGAAG 1860  
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DB 1861 AAATATTTAAAGATGCAAACTTTCTCAGTACTTAATCAGTATGACGATGACTTAA 1920  
QY 1921 TATGACAGATTTGATGTAACCTGCTGATGATTTTACTCAAAAAAGCTTAAT 1980  
DB 1921 TATGACAGATTTGATGTAACCTGCTGATGATTTTACTCAAAAAAGCTTAAT 1980  
QY 1981 CAAAGGATCGGTCATTTTCTTTGGCATTTTAAATCTGAGATGCAATTAACAGTT 2040  
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DB 2101 CACCTTAATAGCAAGTTGAGGCTATGGAAGGCTATTAACCTGATGATGATGATGATG 2160  
QY 2161 CAAAGGAAAGATGAAACAAAGGATACAGATGAAGTTTATGTTGAGCAATTTGG 2220  
DB 2161 CAAAGGAAAGATGAAACAAAGGATACAGATGAAGTTTATGTTGAGCAATTTGG 2220  
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DB 2221 CAGCAGATTTATGATGATGCTCTCCAGGCTTTCTGCTCTTAAACCTGCTCATG 2280  
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DB 2281 CTGGGAAATCTCAGGCTTGAAGGATGCAATTTATGCTCTTGGCAAAAGGCTCATG 2340  
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DB 2341 TTGAATTTGGGAGAACCCAGATCATGTCAGATTAATCTTTGAGAACATGATGATC 2400  
QY 2401 TTTAAATTTGGGAGATTTTACGCGAAATGATGCTTAACCTTGAATTTATGCTATG 2460  
DB 2401 TTTAAATTTGGGAGATTTTACGCGAAATGATGCTTAACCTTGAATTTATGCTATG 2460  
QY 2461 GAAATATCTGGCAAAATCAAGGCTTGAATGCTTGAATGCTTGAATGCTTGAATG 2520  
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DB 2521 ATCGGTGATCTGTTGGGACTTATCGAGGTGTAAGAAATTTCTCACTATTAATGAG 2580  
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DB 2581 CAGTAAAGAGGCTTGAAGGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCT 2640  
QY 2641 CTCAAGACAGAAACAAAGGAGAAATATATGATGCTGCTGATGCTGATGCTGATG 2700  
DB 2641 CTCAAGACAGAAACAAAGGAGAAATATATGATGCTGCTGATGCTGATGCTGATG 2700  
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DB 2701 TGTGCTGATATTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760  
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DB 2761 ATCATGTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820  
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Db 2821 AAGAGAAAAATTTGGTTATTAACGAGAGCGCGTCCGTTTGTGACACAAAGATTTC 2880  
 QY 2881 TTAATAGTATTAAGTAAGAGAGCCCAAGATGCAAAAGACAGAAATTTGAGAGTTT 2940  
 Db 2881 TTAATAGTATTAAGTAAGAGAGCCCAAGATGCAAAAGACAGAAATTTGAGAGTTT 2940  
 QY 2941 CAGAGATGTTTACAAAGCTTATCTAGCTATTTCGCGAGCATGCCAATCTTTCATPAAT 3000  
 Db 2941 CAGAGATGTTTACAAAGCTTATCTAGCTATTTCGCGAGCATGCCAATCTTTCATPAAT 3000  
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 Db 3181 ACAATTAAGCAGATGCTTGAACCTGA 3207

## RESULT 4

US-08-162-081B-34

Sequence 34, Application US/08162081B

Patent No. 582492

GENERAL INFORMATION:

APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
 APPLICANT: Hiles, Waterfield, Michael Derek; Parker, Peter  
 APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,  
 APPLICANT: Stefano, Gout, Ivan Tarasovitch  
 TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Felfe & Lynch  
 STREET: 805 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/162, 081B

FILING DATE: February 7, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/00761

FILING DATE: 13 April 1993

ATTORNEY/AGENT INFORMATION:

NAME: Pasqualini, Patricia A.

REGISTRATION NUMBER: 34,894

REFERENCE/DOCKET NUMBER: LUD 5256

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 3240 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-162-081B-34

Query Match 93.9%; Score 3011.8; DB 1; Length 3240;  
 Best Local Similarity 96.2%; Pred. No. 0;  
 Matches 3085; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 1 ATGCTCCGAAGCCATCATCAGTGAATCTGAGGGGATCCACTTGATGCCCCCAAGATC 60  
 Db 1 ATGCTCCGAAGCCATCATCAGTGAATCTGAGGGGATCCACTTGATGCCCCCAAGATC 60  
 QY 61 CTAGTGAATGTTTACTACCAATGGAGTGAATGACTCTTGAATGCTCCGTGAGGCT 120  
 Db 61 CTAGTGAATGTTTACTACCAATGGAGTGAATGACTCTTGAATGCTCCGTGAGGCT 120  
 QY 121 ACGTTATACGATTAAGATGAACATATTAAAGAAAGAAATACCTCCATGCA 180  
 Db 121 ACGTTATACGATTAAGATGAACATATTAAAGAAAGAAATACCTCCATGCA 180  
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 QY 361 ATCGGCATGCGAGTGTGAAATTCGATATGTTAAAGATCCGAAGTACAGGACTTCCGA 420  
 Db 361 ATCGGCATGCGAGTGTGAAATTCGATATGTTAAAGATCCGAAAGTACAGGACTTCCGA 420  
 QY 421 AGAATATTTCTCAATGTTTGTAAAGAGCTGTGATCTTAGGATCTTATTCACCTCAT 480  
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 QY 481 AGTAGAGCAATGATGTTTATCTCCCAATGAGATCTTCCAGAACTGGCAAGAC 540  
 Db 481 AGTAGAGCAATGATGTTTATCTCCCAATGAGATCTTCCAGAACTGGCAAGAC 540  
 QY 541 ATATATTAATTAATTTGATTAAGGCAAAATATAGTGTGATTTGGGTATATGTTTCCCA 600  
 Db 541 ATATATTAATTAATTTGATTAAGGCAAAATATAGTGTGATTTGGGTATATGTTTCCCA 600  
 QY 601 AATATGACAAACAGATATCTCTGAATCAACATGACTGTGTGCGACAGACAGTA 660  
 Db 601 AATATGACAAACAGATATCTCTGAATCAACATGACTGTGTGCGACAGACAGTA 660  
 QY 661 ATTGCTGAAGCAATCAGGAAAAAACTGGAAGTATGTTGCTATCTGCAACATTAATA 720  
 Db 661 ATTGCTGAAGCAATCAGGAAAAAACTGGAAGTATGTTGCTATCTGCAACATTAATA 720  
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 Db 721 CTCTGTGTTTGAATATCAGGCAAGTATATTTAAAGTGTGATGATGATATAC 780  
 QY 781 TTCTGAGAAAAATCTCTGAGTCAATATTAAGTATTAAGAGCTGTATATGCTGGG 840  
 Db 781 TTCTGAGAAAAATCTCTGAGTCAATATTAAGTATTAAGAGCTGTATATGCTGGG 840  
 QY 841 AGGATGCCCAATTTGATGCTGATGCTGAAGAAAGCCCTTATTCACATCGCAATGAC 900  
 Db 841 AGGATGCCCAATTTGATGCTGATGCTGAAGAAAGCCCTTATTCACATCGCAATGAC 900  
 QY 901 TGTTTTCAATGCAATATTTCCAGAGCATCTTCCAGAGTATCAACATATATGATGCA 960  
 Db 901 TGTTTTCAATGCAATATTTCCAGAGCATCTTCCAGAGTATCAACATATATGATGCA 960  
 QY 961 GAAACATCTCAAAATCCCTTGGGTTTAAATGTCGATCAGATTAATAATCTTTGT 1020  
 Db 961 GAAACATCTCAAAATCCCTTGGGTTTAAATGTCGATCAGATTAATAATCTTTGT 1020  
 QY 1021 GCAACCTATGTGAATGTAAATATTCGAGACATTCGAAAGATTATGTTCCGAACGATATC 1080

Db 1021 GGAACCTATGTGAATGTAATATTCAGACATTGACAAATTTAGTTCGAACAGTATC 1080  
Qy 1081 TACCATGAGAGGAACCCCTATGTGATATGTGAACACTCAAGAGTACTTGTTCAT 1140  
Db 1081 TACCATGAGAGGAACCCCTATGTGATATGTGAACACTCAAGAGTACTTGTTCAT 1140  
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Db 1141 CCAGAGTGAATGAATGCTGTAATTAAGATATATATATATCTCTGATCTTCTGTGTCT 1200  
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Db 1201 CGACTTGTGCTTTCATTTGTTTGTAAAGCCGAAAGGTCCTAAAGAGAACACTGT 1260  
Qy 1261 CCATTGGCCCTGGGAAATATTAACCTGTGTAATTAACAGATACTAGTATCTGAAAA 1320  
Db 1261 CCATTGGCCCTGGGAAATATTAACCTGTGTAATTAACAGATACTAGTATCTGAAAA 1320  
Qy 1321 ATGGCTTTGTAATCTTGGCCAGTACCTCATGACTAGAACATTTGCTGAACCTTATGCT 1380  
Db 1321 ATGGCTTTGTAATCTTGGCCAGTACCTCATGACTAGAACATTTGCTGAACCTTATGCT 1380  
Qy 1381 GTTACTGATCAATCCAAATTAAGAAATCTCCATGTTAGAGTTGAGTTGACTGCTTC 1440  
Db 1381 GTTACTGATCAATCCAAATTAAGAAATCTCCATGTTAGAGTTGAGTTGACTGCTTC 1440  
Qy 1441 AGCAGTGTGTAAGTTCCAGATATGTCAGTGAATTAGAGAGTCCAAATGCTGTGA 1500  
Db 1441 AGCAGTGTGTAAGTTCCAGATATGTCAGTGAATTAGAGAGTCCAAATGCTGTGA 1500  
Qy 1501 TCCCGTGAAGAGATTTAGTATTTCCATGTCAGAGTCTGATTAACAGTATGCTAGAC 1560  
Db 1501 TCCCGTGAAGAGATTTAGTATTTCCATGTCAGAGTCTGATTAACAGTATGCTAGAC 1560  
Qy 1561 AATGAATTAAGAGAAATGATTAAGAACAGCTCCGAGCAATTTGTACAGAGATCTCTA 1620  
Db 1561 AATGAATTAAGAGAAATGATTAAGAACAGCTCCGAGCAATTTGTACAGAGATCTCTA 1620  
Qy 1621 TCTGAATATCATGACAGAGAGAAAGATTTCTGTGAGCCACAGACACTATTTGTAACT 1680  
Db 1621 TCTGAATATCATGACAGAGAGAAAGATTTCTGTGAGCCACAGACACTATTTGTAACT 1680  
Qy 1681 ATCCCGAAATCTACCCCAATTTGCTGTCTGTCTGTTAAATGGAATCTTAGAGATGA 1740  
Db 1681 ATCCCGAAATCTACCCCAATTTGCTGTCTGTCTGTTAAATGGAATCTTAGAGATGA 1740  
Qy 1741 GCTCAGATGTAATGCTGTTGTAAGAAATTTGCTCCAAATCAAGCTGAACAGGCTATGAG 1800  
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Qy 1801 CTTTCTGAGTGAATTAACCCAGATCTATGTTGAGAGTTTGTGCTGCTGCTTAA 1860  
Db 1801 CTTTCTGAGTGAATTAACCCAGATCTATGTTGAGAGTTTGTGCTGCTGCTTAA 1860  
Qy 1861 AATATTTTAACAGATGACAAACTTTCTCAGTATTTAATCAGTACAGGCTCTAA 1920  
Db 1861 AATATTTTAACAGATGACAAACTTTCTCAGTATTTAATCAGTACAGGCTCTAA 1920  
Qy 1921 TATGAACAGTATTTGTAACCTGCTTGTGAGATTTTACTCAAAAAAGGCTTAAT 1980  
Db 1921 TATGAACAGTATTTGTAACCTGCTTGTGAGATTTTACTCAAAAAAGGCTTAAT 1980  
Qy 1981 CAAGAGTGTGCTTCTTCTTGTGATTTAAATCTGAGATGCAATTAACAGTT 2040  
Db 1981 CAAGAGTGTGCTTCTTCTTGTGATTTAAATCTGAGATGCAATTAACAGTT 2040  
Qy 2041 AGTCAAGAGTGTGCTTCTTGTGAGTCTTATGCTGCTGAGATGGAATGATCTGA 2100  
Db 2041 AGTCAAGAGTGTGCTTCTTGTGAGTCTTATGCTGCTGAGATGGAATGATCTGA 2100  
Qy 2101 CACCTTAATAGCAAGTTGAGGCTATGGAAGGCTCATTAATCTGACATCTCA 2160  
Db 2101 CACCTTAATAGCAAGTTGAGGCTATGGAAGGCTCATTAATCTGACATCTCA 2160

Db 2101 CACCTTAATAGCAAGTTGAGGCTATGGAAGGCTCATTAATCTGACATCTCA 2160  
Qy 2161 CAAGAGAGAGAGATGAACAACAAGGCTACATGAGTATTTAGTTAGCAATGCG 2220  
Db 2161 CAAGAGAGAGAGATGAACAACAAGGCTACATGAGTATTTAGTTAGCAATGAG 2220  
Qy 2221 CGACCAATTTCAATGATGCTCTCCAGGGCTTGTGCTGCTTAAACCTGCTCATAG 2280  
Db 2221 CGACCAATTTCAATGATGCTCTCCAGGGCTTGTGCTGCTTAAACCTGCTCATAG 2280  
Qy 2281 CTGGGAATCTCAGGCTTGAAGAGTGTGAATTAATGCTTCTGCAAAAAGGCTGTG 2340  
Db 2281 CTGGGAATCTCAGGCTTGAAGAGTGTGAATTAATGCTTCTGCAAAAAGGCTGTG 2340  
Qy 2341 TTGAATTTGGAGAACCCAGACATCATGCAATTAATCTTCAACAATGATGATC 2400  
Db 2341 TTGAATTTGGAGAACCCAGACATCATGCAATTAATCTTCAACAATGATGATC 2400  
Qy 2401 TTTAAAAATGGGAGTATTTAGCGCAAGATATGCTAACCCCTCAGATTATGCA 2460  
Db 2401 TTTAAAAATGGGAGTATTTAGCGCAAGATATGCTAACCCCTCAGATTATGCA 2460  
Qy 2461 GAAAAATATCGGCAAAATCAAGGCTTGAATCTTGAATGTTACCTTATGATGCTGA 2520  
Db 2461 GAAAAATATCGGCAAAATCAAGGCTTGAATCTTGAATGTTACCTTATGATGCTGA 2520  
Qy 2521 ATCGGTGACTGTGTGGACTTATCGAGTGTGAGAAATTTCCACCTAATGAGAT 2580  
Db 2521 ATCGGTGACTGTGTGGACTTATCGAGTGTGAGAAATTTCCACCTAATGAGAT 2580  
Qy 2581 CAGTGAAGAGAGCCCTGAAGAGTGCATGCAATTAACAGCCACACTCATGAGTG 2640  
Db 2581 CAGTGAAGAGAGCCCTGAAGAGTGCATGCAATTAACAGCCACACTCATGAGTG 2640  
Qy 2641 CTCAAGACAAAGAACAAAGGGAATATATGATGCGCCATGATGATTTGTTAACATCA 2700  
Db 2641 CTCAAGACAAAGAACAAAGGGAATATATGATGCGCCATGATGATTTGTTAACATCA 2700  
Qy 2701 TGTGCTGATATGTTGTGCACTTCAATTTTGGAAATGGAATGCTCAATAGTAT 2760  
Db 2701 TGTGCTGATATGTTGTGCACTTCAATTTTGGAAATGGAATGCTCAATAGTAT 2760  
Qy 2761 ATCATGTTAAAGATGATGACAACTGTTCAATATGATTTGAGACATTTTGGATCAC 2820  
Db 2761 ATCATGTTAAAGATGATGACAACTGTTCAATATGATTTGAGACATTTTGGATCAC 2820  
Qy 2821 AAGAAAGAAAAATTTGTTAATAACAGAGCGCTGCGTGTGTTTGAACAAGATTC 2880  
Db 2821 AAGAAAGAAAAATTTGTTAATAACAGAGCGCTGCGTGTGTTTGAACAAGATTC 2880  
Qy 2881 TTAATAGTATTAAGTAAGAGAGCCCAAGATGACAAAGAACAAAGAAATTTGAGAGTT 2940  
Db 2881 TTAATAGTATTAAGTAAGAGAGCCCAAGATGACAAAGAACAAAGAAATTTGAGAGTT 2940  
Qy 2941 CAGGAGATGTGTTAACAAGCTTATCTAGCTATTTCAACAGATGCCAATCTCTTAAT 3000  
Db 2941 CAGGAGATGTGTTAACAAGCTTATCTAGCTATTTCAACAGATGCCAATCTCTTAAT 3000  
Qy 3001 CTTTCTCAATGATGCTGCTCTGGAATGCCAGATGCAATCTTTTGTGATGATGA 3060  
Db 3001 CTTTCTCAATGATGCTGCTCTGGAATGCCAGATGCAATCTTTTGTGATGATGA 3060  
Qy 3061 TACATTCGAAGAGCCCTAGCTTAAATTAACCTGAGCAGAGGCTTTGAGATTTCA 3120  
Db 3061 TACATTCGAAGAGCCCTAGCTTAAATTAACCTGAGCAGAGGCTTTGAGATTTCA 3120  
Qy 3121 AAAAATGAATGATGACACACATGCTGCTGAGCAACAATAATGATGATCTTCAC 3180  
Db 3121 AAAAATGAATGATGACACACATGCTGCTGAGCAACAATAATGATGATCTTCAC 3180  
Qy 3181 ACAATTAAGAGAGCTTTGAAGTGA 3207  
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Db 3207 ACAATTAAGAGAGCTTTGAAGTGA 3207

RESULT 5  
US-08-780-872-34  
Sequence 34, Application US/08780872  
Patent No. 5846824  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph, Oesu; Masayuki; Panayotou, George; Volintu,  
APPLICANT: Stefano; Gout, Ivan Tarasovich  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felle & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/780,872  
FILING DATE: 09-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/162,081  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-780-872-34

Query Match 93.9% Score 3011.8; DB 2; Length 3240;  
Best Local Similarity 96.2%; Pred. No. 0;  
Matches 3085; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 1 ATGCTCCAGACATCATCAGGTGAGTGGGGCATCCCTGATGCCCCCAAGATC 60  
DB 1 ATGCTCCAGACATCATCAGGTGAGTGGGGCATCCCTGATGCCCCCAAGATC 60  
QY 61 CTAGTAGAATGTTTACTACCAATGGAGTAGATGACTTTAGAAATGCTCGTAGAGCT 120  
DB 61 CTAGTAGAATGTTTACTACCAATGGAGTAGATGACTTTAGAAATGCTCGTAGAGCT 120  
QY 121 AGCTTAATAAGATAAGATGATATTTAAAGAAAGAAATACCTCTCCATCAA 180  
DB 121 ACATTAGTAAGATAAGATGATATTTAAAGAAAGAAATACCTCTCCATCAA 180  
QY 181 CTTCTTCAAGATGATCTTCTTACATTTTCTAGTGTATACCAAGAGAGAGAGGA 240  
DB 181 CTTCTTCAAGATGATCTTCTTACATTTTCTAGTGTATACCAAGAGAGAGAGGA 240  
QY 241 GAATTTTGTATGAACAAGACGACTTTGTGACTCTTGGCTTTTCAACCTTTTAA 300  
DB 241 GAATTTTGTATGAACAAGACGACTTTGTGACTCTTGGCTTTTCAACCTTTTAA 300

QY 301 GTAATTGAACAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAAGAAATGGTTTGGCT 360  
DB 301 GTAATTGAACAGTAGGCAACCGTGAAGAAAGATCCTCAATCGAAGAAATGGTTTGGCT 360  
QY 361 ATCGGATCCAGGTGTGAAATTCGATATGTTAAAGATCCAGAGTACAGAGCTTCCGA 420  
DB 361 ATCGGATCCAGGTGTGAAATTCGATATGTTAAAGATCCGAGTACAGAGCTTCCGA 420  
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DB 421 AAAAAATTTCTTAAGTGTGTAAGAAAGCTGTGATCTTAGGATCTTAATTCACCTCAT 480  
QY 481 AGTAGAGCAATGATGTTATCTCCTCAAAATGATGATCTTCAACCAAGTCCCAAGCAC 540  
DB 481 AGTAGAGCAATGATGTTATCTCCTCAACCAAGTGTGATCTTCAACCAAGTCCCAAGCAC 540  
QY 541 ATATATTAATTAATTTGGATTAAGGCAATTAATAGTGTGATTTGGGTAAATAGTTTCTCCA 600  
DB 541 ATATATTAATTAATTTGGATTAAGGCAATTAATAGTGTGATTTGGGTAAATAGTTTCTCCA 600  
QY 601 AATTAATGACAAACAGAGTATCTGAAATCAACATGACTGTGTCCAGAACAGTA 660  
DB 601 AATTAATGACAAACAGAGTATCTGAAATCAACATGACTGTGTCCAGAACAGTA 660  
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DB 661 ATTGCTGAAGCAATGAGGAAAAAACTCGAAGTATGTTGCTTCACTGGAACAACCTAAA 720  
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DB 781 TTCTTGAAGAAATATCTCTGAGTGAATGAATATGAAGCTGTATTAATGCTTGGG 840  
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DB 841 AGGATGCCAATTTGATGATGCTGATGCTGAAGAAAGAAAGCTTATTCACATCGCAATGAGC 900  
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DB 901 TGTTTTCAAGTCCATCATATTTCCAGAGCATCTCAGAGCTACGCAATATATGATGA 960  
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DB 1021 GCAACCTATGCAATGTAATATTTTCGAGACATTCGACAGATTTATGTTGCAACAGTATC 1080  
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DB 1081 TACCATGAGAGAAACCTTATATGATATGATGATGATGATGATGATGATGATGATGAT 1140  
QY 1141 CCCAGGTGAATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
DB 1141 CCCAGGTGAATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
QY 1201 CGACTTTGCTTTTCAATTTGCTGTTAAAGCCGAAAGGATGCTTAAAGAGAACATGCT 1260  
DB 1201 CGACTTTGCTTTTCAATTTGCTGTTAAAGCCGAAAGGATGCTTAAAGAGAACATGCT 1260  
QY 1261 CCATTGGCTGGGAAATATTAACCTGTTGATTAACAGATCTTATGATGATGATGATGAT 1320  
DB 1261 CCATTGGCTGGGAAATATTAACCTGTTGATTAACAGATCTTATGATGATGATGATGAT 1320  
QY 1321 ATGCTTTGAATCTTTTGGCAGTACCTCATGAGTAAAGATTTGCTGAACCTTATGGT 1380  
DB 1321 ATGCTTTGAATCTTTTGGCAGTACCTCATGAGTAAAGATTTGCTGAACCTTATGGT 1380



QY 1381 GTTACTGATCAATTCAAATTAAGAAACTCCATGTTTAGTGGAGTTGATGCTTC 1440  
 DB 1381 GTTACTGATCAATTCAAATTAAGAAACTCCATGTTTAGTGGAGTTGATGCTTC 1440  
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 DB 1441 AGCAGTGTGTAAGTTCCAGATATGTGATGATGAAGAGATCCAAATGGTGTGA 1500  
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 DB 1501 TCCCGTGAAGCAGATTTTATTTCCATGCGAGCTGATGATCAAGACTAGTATAGAC 1560  
 QY 1561 AATGAATTAAGAAATGATTAAGAAAGAGCTCCGAGCAATTTGTACAGAGATCCCTA 1620  
 DB 1561 AATGAATTAAGAAATGATTAAGAAAGAGCTCCGAGCAATTTGTACAGAGATCCCTA 1620  
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 DB 1621 TCTGAATCTGAGCAAGAAAGATTTTCTGTGAGCAGACAGACTATTTGTACT 1680  
 QY 1681 ATCCCGAAATTTCTACCAATTTGCTTCTGTGATTAATGAATCTTGAATGAATGA 1740  
 DB 1681 ATCCCGAAATTTCTACCAATTTGCTTCTGTGATTAATGAATCTTGAATGAATGA 1740  
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 DB 1741 GCTCAGATGATGCTGTTGTTAAAGATTTGGCTTCCATCAAGCTGAAAGAGCTATGAG 1800  
 QY 1801 CTTTGTGATGCTGATTTCCGAGATCTATGATGATGATGATGATGATGATGATGAT 1860  
 DB 1801 CTTTGTGATGCTGATTTCCGAGATCTATGATGATGATGATGATGATGATGATGAT 1860  
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 DB 1861 AATATTTTAAGAGATGACAACTTCTGATGATGATGATGATGATGATGATGATGAT 1920  
 QY 1921 TATGAACAGATTTTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
 DB 1921 TATGAACAGATTTTGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980  
 QY 1981 CAAAGGATGCTGATTTTCTTTGGATTTAAATCTGAGATGACAAATGAACAGTT 2040  
 DB 1981 CAAAGGATGCTGATTTTCTTTGGATTTAAATCTGAGATGACAAATGAACAGTT 2040  
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 DB 2041 AGTCAGATGCTGCTGCTTTTGGATGATGATGATGATGATGATGATGATGATGAT 2100  
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 DB 2101 CACCTTAATAGGCAAGTTGAGCTATGAAAGAGCTTCACTTAAGTGAAGATGCTCAAA 2160  
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 DB 2221 CGACGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2280  
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 QY 2401 TTTAAATAATGGGATGATTTACGCAAGATATGCTTCAATTTGATGATGATGATGAT 2460  
 DB 2401 TTTAAATAATGGGATGATTTACGCAAGATATGCTTCAATTTGATGATGATGATGAT 2460  
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DB 2461 GAAATATCTGGCAAAATCAAGGCTTGTGAAATGTTACTTATGATGATGATGATGAT 2520  
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 DB 2521 ATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580  
 QY 2581 CAGTGAAGAGAGGCTTGAAGAGTGTGAATATGCTTCTGCAAAAGCCGCTGCTGCTG 2640  
 DB 2581 CAGTGAAGAGAGGCTTGAAGAGTGTGAATATGCTTCTGCAAAAGCCGCTGCTGCTG 2640  
 QY 2641 CTGAAGAGAGAGAGGCTTGAAGAGTGTGAATATGCTTCTGCAAAAGCCGCTGCTGCTG 2700  
 DB 2641 CTGAAGAGAGAGAGGCTTGAAGAGTGTGAATATGCTTCTGCAAAAGCCGCTGCTGCTG 2700  
 QY 2701 TGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760  
 DB 2701 TGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2760  
 QY 2761 ATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820  
 DB 2761 ATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2820  
 QY 2821 AAGAGAGAGAGAGGCTTGAAGAGTGTGAATATGCTTCTGCAAAAGCCGCTGCTGCTG 2880  
 DB 2821 AAGAGAGAGAGAGGCTTGAAGAGTGTGAATATGCTTCTGCAAAAGCCGCTGCTGCTG 2880  
 QY 2881 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940  
 DB 2881 TTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2940  
 QY 2941 CAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000  
 DB 2941 CAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3000  
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 QY 3061 TACATGAGAGAGAGGCTTGAAGAGTGTGAATATGCTTCTGCAAAAGCCGCTGCTGCTG 3120  
 DB 3061 TACATGAGAGAGAGGCTTGAAGAGTGTGAATATGCTTCTGCAAAAGCCGCTGCTGCTG 3120  
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 DB 3121 AAGAGAGAGAGAGGCTTGAAGAGTGTGAATATGCTTCTGCAAAAGCCGCTGCTGCTG 3180  
 QY 3181 ACAATTAAGAGAGGCTTGAAGAGTGTGAATATGCTTCTGCAAAAGCCGCTGCTGCTG 3240  
 DB 3181 ACAATTAAGAGAGGCTTGAAGAGTGTGAATATGCTTCTGCAAAAGCCGCTGCTGCTG 3240

RESULT 6  
 US-09-085-957-34  
 ; Sequence 34, Application US/09085957  
 ; Patent No. 6274327

# GENERAL INFORMATION:

APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
 APPLICANT: Balaj, Waterfield, Michael Derek; Parker, Peter  
 APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,  
 APPLICANT: Stefano, Gout, Ivan Tarasovitch  
 TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
 TITLE OF INVENTION: THEIR PREPARATION AND USE  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pelfe & Lynch  
 STREET: 805 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10022

COMPUTER READABLE FORM:  
 MEDIUM type: Diskette, 5.25 inch, 360 kb storage



COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/085,957  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/780,872  
FILING DATE: 09-JAN-1997  
APPLICATION NUMBER: 08/162,081  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-085-957-34

Query Match 93.9%; Score 3011.8; DB 3; Length 3240;  
Best Local Similarity 96.2%; Pred. No. 0;  
Matches 3085; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

1 ATGCTCCAGAGCCATCATCAGGTGAAGTGGGGGATCCACTGATGACCCCAAGAAATC 60  
1 ATGCTCCAGAGCCATCATCAGGTGAAGTGGGGGATCCACTGATGACCCCAAGAAATC 60  
61 CTAGTGAATGTTTACTACCAATGGAATGATAGTGAATGCTTCGATGAGCT 120  
61 CTAGTGAATGTTTACTACCAATGGAATGATAGTGAATGCTTCGATGAGCT 120  
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121 AGCTTAATACGATTAAGGATGATGATTAAGAGCAAGAAATACCTTCATCAA 180  
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241 GAATTTTGTATGAAGCAAGAGCACTTTGTGACCTTGGCTTTTCAACCTTTTAAAA 300  
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301 GTAAATGAACCGATGAGCAACCGTGAAGAAAGATCTCAATCGAATGTTTGTGCT 360  
301 GTAAATGAACCGATGAGCAACCGTGAAGAAAGATCTCAATCGAATGTTTGTGCT 360  
361 ATGGCAGTCCAGTGTGTAATGATATGTTAAGATCCAGAGTACAGAGCTTTCCGA 420  
361 ATGGCAGTCCAGTGTGTAATGATATGTTAAGATCCAGAGTACAGAGCTTTCCGA 420  
421 AGAATATTTCTCAATGTTTGAAGAGAGCTGTGATCTTAGGATCTTAATTCACCTAT 480  
421 AGAATATTTCTCAATGTTTGAAGAGAGCTGTGATCTTAGGATCTTAATTCACCTAT 480  
481 AGTAGAGCAATGATGTTTATCTCCCAATGATGATCTTCAACGAACTGCAAGAGAC 540  
481 AGTAGAGCAATGATGTTTATCTCCCAATGATGATCTTCAACGAACTGCAAGAGAC 540  
541 AGTAGAGCAATGATGTTTATCTCCCAATGATGATCTTCAACGAACTGCAAGAGAC 540  
541 ATATATTAATTAATGATGATGAGGCAATTAATAGTGTGATTTGGTATATGTTTCTCA 600  
541 ATATATTAATTAATGATGATGAGGCAATTAATAGTGTGATTTGGTATATGTTTCTCA 600

601 AATATGACAAACAGAGTATACCTGAAATTAACCATGATGATGTGCGAAGAGTA 660  
601 AATATGACAAACAGAGTATACCTGAAATTAACCATGATGATGTGCGAAGAGTA 660  
661 ATTGCTGAAGCAATCAGAGAAATTAACCTGAGATGTTGCTATCATCTGAACACTAAA 720  
661 ATTGCTGAAGCAATCAGAGAAATTAACCTGAGATGTTGCTATCATCTGAACACTAAA 720  
721 CTCTGTGTTTGAATATCAGGCAAGTATTTTAAAGTGTGCGAGATGATGATAC 780  
721 CTCTGTGTTTGAATATCAGGCAAGTATTTTAAAGTGTGCGAGATGATGATAC 780  
781 TTCTAGAAATTAATCTCTGAGTCAATATGATATATAGAGCTGATTAATGCTGGG 840  
781 TTCTAGAAATTAATCTCTGAGTCAATATGATATATAGAGCTGATTAATGCTGGG 840  
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961 GAAACATCTACAAATCCCTTGGGTTATTAATAGAGCTGATTAATGATGATGGA 1020  
961 GAAACATCTACAAATCCCTTGGGTTATTAATAGAGCTGATTAATGATGATGGA 1020  
1021 GCAACCTATGTAATGTAATTAATTCAGAGCAATTCAGAGCTGATTAATGATGATG 1080  
1021 GCAACCTATGTAATGTAATTAATTCAGAGCAATTCAGAGCTGATTAATGATGATG 1080  
1081 TACCATGAGAGAGAACCTTATGATATATGTAATGTAATGTAATGTAATGTAAT 1140  
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1141 CCCAGTGAATGTAATGTAATTAATTCAGAGCAATTCAGAGCTGATTAATGATGATG 1200  
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1261 CCATTGGCTGGGAAATATTAACCTGTTGATTAACAGATTAATCTGATGATGGA 1320  
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1321 ATGGCTTGAATCTTTGGCCAGTACCTCATAGAGATTTGCTGAACCTTATGCT 1380  
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1441 AGCAGTGTGTAAGTTTCCAGATATGTCAGTATTAAGAGCATGCCAATGTTGCTGA 1500  
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1501 TCCCGTGAAGAGATTTAGTTATTTCCATGAGAGCTGATTAACACTGATGAGAGC 1560  
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1561 AATGAATTAAGAGAAATGATTAAGAGAGCTCCGAGCAATTTGTACAGAGATCTCTA 1620  
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1621 TCTGAATTAATGAGAGAAATGATTTCTGTGAGGCAAGAGCAATTTGTGTAAT 1680  
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RESULT 7  
US-08-162-081B-32  
Sequence 32. Application US/08162081B  
Patent No. 5824492  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefano, Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
TITLE OF INVENTION: THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,081B  
FILING DATE: February 7, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 688-3884  
INFORMATION FOR SEQ. ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3412 base pairs  
type: nucleic acid

STRANDEDNESS: single or double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..3204  
OTHER INFORMATION: /standard\_name= "CDS"  
US-08-162-081B-32

Query Match 93.8%; Score 3008.6; DB 1; Length 3412;  
Best Local Similarity 96.1%; Pred. No. 0;  
Matches 3083; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

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QY 361 ATGCGCATGCGAGTGTGTGATTCGATGATGTTTAAAGATCAGAGATGACAGA 420  
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DB 661 ATTGCTGAAGCAATCGAGAAAAAACTCGAAGATGTTGCTATCATCTGAACAACATTA 720  
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RESULT 8
US-08-780-872-32
; Sequence 32, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano; Gout, Ivan Tarasovich
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,872
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 658-3884
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3412 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single or double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3204
; OTHER INFORMATION: /standard_name= "CDS"
; US-08-780-872-32

Query Match 93.8%; Score 3008.6; DB 2; Length 3412;
Best Local Similarity 96.1%; Pred. No. 0;
Matches 3083; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

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Db	661	ATTGCTGAAGCAATCAGGAAAAAACTGAAAGTATGTTGCATCATCTGCAACACTATAA	720
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OY	1141	CCGAGGTGAATGAATGGCTGAATTAAGATATATCATTTCTGATCTTCTGTGCTGCT	1200
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QY	1201	CGACCTTTGCTTTTCCATTGTTCTGTGTAAGGCGGAAAGGGTGTAAAGAGGAACCTGT	1260
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QY	1261	CCATTGGCCTGGGGAAATTAACCTTGTGATTACACAGATACTTACTTCTGGAAAA	1320
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Db 2341 TTGAATTTGGGAAACCCAGACATCATCTCAGAAATTTACTCTTTCAGAAACATGAGATCATC 2400  
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RESULT 9  
US-09-085-957-32  
Sequence 32, Application US/09085957  
Patent No. 6274327

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APPLICANT: Joseph, Otsu, Masayuki, Panayotou, George, Volinia,  
APPLICANT: Stefano, Gout, Ivan Tarasovitch

TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
TITLE OF INVENTION: THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felle & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
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ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/085,957  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/780,872  
FILING DATE: 09-JAN-1997  
APPLICATION NUMBER: 08/162,081  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
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TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3412 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single or double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..3204  
OTHER INFORMATION: /standard\_name="CDS"  
US-09-085-957-32  
Query Match 93.8%; Score 3008.6; DB 3; Length 3412;  
Best Local Similarity 96.1%; Pred. No. 0;  
Matches 3083; Conservative 0; Mismatches 124; Indels 0; Gaps 0;  
Qy 1 ATGCTCCAGAGACCATCATGAGTGAAGTGGGGCATCCACTTGATGCCCCCAAGATC 60  
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Qy 61 CTATAGATGTTTACTACCAATGAGATGATGATGATGATGATGATGATGATGATGATGATG 120  
Db 61 CTATAGATGTTTACTACCAATGAGATGATGATGATGATGATGATGATGATGATGATGATG 120  
Qy 121 ACGTTAATACGATTAAGGATGAACTATTTAAAGACAGAAATACCTCCATCAAA 180  
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Qy 181 CTTCTTCAAGATGATCTTTCTTACATTTTGTAGTGTACCAAGAGAGGAA 240  
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Db 241 GAAATTTTGTATGAAACAGACCTTGTGATCTTGCGCTTTTCAACCTTTTAAAA 300  
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QY 361 ATGGGCAATGCGAGTGTGTAATTCGATATGATTAAAGATCCAGATACAGGACTTCCGA 420  
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Db 421 AGAAATATTTCTCATGTTTGTAAAGAGCTGTGGATCTTAGGGGACTTAATTCACCTCAT 480  
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Db 541 ATATATATTAATTTGGATTAAGGCAAAATATATGTGGTGAATTTGGGTAAATGTTTCTCA 600  
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Db 601 AATATATGACAAAGAGTATCTGTAATAATCAACCATGACGTGTGGCCAGAAACAAAGTA 660  
QY 661 ATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTGGTATCATCTGAACAACCTAAAA 720  
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Db 1081 TACCATGAGAGAAACCTTATGTGATTAATGTGAACACTCAAGAGTACCTTGTCCAAAT 1140  
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QY 1321 ATGGCTTTGAATCTTTGGCCAGTACTCATGACATTAAGAAATTTGTTGAACCTTATGGT 1380  
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Db 1501 TCCCGTAGACAGATTTTACTTATTTCCCATGACGAGTGAATACAGACTAGTAGAC 1560  
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[illegible]

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Qy 1412 CATGTTAGATTTGAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAG 1471  
Dh 1424 CATGGAACCTGTTCAACCAATCCATATATCTGAAATGCAACAGCTTGCATGTTAAAT 1483  
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Qy 1820 CAGATCTTAATGTTGAGGTTTGTCTGTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1879  
Dh 1844 CAGACAGTACGTTGAGAAATATGCTGAGGCTGCT---GCCAGATGATGATGAAG 1900  
Qy 1880 AACTTCTGATACCTAATTCAGCTAGTACAGGATCAAAATTAAGAAAGTGAATTTGAT 1939  
Dh 1901 AACTTCTGATACCTTAACTTAACTGATGCAAGTGAATTAATTAAGTGAATTTGAT 1960  
Qy 1940 AACTGCTTGTGATTTTAACTCAAAAAAGCTTAACTAATCAAGATGCTGATCTTT 1999  
Dh 1961 GTGCCCTCTGATTTCTTAATTAAGAAAGCACTTGTATGAGAGATTAAGGCACTTTC 2020  
Qy 2000 TCTTTTGGATTTAAATCTGAGATCAATTAAGAAAGTGAAGTGAAGTGAAGTGAAGTGA 2059  
Dh 2021 TATTTTGGATCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2080  
Qy 2060 TTTTGGATCTTATGCGGATGATGAGATGATGATGATGATGATGATGATGATGATGATG 2119  
Dh 2081 TCTTTGAAGATACCTGCGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2140  
Qy 2120 AAGCTATGAAAAAGCTATTAATCTGATGATGATGATGATGATGATGATGATGATGATG 2179  
Dh 2141 AAGCACTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2200  
Qy 2180 CACAAAAGGTACAGATGAAGTTTATGTTGAGCAAAATGCGGAGCAAGATTTTCATGATG 2239  
Dh 2201 ACAGAGCCAAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2260

Qy 2240 CTCTCAGGAGCTTTCTGCTCTCTTAACCCCTGCTATCAGTGGGAAATCTCAGGCTTG 2299  
Dh 2261 CCTCTCTGACCTGCAAGTCAACCCCTGATACCTGATATCTCTCAAGAACTCTATGTTG 2320  
Qy 2300 AAGAGTGTGAATTAATGCTTCTGCAAAAAAGGCACTGTTGTTGTTGTTGTTGTTGTTG 2359  
Dh 2321 AAAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2380  
Qy 2360 ACATCATGTCAGAAATTAATCTTTCAGAACATTAATTAATTAATTAATTAATTAATTA 2419  
Dh 2381 TATTTGAGAGATTAAT-----TGAGTGAATTTTAAATTAATTAATTAATTAATTA 2428  
Qy 2420 TACGCAAGATATGATCAACCCCTGATTAATTAATTAATTAATTAATTAATTAATTA 2479  
Dh 2429 TACGCAAGATATGATCAACCCCTGATTAATTAATTAATTAATTAATTAATTAATTA 2488  
Qy 2480 AAGCTTTGATCTTGAATGTTTACCTTAATGATGATGATGATGATGATGATGATGATG 2539  
Dh 2489 CTGTTTGAATCTTGGATGTTGCTTATGAGTGTGTTAGCAACAGAGATCGCTGGCC 2548  
Qy 2540 TTATCAGAGTGTGAAGAAATTTCACTATTAATGAGATTCAGTTAAAGAGC---C 2596  
Dh 2549 TCATTGAAGTGTGACACCTCTGAACCAATGCTGACATTCAGCTGAACAGTGAAGATG 2608  
Qy 2597 TGAAGGTGACCTGAGTTTAAACAGCCACACTCATGATGATGATGATGATGATGATGATG 2656  
Dh 2609 TGCTCTGAGAGGCTTCAACAAAGATGCTTGTGAATGCTTAAAGATTAACAT 2668  
Qy 2657 AAGGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2716  
Dh 2669 CTGGGATGACCTGAGCCAGAGCTTGAAGATTAATTAATTAATTAATTAATTAATTA 2728  
Qy 2717 TTGCACTTCAATTTGGAAATGAGATGTCACATTAATTAATTAATTAATTAATTAATTA 2776  
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Qy 2777 ATGGAACATGTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2836  
Dh 2789 CTGGCAGCTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2848  
Qy 2837 GTTATTAACGAGAGGCGTGGCTTTGTTTGAACAAAGTTTCTTAATTAATTAATTAATTA 2896  
Dh 2849 GCATTTAAAGGAGAGAGGAGGCTTTTATTTATTAATTAATTAATTAATTAATTAATTA 2908  
Qy 2897 AAGAGCCCAAGATGACAAAGAGAAATTTGAGAGTTTCAGAGATGTTTACA 2956  
Dh 2909 AAGGAAAAACAGG-----AAATACAGAAAGTTTGGCCGTTCCGAGTGTGAGG 2962  
Qy 2957 AAGCTTATCTATCTATTTGGCAGATGCAATCTCTTCAATTAATCTTTCTCAATGATG 3016  
Dh 2963 ATGATATATCTATTTTACAGAGGAGGAGGAAATCTCTTCACTCTTTTGGCGTGAATG 3022  
Qy 3017 TTGGCTCTGATGTCAGAACTGCAATCTTTGATGATTAATTAATTAATTAATTAATTA 3076  
Dh 3023 TGACTGCAAGGCTCTCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 3082  
Qy 3077 TAGCTTTAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3136  
Dh 3083 TTGCAATTTAGGAAAGATGAAGAAAGCACTCAAAACAGTTTAAAGAAATTTGATGA 3142  
Qy 3137 CACACCATGATGCTGAGCAACAAAGAAATGATGATCTTCAACATTAATTAAGCA 3191  
Dh 3143 CGCTCAGGAGAACTGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3197

RESULT 11  
US-09-194-640A-2  
; Sequence 2, Application US/09194640A  
; Patent No. 6482623  
; GENERAL INFORMATION:  
; APPLICANT: Van Hasebroeck, Bart  
; APPLICANT: Waterfield, Michael D.



Query Match 10.5%; Score 336.2; DB 3; Length 3868;  
 Best Local Similarity 53.5%; Pred. No. 2.9e-88;  
 Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;

1682 TCCCGGAAATTTACCCAAATGCTTCTGCTTAAATGGAACCTAGAGATGAAGTAG 1741  
 1821 TCCCGAGGCGCTAGCCCGCTGCTGCTGCTACCAAGTGAACAGCATGAGAAATGTG 1880  
 1742 CTCAGATGACTGCTTGTGTAAGATTGGCTCAATCAAGCTGAACAGGCTGAGAG 1801  
 1881 CCCAGATGCTTACCTGCTGTGCTCTGCGCGGAGAGCTGCCCGCTGAGGCGCTGAGC 1940  
 1802 TTCAGATGCAATTAACCAAGATCTATGATGAGGTTTGTGTTGCTGCTTGA 1861  
 1941 TCTTACACTTCACTTCCCGAATGGCAGTAGGCTCTTCCGCTCAAGTCCGCTCGGA 2000  
 1862 AATATTATACAGATGCAAACTTTCTCACTACTAATTCAGCTACATGATGATGAAAT 1921  
 2001 AAC--TGACGACGATGAGCTGCTTCCAGTACTGCTGACGCTGAGCTGCTCAAGT 2057  
 1922 ATGAACAGATTTGATGATACTGCTTGTGAGATTTTAACTCAAAAAGGCTTAATATC 1981  
 2058 AGAGATCTTACCTGAGCTGAGCTGACCAAAATCTGCTGACCGGCGCTGCGCAAC 2117  
 1982 AAAGATCGGTCACTTTTCTTTGGCATTAAATCTGAGATGACCAATAAACAGTTA 2041  
 2118 GCAAGATCGGCACCTTTCTTGGCACCTCGCTCCGAGATGACGATGCCGCTGGTGG 2177  
 2042 GTCAGAGTTTGGCCCTGCTTTGGAGTCTTATGCTGCTGATGATGAGATGTATGAAC 2101  
 2178 CCTGGCTTGGCCCTCATCTGAGAGCTTACTGCGAGGCGGAGCAACCAATGAAAG 2237  
 2102 ACCTTAATAGCAAGTTGAGGCTATGAAAGCTCAATTAAGCTGACATTTCAAA 2161  
 2238 TGTGATGAGAGAGGAGGAGAGCACTGACAACTGAAGGCTCTGATGCTTGTAAAG 2297  
 2162 AAGAGAGAGAGATGAACACAAAGATACAGTGAATTTTAACTTGAACAAATGCGGC 2221  
 2238 TGAGCTCTAGAAAGACCCCAAGCCCAAGACCAAGAGCTGATGACTTGTGATCGGC 2357  
 2222 GACCAATTTTATGATGCTCTTCAAGGCTTTCTGCTCTCTTAACTTCTGCTATGAG 2281  
 2358 AGAGGCTTACCTAGAGGCTCTTCCACCTGACAGTCCACCTGACAGCCAGACCTTGC 2417  
 2282 TGGAAATCTCAGGCTTGAAGAGTGCATATATGCTTCTGCAAAAAGGCACTGTGGT 2341  
 2418 TGGCTGAAGTCTGCTGAGAGAGTGCATCTTCAAGTCTCAAGATGAAGCCCTGTGGA 2477  
 2342 TGAATTTGGAGAACCCAGACATCATGTCAAAATTAATCTTTTGAAGCAATGATCATCT 2401  
 2478 TCATGTACAGCAAGAGAG-----GCAAGGACGCGGCGGAGCTGGGATCATCT 2528  
 2402 TTTAAAAATGGGATGATTTTACGGCAAGATATGCTAACCTTCAAGATTTTGGCATTTAG 2461  
 2529 TTTAAACCGGGATGACCTCCGAGAGATCTGACCTCTGAGATGATCCAGCTCATG 2588  
 2462 AAAATATCTGGCAAAATCAAGGCTTGTATCTTGAATGTTTACTTATGATGATGCTGCA 2521  
 2589 AGCTCTGTGAGAGAGAGGAGGAGCTGAGCTTGAAGATGAGCCCTTATGCTGCTCTCCA 2648  
 2522 TCGATGATGTTGTGGACTTATCGAGTGTGTAAGAAATTTCTCACTATATGAGATTC 2581  
 2649 CCGGGAGCGGACAGGCGCTCATTTAGAGTGTACTCGCTTCAACACATCGGCAACATCC 2708  
 2582 A---GTGTAAGAGAGGCTGAAAGGTGCACTCAGTTTAAAGCCACACATCTCATGCT 2638  
 2709 AACTCAACAGAGCAACATGAGCAGCCAGCCCTTCAACAGAGATGCTGCTCAACT 2768  
 2639 GAGCTCAAAAGACAAAGCAAGAGGAGAAATATATGATGCGGCGCTGATTTGTTTAAAGAT 2698  
 2769 GAGCTAAAGTCAAGAACCGGGAGAGGCGCTGATGAGCCATTTAGAGATTCACCTCTT 2828  
 2699 CATGTCTGATGATTTGTGTTGCACTTTCATTTTGGAAATTTGAGATCTGCAAAATAGTA 2758

Db 2829 CCGTCTGCTGATTTGTGTGGCCACATATGTGCTGGGCAATGGCATGCGACAGCGACA 2888  
 QY 2759 ATATCATGTGTTAAAGATGATGACAACTTTTCAATTAATTTTGAACATTTTGGATC 2818  
 Db 2889 ACATCATGATCCGAGAGAGTGGGCACTGTTCCACATTAATTTTGGCACATTTCTGGGA 2948  
 QY 2819 ACAGAGAGAAATTTGTTTAAACGAGAGGCGCTGCTTGTGTTGACACAAAT 2878  
 Db 2949 ATTTCAAGACAAAGTTTGAATTCACCGAGAGCTGTCCCATTTACCTTACCTAGACT 3008  
 QY 2879 TCTTAATAGTATTAAGTAAGAGCCCAAGAAATGCAAAAGCAAGAGATTTGAAGGT 2938  
 Db 3009 TTGTTCATGATGATTCAGCAGG-----GAACTAATTAATGTGAATTTGAACGGT 3062  
 QY 2939 TTCAGAGATGTGTTTCAAGGCTTATCTATGCTATTTGGCAGCATGCCAATCTTCA 2998  
 Db 3063 TCCGGGCTACTGTGTAAGAGGCTTACACCATCTGCGGCGGCAAGGCTTCTCTCC 3122  
 QY 2999 ATCTTTCTCAATGATGCTTGGCTGGAATGCCAAGCTGCAATCTTTGATGATATG 3058  
 Db 3123 ACCTCTTTCCTGATGCTGCGGCGGAGGCTGCTGAGCTCAGCTGCTCAAGACATCC 3182  
 QY 3059 CATACATTCGAAAGACCTAGCTTTAGATTAATCTGAGCAAGAGGCTTTGAGATTTGA 3118  
 Db 3183 AGATCTCAAGAGACTCCCTGACACTGGGGAACAGAGAGAGGACATGAGCACTTCC 3242  
 QY 3119 TGAACAAATGATATGACACCACTGCTGCTGCAACAAATTTGATTTGCTTCC 3178  
 Db 3243 GAGTGAAGTTTAAAGAGCCCTCGTGAAGCTGGAACCAAGTGAATGGCTGGGCC 3302  
 QY 3179 ACA 3181  
 Db 3303 ACA 3305

RESULT 13  
 US-08-777-405A-1  
 ; Sequence 1, Application US/08777405A  
 ; Patent No. 5858753  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chantry, David  
 ; APPLICANT: Hoekstra, Mel F.  
 ; APPLICANT: Holzman, Douglas A  
 ; TITLE OF INVENTION: No. 5858753el Lipid Kinase  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
 ; STREET: 6300 Sears Tower/233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/777,405A  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: No. 5858753and, Greta E.  
 ; REGISTRATION NUMBER: 35,302  
 ; REFERENCE/DOCKET NUMBER: 27866/33441  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (312) 474-6300  
 ; TELEFAX: (312) 474-0448  
 ; TELE: 25-3856  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5220 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 196..3327  
US-08-777-405A-1

Query Match 10.5%; Score 336.2; DB 2; Length 5220;  
Best Local Similarity 53.5%; Pred. No. 3.5e-88;  
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;

1682 TCCCGGAATTTCTACCAATTTGCTTCTGTTAAATGGAATCTTAGAGTGAAGT 1741  
1820 TCCCGAGGCGGTACCGCGCTGCTGTGTCAACCAAGTGAACAAGCATGAGATGTG 1879  
1742 CTCAGATGCTGCTTGTGTAAGATGGCTTCCAATCAAGCTGAACAGGCTATGAGC 1801  
1880 CCCAGATGCTTACCTGCTGTGCTCTGCGCGAGCTGCCCTCTGAGCGCCCTGAGC 1939  
1802 TTCTGACCTGCAATTTCCAGATCCATAGTGTGAGTCTTGTGCTGCTTGAAGA 1861  
1940 TCTTACACTTCAAGCTTCCCGATTCGACGTAGGCTCTTCCGACATCAAGTGTGCG 1999  
1862 AATATTATACAGATGCAAACTTCTCAGTACCTTAATCAGTATGACAGTAAAT 1921  
2000 AAC--TGACGACGATGAGCTGTTCAGTACCTGCTGACGTGTCAGTCTCAAGT 2056  
1922 ATGACAGATTTTGGATTAACCTGCTGTGAGATTTTCTCAAAAAGGCTTAATATC 1981  
2057 ACAGATCTTACCTGACTGCGAGCTGACCAAAATCTGCTGAGACGGGCCCTGCAAC 2116  
1982 AAGGATCGCTCTTTTCTTTGGCATTTAAATCTGAGATGACACATTAACAGT 2041  
2117 GCAGATCGGCACTTCTTTCTGCACTCCGCTCCGAGATGCAAGTGTGCGTGG 2176  
2042 GTGAGATTTGGCTCTTTTGGAGTCTTATGCTGCTGATGAGATGTATCTGAAGC 2101  
2177 CCTGCGCTTCGCTCATCTGAGGCTTACTGAGGGCTACTGAGGGCAGCACCAACATGAAG 2236  
2102 ACCTTAATAGGCAAGTGAAGCTTATGAAAAGCTTAACTTACTGACATCTCAAC 2161  
2237 TGCTGATGAAGCAGGGGAGACACTGAGCAATGAAGGCTTAATGACTTCTCAAGC 2296  
2162 AAGGAAAGAGATGAACAACAAGATGACATGAATTTTATGAGCAATGCGGC 2221  
2297 TGAGCTCTCAGAAAGCCCCCAAGCCCCAGACCAAGAGCTATGACATTTGATGCGGC 2356  
2222 GACCAATTTGATGATGCTCTCCAGGCTTCTGCTCTCTTAAACCTGCTCATGAC 2281  
2357 AGGAGGCTTACTAGAGCCCTCTCCACCTGCACTCCCACTCCACCCAGCACCTGCG 2416  
2282 TGGGAATCTCAGGCTTGAAGATGTCGAATTAATCTTCTGCAAAAAGGCACTGTGT 2341  
2417 TGGCTGAAGTCTGCTGAGAGCTGACCTTATGATGATCCCAAGATGAAGCCCTGTGA 2476  
2342 TGAATTTGGAGAACCCAGACATCATGTGCAATTAATCTTCTGCAACAATGATCATCT 2401  
2477 TCATGTACAGCAAGAGAG-----GCAAGCAGCGCGCGAGCGTGGGATCATCT 2527  
2402 TTAATAATGGGATGATTTACGCAAGATATGCTAAACCTTGAAGTATTTGCATATG 2461  
2538 TTAAGAACGGGATGACCTCCGAGAGACATGCTGACCTGAGATGATCCAGCTCATG 2587  
2462 AAAATATCTGGCAAAATCAAGCTTGTATCTTGAATGTTACTCTTATGATGCTGTCA 2521  
2588 AGCTCTGTGGAAGCAGAGGCTGACCTGAGATGAACCCCTTATGCTGCTCCCA 2647  
2522 TGGTACTGTGTGGACTTATGAGTGTGTGAATTTCTACATATATGCAATTC 2581  
2648 CCGGGAGCGCACAGGCTCTATTGAGGTGTAATCTCGGTTCAGACATGCCAATCC 2707

2582 A---GTGTAAAGAGGCGCTGAAGGTGCTGACATTTAAAGCCACACACTCCATCAGT 2638  
2708 AACTCAACAGAGCAATGCGACCCACAGCGCCCTTCAACAGAGTCCCTGTCAACT 2767  
2639 GGTCAAAAGCAAGACAGGGGGAATATATGATGCGGCCCATGATTTGTTTACAGAT 2698  
2768 GGTGAAGTCCAAAGACCCGGGAGGCGCCCTGATCCAGATGAGAGTTCACCTCT 2827  
2699 CATGCTGATATTTGTTGTCACCTTCAATTTTGGATTTGAGATGTCACAAATGTA 2758  
2828 CTTGCTGCTGATTTGTGTGCGACATATGTGCTGGCATTTGGGATGCGACAGCA 2887  
2759 ATATCATGTTAAGATATGACACCTTTTCAATATGATTTTGGACACTTTTGGATC 2818  
2888 ACATCATATCCGAGAGAGTGGCGAGCTGTTCCACATTTGATTTTGGCCACTTTTGGGGA 2947  
2819 ACAAGAAAAAATTTGTTATTAACGAGAGCGGCTCCGTTGTTTGAACAAGATT 2878  
2948 ATTTCAAGCCAGTTTGAATCAACCGGAGCGTCCCATTTATCTTCACTATGACT 3007  
2879 TCTTAATGATGATTAAGAGAGCCCAAGATGCAACAAGCAAGATTTGAGAGT 2938  
3008 TTGTCATGCTGATTCAGCAGG-----GAAGACTAATATATGTAGAAATTTGAACGT 3061  
2939 TTCAAGAGATGTTTCAAGGCTTATCTAGCTATTCGAGAGTGCATCTTTCATTA 2998  
3062 TCCGGGCTACTGTGAAGAGGCTTACACCATCTGCGGCGCCACGGCTTCTTCTCC 3121  
2999 ATCTTTCTCANTGATGCTGCTGCTGAGATCCGACATGCAATCTTTTGAATATTTG 3058  
3122 ACCCTTTGCTGATGAGCGGCGGCGAGGCTGCTGATGCTCTCAAGACATCC 3181  
3059 CATACATTCGAAAGACCTTACTTATGATTAATCTGACAAAGGCTTTGAGATATTGA 3118  
3182 AGTATCTCAAGACCTCCCTGGCACTGGGGAACAGAGAGGAGCACTGAACACTTCC 3241  
3119 TGAACAAATGAATGATGACACCATGCTGCGCAACAAATGATGATCTTCC 3178  
3242 GAGTGAAGTTTAAAGAAAGCCCTCGTAGAGCTGGAACCAAGATGAACTGGCTGCC 3301  
3179 ACA 3181  
3302 ACA 3304

RESULT 14  
US-08-977-871A-1  
Sequence 1, Application US/08977871A

Patent No. 5882910  
GENERAL INFORMATION:  
APPLICANT: Chantry, David  
APPLICANT: Hoekstra, Merl F.  
APPLICANT: Holzman, Douglas A  
TITLE OF INVENTION: No. 5882910el Lipid Kinase  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun  
STREET: 6100 Sears Tower/233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/977,871A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/777,405

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?      FILING DATE:
?      ATTORNEY/AGENT INFORMATION:
?      NAME: No. 5882910and, Greta E.
?      REGISTRATION NUMBER: 35,302
?      REFERENCE/DOCKET NUMBER: 27866/334441
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: (312) 474-6300
?      TELEFAX: (312) 474-0448
?      TELEX: 25-3856
?      INFORMATION FOR SEQ ID NO: 1:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 5220 base pairs
?      TYPE: nucleic acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?      MOLECULE TYPE: cDNA
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 196..3327
?      US-08-977-871A-1

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Query Match	10.5%;	Score 336.2;	DB 2;	Length 5220;
Best Local Similarity	53.5%;	Pred. No. 3.5e-88;		
Matches 804;	Conservative	0;	Mismatches 678;	Indels 21;
				Gaps 4;

QY	1682	TCGCCGAATTCACCCAAATGCTTCGTGTTAAATGGAACCTTGAGATGAAAGT	174
Dp	1820	TCCCGGAGGCGCTACCCGGCGCTGCTGCTGTCACCAAGTGGAAACAGATGGAGATGTGG	1875
QY	1742	CTCAGATGTACTGCTTGGTAAAAAGATTGGCCTCCAAATCAAGCTTGACAGCTATAGAGC	1801
Dp	1880	CCCGAGATGCTTACTCTGCTGTGCTCTGGCCGAGACTGCCGCTCTGAGCGCCCTGGAGC	1935
QY	1802	TTTCGAGATGTCAATTACCCAGATCCTATAGTTTCAGAGTTTTCGTTCGGTCTTAGAA	186
Dp	1940	TGCTTAGACTTACGCTTCCCGATTGGCCACGTAGGCTCCTTGGCCATCAAGTGGCTGGGA	1995
QY	1862	AATATTTAACAGATGACAAACCTTTCACGATCTAATTACGCTACTACAGGACTTAAAT	192
Dp	2000	AAC---TGACGAGACGATGAGCTGTTCCAGTACCTGCTCAGCTGTGTGACGGTGCCTCAAGT	205
QY	1922	ATGGAACGATTTTGGATATACCTGCTGTGGAGATTTTACTCAAAAAGCGTTAACTAATC	1981
Dp	2057	ACGAGTCTTACTTGACACTGACGACGCTGACAAATTCCTGCTGAGACCGGCGCCCTGGCAAC	2118
QY	1982	AAGAGATCGACGACTTTTCTTTTGGACATTTAAATCGAGATGACACATTAACAGTTA	2041
Dp	2117	GCAAGATGGGCACTTCCTTTCTTGGACACTCCGCTCCGAATGACAGTGGCGGTGGTGG	2178
QY	2042	GTCAGAGTTTGGCCTGCTTTTGGAGTCTTATTGCCGTGCATGTGGGATGTATCTGAAGC	2101
Dp	2177	CCCTGCGCTTGCGGCTCATCTCTGGAGGCTCTGACGGGGGACGACCCACCAACATGAAGG	2238
QY	2102	ACCTTAATAGGCAAGTTGAGGCTATGGAAGAAAGCTCATTAACCTGACATTCCTCAAC	2161
Dp	2237	TGCTGATGAAAGGAGGGGAGACACTGAGCAAACTGAAAGCCCTGTATATCTTCTGTAAGC	2298
QY	2162	AAGAGAAAGAGATGAACAACAAAAGGTACAGATGAAGTTTATTGTTAGGCAAAATGCGGC	2221
Dp	2297	TGAGCTCTCAGAAAGACCCCAAGCCCCAGACCAAGAGAGCTATGTGACTTTGTGATGGCGC	2356
QY	2222	GACCAAGTTTCATGGATGTCCTCCAGGGCTTCTGTCTCCTCTAAACCTTCCTATCAAGC	2281
Dp	2357	AGGAGGCTTACTTGAAGGCGCTCTCCCACTGCAAGTCCCACTGACCCCAAGCAACCTTGC	2416
QY	2282	TGGGAAATCTCAGGCTTGAAAGGTGCGAATTTATGTCTTCTGCAAAAAGCCACCTGTGGT	2341
Dp	2417	TGGCTGAAGTGTGCTGGAGCAGTGCACTTCATGAGACTCCAAGTGAAGCCCTGTGGGA	2476
QY	2342	TGAATTGGGAAACCCAGACATCATGTGCAAAATTACTTTTCAGAACATAGATCATCT	2401
Dp	2477	TCATGTACAGCAAGAGAG-----GAGGCGACGGGGGAGCGCTGGGCACTCATCTT	2527

OY	2402	TTAAAAAAGGGGATGATTTACGGCAAGATATGCTAACCCCTTCAGATTAATTCGATTTATNG	2461
Db	2508	TTTAAGAAAGGGGAATGACCTCCGGACGACATGCTGACCTTCGACATATGATTCAGCTCATGG	2587
OY	2462	AAAAATATCTGGCAAAATCMAAGTCTTGATCTTCGAATGTTACTTATGATGATGTCTCA	2521
Db	2588	ACGTCTCTGTGAACGACGAGGAGGGCTGGACCTGAGAGATGACCCCTTATNGGCTCTCCCA	2647
OY	2522	TCGGTGACTGTGTGGGACTTATCGAGTGTGTGAAGAAATTCACACTATAATGCAATTC	2581
Db	2648	CCGGGGACCGACAGGCGCTCATTTAGGTGTGATCTCCGTTACAGACCATCGCCAAACATCC	2707
OY	2582	A---GTGTAAAGAGAGCCCTGAAAGGTGCATCGACAGTTTAAACAGCCACACTCCATAGT	2638
Db	2708	AACTCAACAGACGCAATGCGACGCCACAGCCGCTTCACACAGAGATGCCCTGCTCACT	2767
OY	2639	GGCTCAAAAGACMAAGACMAAGGGGGAAATATATGATGCGCCATGATTTGTTTTACAGAT	2698
Db	2768	GGCTGAAGATCCMAAGAACCCGGGGGAGGCCCTCGATCGACCATTTAGAGAGTTACCCCTCT	2827
OY	2699	CATGTGCTGGAATATTTGTTTGTCCACTTCATATTTGGGAATTTGGAGATGCTCACATATGTA	2758
Db	2828	CCGTGTGCTGCTATTTGTGTGCGCAATATGTGCTGGGCATTGGCGATCGGCACAGCACA	2887
OY	2759	ATATCATGTTTAAAGATGATGACCAACCTGTTTCATATAGATTTTGGACACTTTTGGATC	2818
Db	2888	ACATCATGATCCGAGACAGATGGCAGCTGTTCACATGATTTTGGCACTTTTGTGGGGA	2947
OY	2819	ACAAGAAAGAAAAATTTGGTTATTAACGAGAGCGCGTGCCGTTGTTTGAACAAGATT	2878
Db	2948	ATTTCAAGACCCAAAGTTTGGAAATCAACCGCAGCGGTGTCCATTATCTCTCACTATGACT	3007
OY	2879	TCTTAATATGATATAGTAAGAGAGCCCAAGATGCCAACAAGACAAGAAATTTGAGAGGT	2938
Db	3008	TTGTTCATGTGATTCAGCAGGG-----GAAAGACTAATAATGTAGAGAAATTTGAAAGGT	3061
OY	2939	TTCAAGAGATGTGTTACAGAGCTTATCTAGCTATTCGGCAGCATGCCAAATCTCTTCAFA	2998
Db	3062	TCCGGGGCTACTGTGAAGAGGGCTTAACACATCTCGGGCGCCACAGGGCTTCTTCTCTCC	3121
OY	2999	ATCTTTTCTCAATGATGCTTTGGCTCTGGAATGCCAGAACTGCAATCTTTTGATGATATTTG	3058
Db	3122	ACCTCTTTGCCCTGTATCCGGCGCGCAGCCCTGCTGCTGACTGCTCCAAAGACATCC	3181
OY	3059	CATACATTTCGAAGAGACCTTAGCTTTAATAAATGAGCAAGAGGCTTTGAGATATTCA	3118
Db	3182	AGTATCTCAAGAGACTCCCTGTGCACTGGGGAAACAGGGAGAGGACCTAAGACATTC	3241
OY	3119	TGAACAAATGAATGATGACACACCATGTGTGCTGACACAAACAAATGATTTGATCTTCC	3178
Db	3242	GAGTGAAGTTTAACGAAGCCCTCCGTGATGAGCTGGAAAAACAAAGTGAATCGGTGGCCCC	3301
OY	3179	ACA 3181	
Db	3302	ACA 3304	

RESULT 15  
 US-09-225-951-1  
 : Sequence 1, Application US/09225951  
 : Patent No. 5985589  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Chantry, David  
 :  
 : APPLICANT: Hoekstra, Weir F.  
 :  
 : APPLICANT: Holzman, Douglas A  
 :  
 : TITLE OF INVENTION: No. 5985589e1 Lipid Kinase  
 :  
 : NUMBER OF SEQUENCES: 17  
 :  
 : CORRESPONDENCE ADDRESSES:  
 :  
 : ADDRESSEE: Marshall O'Toole Gerstein Murray & Borum  
 :  
 : STREET: 6300 Sears Tower/233 South Wacker Drive  
 :  
 : CITY: Chicago  
 :  
 : STATE: Illinois  
 :  
 : COUNTRY: USA  
 :

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      ZIP: 60606
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.30
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/09/225,951
      FILING DATE:
      CLASSIFICATION:
      ATTORNEY/AGENT INFORMATION:
      NAME: No. 5985589and, Greta E.
      REGISTRATION NUMBER: 35,302
      REFERENCE/DOCKET NUMBER: 27866/33441
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (312) 474-6300
      TELEFAX: (312) 474-0448
      TELEX: 25-3856
      INFORMATION FOR SEQ. ID NO: 1:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 5220 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: cDNA
      FEATURE:
      NAME/KEY: CDS
      LOCATION: 196..3327
      US-09-225-951-1

Query Match      10.5%: Score 336.2; DB 2; Length 5220;
Best Local Similarity 53.5%; Pred. No. 3.5e-88;
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;

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      1742 CTCAGATGTACTGCTTGTGTAAGAATGCGCTCCCAATACAGCTGGAACAGCTATGAGC 1801
      1880 CCGAGATGCTTACTGCTGTGCTCTGCTGCGGAGCTGCCGCTCTGAGCGCCCTGAGGC 1939
      1802 TTCGGAATGCAATTAACCAATGCTATGCTGAGGTTTGTGCTGCTGCTTAA 1861
      1940 TGCTAGACTTCAAGCTTCCCGATGTCAGAGTACGCTCTGCTGAGGCTGCAAGT 1999
      1862 AATATTTAAGATGACAAATTTCTCAGTACCTTAATCAAGTACTAGTACAGTAAAT 1921
      2000 AAC--TACGAGCATGAGCTGTTCCAGTACCTGCTGAGCTGCTGAGGCTGCAAGT 2056
      1922 ATGAACAGTATTTGGATTAACCTGCTTGTGAGATTTTACTCAAAAAAGCTTAATTC 1981
      2057 ACGACTCTTACTGAGTCTGAGCTGACCAAAATTCCTGTGAGCGGCGCTGCGCAAC 2116
      1982 AAAGATGCTTCACTTTTCTTTGGCATTAAATCTGAGTGAACAATAAAGATT 2041
      2117 GCMAATGCGGCACCTTCTTTCTGGACCTCCGCTCGAGATGACGTCGCGGTGG 2176
      2042 GTCAAGGTTTGGCTGCTTTTGAAGTCTTATGCGGTGATGAGTGTATCTGAAGC 2101
      2177 CCTGCGCTTGGCGCTTCACTCTGAGAGCTTACTGCAAGGAGCAACCAACATGAAAG 2236
      2102 ACCTTAATAGGCAAGTGAAGGCTATGAAAGTCAATTAATCTGATGACATTCGAAC 2161
      2237 TGTGATGAAGCAGGGGAGCACTGAGCAAACTGAAGCCCTGATGACTTGTGAAGC 2296
      2162 AAGAGAGAGATGAACAACAAGTACAGATGAAGTTTATGTTAGTGAACAATGCGGC 2221
      2297 TGAGCTCTGAGAAAGCCCCAAGCCCCAAGCAAGAGAGCTGATGACTTGTGATCGGC 2356
      2222 GACCAATTTTCAATGATGCTCTCAGGGCTTTTGTCTCTTAAACCTGCTCATAGC 2281
      2357 AGGAGGCTTACTAGAGGCTTCTCCCACTGCAAGTCCCACTGACCCCAAGCACCCTGC 2416

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      2282 TGGAAATCTCAGGCTTGAAGAGTGTGCAATTATGTCTTTCGAAAAAGGCCACTGTGT 2341
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      2342 TGAATTGGGAGAACCCAGACATCATGTGCAATTACTCTTTTCAGAAATGATGATCATCT 2401
      2477 TCATGTACGCAACCAAGAG-----GCAAGGAGGGGGGAGCGGTGGGATCATCT 2527
      2402 TTAATAATGGGATGATTTACGGCAAGATATGCTAAACCTTTCAGATTATTCGCAATTATGG 2461
      2528 TTAAGAACGGGATGACCTCCGGCAGGACATGCTACCTGTGAGATGATCCAGCTCATGG 2587
      2462 AAAATATCTGCGAAATATCAAGCTCTTGAATCTTCGAATGTACTTATGATGATGTCTGCA 2521
      2588 AGTCTCTGTGGAAGCAGGAGGGGCTGAGCTGAGATGACCCCTATGTGCTGCTCCCA 2647
      2522 TGGTGAATGTGTGGGACTTATCGAGTGTGAGAAATTCACATATATATGCAATTC 2581
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      3179 ACA 3181
      3302 ACA 3304

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Search completed: November 7, 2003, 13:16:14  
 Job time : 156.839 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 04:07:07 ; Search time :40.233 Seconds  
(without alignments)  
16024.736 Million cell updates/sec

Title: US-09-325-095-35

Perfect score: 3207  
Sequence: 1 ATGCCTCCAGACATCATC.....AGCAGCATGCTTGAACGTA 3207

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
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2: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1980.DAT.\*  
3: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA1981.DAT.\*  
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24: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA2001B.DAT.\*  
25: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA2002.DAT.\*  
26: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3207	100.0	3207	14	AA051155
2	3202.2	99.9	3498	15	AA057012
3	3008.6	93.8	3412	14	AA051156
4	3008.6	93.8	3424	24	AB159523
5	3008.6	93.8	3424	24	AB151465
6	519.2	16.2	741	21	AA02190
7	448.2	14.0	3213	21	AA06590
8	448.2	14.0	3213	24	ABV78026

9	448.2	14.0	3213	24	AA514366
10	408.8	12.7	412	25	ABX37274
11	336.2	10.5	3387	19	AAV16533
12	336.2	10.5	3688	21	AA131554
13	336.2	10.5	3688	24	ABK84750
14	336.2	10.5	3688	24	AA514363
15	336.2	10.5	5220	19	AAV31340
16	336.2	10.5	5220	20	AAV31340
17	336.2	10.5	5220	21	AA232882
18	323.4	10.1	3525	24	ABK84381
19	297.4	9.3	3733	23	ABU07215
20	288.8	9.0	5162	20	AAV74104
21	288.8	9.0	5162	21	AA286814
22	288.8	9.0	5397	24	AB159522
23	288.8	9.0	5397	24	AB151467
24	285	8.9	4134	17	AAV58545
25	285	8.9	4137	17	AAV58545
26	277.6	8.7	3808	19	AAV04634
27	277.6	8.7	3808	20	AAV74100
28	277.6	8.7	3808	21	AA286813
29	262.6	8.2	4074	22	AA137431
30	262.6	8.2	4074	22	ABK07289
31	262.6	8.2	4074	22	ABK07290
32	262.6	8.2	4074	22	AAK89934
33	262.6	8.2	4074	22	AAK89935
34	262.6	8.2	4074	25	ABX60419
35	233.6	7.3	1074	23	AA573988
36	222.8	6.9	5285	18	AAV80199
37	218.4	6.8	5061	19	AAV42920
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39	198.2	6.2	4491	23	AA571517
40	198.2	6.2	4878	24	ABV59725
41	183	5.7	5990	24	ABK62570
42	173	5.4	4498	23	AA568360
43	173	5.4	4747	22	ABK08693
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45	148.4	4.6	170	24	AB136640

#### ALIGNMENTS

RESULT 1	AA051155	standard; cDNA; 3207 BP.
ID	AA051155	
AC	AA051155	
XX		
DT	25-MAR-2003	(updated)
DT	09-JUN-2003	(updated)
DT	12-APR-1994	(first entry)
XX		
DE	p110 cDNA.	
XX		
KW	Phosphoinositide kinase; PI; p85 subunit; screening; agonist;	
KW	antagonist; cell proliferation; inhibition; prophylaxis; therapy;	
KW	platelets; neutrophil activity; 3-phosphorylated phosphoinositides;	
se.		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..3207
FT		/+tag= a
FT		/note= "PI3- kinase p110"
XX		
PN	W09321328-A1.	
XX		
PD	28-OCT-1993.	
XX		
PF	13-APR-1993.	93WO-GB00761.
XX		
PR	13-APR-1992.	92GB-0008135.

cDNA encoding huma  
Bovine EST associa  
cDNA encoding mamm  
Human phosphatidy  
Human cDNA differe  
cDNA encoding huma  
Human phosphatidy  
cDNA sequence enco  
Human PI 3-kinase  
Human cDNA differe  
Drosophila melanog  
Human G-protein re  
Human p120 regulat  
Human phosphatidy  
cDNA encoding huma  
Human phosphatidy  
Human phosphatidy  
Porcine phospholip  
Porcine G-protein  
Pig p120 regulator  
Human musclookete  
Human pancreatic c  
Human pancreatic c  
Human digestive sy  
Human digestive sy  
cDNA encoding nove  
DNA encoding nove  
phosphatidy inosi  
cDNA encoding a hu  
Androgen-independe  
DNA encoding nove  
Novel human coding  
Rat sequence diffe  
DNA encoding nove  
Human PI3-kinase h  
Human protein enco  
Human colon tumour







QY 1621 TCTGAATCACTGAGCAAGAAAGATTTTCTGTGAGCCACAGACACTATGTGTAAT 1680  
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 QY 1861 AAATATTTAACAATGCAAACTTTCTCAGTACCTAATTCAGCTATGACAGTACTAAA 1920  
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 QY 1921 TATGAACAGTATTTGATTAACCTGCTTGTGAGATTTTAACTCAAAAAGGCTTAAT 1980  
 Db 1921 TATGAACAGTATTTGATTAACCTGCTTGTGAGATTTTAACTCAAAAAGGCTTAAT 1980  
 QY 1981 CAAGAGATCGGTCACTTTTCTTTGGCATTAAATCTGAGATGCAATATAAACAGTT 2040  
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 Db 2041 AGTCAGAGGTTTGGCTGCTTTTGGAGTCTTATTTGCGGTGATGAGGATGTAATCTGA 2100  
 QY 2101 CACCTTAATAGCAAGTTGAGGCTATGGAAGGCTCAATTAAGTCACTGATTTCTCAA 2160  
 Db 2101 CACCTTAATAGCAAGTTGAGGCTATGGAAGGCTCAATTAAGTCACTGATTTCTCAA 2160  
 QY 2161 CAAGAGAGAGATGAAACAAAGAGTAAGATGAAGTTTGTGAGCAAAATGCGG 2220  
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 Db 2581 CAGTGTAAAGAGAGGCTGAAAGGTGCACTGCAATTTAAACGCCACACATCCTCAGTGG 2640  
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Db 2701 TGTGCTGATATTTGTGTGCACTTCAATTTGGAAATGAGATGCTCAATAGTAAT 2760  
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 Db 2821 AAGAGAAAAATTTGGTTTAAACGAGAGCGGTGCTTTGTGTTTGAACAGATTTTC 2880  
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 Db 3121 AACAATATGATATGACACCACTGCTGAGCAACAAATATGATTTGATCTTCAC 3180  
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 Db 3181 ACAATTAGCAGATGCTTTGAATGCA 3207

RESULT 2  
 AA057012  
 ID AA057012 standard; cDNA to mRNA, 3498 BP.  
 XX  
 AC AA057012;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 31-AUG-1994 (first entry)  
 XX  
 DE Pcdins 3-kinase 110 kD catalytic subunit cDNA.  
 XX  
 KW 110 kD catalytic subunit; phosphatidylinositol 3-kinase;  
 KW transformation; Schizosaccharomyces pombe; mtc promoter; choline;  
 KW Pcdins 3-kinase; assay; detection; cell growth; regulation; cancer;  
 KW blood vessel plaques; ss.  
 XX  
 OS Bos taurus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..3207  
 FT /tag= a  
 FT /product= P110  
 XX  
 PN W09403609-A1.  
 XX  
 PD 17-FEB-1994.  
 XX  
 PF 05-AUG-1993; 93WO-GB01651.  
 XX  
 PR 05-AUG-1992; 92GB-0016654.  
 XX  
 PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
 PI Goode NT, Nurse PM, Parker PUJ, Waterfield MD;  
 XX WPI; 1994-065697/08.  
 DR P-PSDB; AAR46294.

XX Eukaryotic cells transformed with mammalian phospholipid or  
 PT protein kinase DNA - useful in assays for compounds involved in  
 PT cell growth regulation and for treating cancers  
 XX  
 PS Disclosure; Fig 1; 71pp; English.

XX This sequence encodes the 110 kD catalytic subunit of the phosphatidy-  
 CC inositol 3-Kinase. This sequence was transformed into  
 CC Schistosomacromyces pombe cells under the regulatory control of the  
 CC nmt promoter in an embodiment of the invention. In the presence of  
 CC thiamine the promoter is inactive and the cells carrying the pIdins  
 CC catalytic subunit plasmid grow as the parental strain. In the absence  
 CC of thiamine the nmt promoter functions and the pIdins 3-kinase  
 CC catalytic subunit is induced. pIdins activity is substantially  
 CC increased under these conditions. Cells containing constructs such as  
 CC this, are useful in assays for detecting compounds involved in cell  
 CC growth regulation. It is also used as the basis for detecting  
 CC compounds for treating cancers and the formation of blood vessel  
 CC plaques.  
 CC (updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX

Sequence 3498 BP; 1148 A; 627 C; 721 G; 1002 T; 0 other;

Query Match 99.9%; Score 3202.2; DB 15; Length 3498;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 3204; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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 Db 61 CTAGTAGAATGTTTACTTACCAATGGATGATAGTACTTAAATGCTTCCTGGAGGCT 120  
 QY 121 ACGTATAAGATGAATGAAGCATGTAATTTAAGACAGAAATACCTCTGCATCAA 180  
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 QY 181 CTTCTTCAGATGATCTTCTTACATTTTGTAAAGTGTACCCAGAAAGCAGAAAGGAA 240  
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 Db 241 GAATTTTGTATGAACAAAGACGACTTGTGACCTTGGCTTTTCAACCTTTTAAAA 300  
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 Db 541 ATATATATTAATTTGATTAAGGCAAAATATATAGTGTGATTTGGTAAATGTTTCTCA 600  
 QY 601 AATATATGAACAAAGATATCTGTGAATAATCAACATGACTGTGTGCCAGAAAGATA 660  
 Db 601 AATATATGAACAAAGATATCTGTGAATAATCAACATGACTGTGTGCCAGAAAGATA 660  
 QY 661 ATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATGATCTGAACAACTAAAA 720

Db 661 ATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGCTATGATCTGAACAACTAAAA 720  
 QY 721 CTCTGTGTTTAAATATCAGGCAAGATATTTTAAAGCTGTGTGATGTAATAC 780  
 Db 721 CTCTGTGTTTAAATATCAGGCAAGATATTTTAAAGCTGTGTGATGTAATAC 780  
 QY 781 TTCTGTAATAAATATCTCTGAGTCACTATGATATATGAAGCTGTAAAGCTTGGG 840  
 Db 781 TTCTGTAATAAATATCTCTGAGTCACTATGATATATGAAGCTGTAAAGCTTGGG 840  
 QY 841 AGGATGCCCAATTTGATGCTGATGCTTAAAGAAAGCTCTATTTCTCACTGCCAATGAC 900  
 Db 841 AGGATGCCCAATTTGATGCTGATGCTTAAAGAAAGCTCTATTTCTCACTGCCAATGAC 900  
 QY 901 TGTTTTAAATGCGCATATATTCAGACGATCTCCACAGCTACGCTATATGAATGGA 960  
 Db 901 TGTTTTAAATGCGCATATATTCAGACGATCTCCACAGCTACGCTATATGAATGGA 960  
 QY 961 GAAACATCTACAAATCCCTTGGTTATTAATGATGCACTCAGAAATTAATTTCTTGT 1020  
 Db 961 GAAACATCTACAAATCCCTTGGTTATTAATGATGCACTCAGAAATTAATTTCTTGT 1020  
 QY 1021 GCAACCTATGTAATGTAATATTTGAGACATTTGACAGATTTATGTTGCAACAGTATC 1080  
 Db 1021 GCAACCTATGTAATGTAATATTTGAGACATTTGACAGATTTATGTTGCAACAGTATC 1080  
 QY 1081 TACCATGAGAGAACCTTATATGATATATGTAACATCTCAAGAGTACTTGTCCAAT 1140  
 Db 1081 TACCATGAGAGAACCTTATATGATATATGTAACATCTCAAGAGTACTTGTCCAAT 1140  
 QY 1141 CCCAGGTGAATGAATGGGCTGAATTAAGATATATTAATTCCTGATCTCTGCTGCT 1200  
 Db 1141 CCCAGGTGAATGAATGGGCTGAATTAAGATATATTAATTCCTGATCTCTGCTGCT 1200  
 QY 1201 CGACTTTCCTTCAATTTGTTCTGTTAAAGCCGAAAGGCTCTAAAGAGAACCTGT 1260  
 Db 1201 CGACTTTCCTTCAATTTGTTCTGTTAAAGCCGAAAGGCTCTAAAGAGAACCTGT 1260  
 QY 1261 CCAATGGCTCTGGGAAATATAACTTGTGATTAACACATCTAGTATCTGAAAA 1320  
 Db 1261 CCAATGGCTCTGGGAAATATAACTTGTGATTAACACATCTAGTATCTGAAAA 1320  
 QY 1321 ATGGCTTTGAATCTTGGCCAGTACCTCATGACTGAAGATTTGCTGAACCTTATGGT 1380  
 Db 1321 ATGGCTTTGAATCTTGGCCAGTACCTCATGACTGAAGATTTGCTGAACCTTATGGT 1380  
 QY 1381 GTTACTGATCAATCCAAATTAAGAACTCAATGTTAGAGTTGAGTCTGGTTC 1440  
 Db 1381 GTTACTGATCAATCCAAATTAAGAACTCAATGTTAGAGTTGAGTCTGGTTC 1440  
 QY 1441 AGCAGTGTGTAAGATTTCCAGATATGCTGATTTGAAAGACATGCTCAATTTGGTCTGTA 1500  
 Db 1441 AGCAGTGTGTAAGATTTCCAGATATGCTGATTTGAAAGACATGCTCAATTTGGTCTGTA 1500  
 QY 1501 TCCCGTGAACAGAGATTTAGTTATTCCTCATGACGAGCTGATTAACAGACTAGTAGAC 1560  
 Db 1501 TCCCGTGAACAGAGATTTAGTTATTCCTCATGACGAGCTGATTAACAGACTAGTAGAC 1560  
 QY 1561 AATGAATTAAGAAAAATGATTAAGAAACAGCTCCAGCAATTTGTACAGAGATCTCTTA 1620  
 Db 1561 AATGAATTAAGAAAAATGATTAAGAAACAGCTCCAGCAATTTGTACAGAGATCTCTTA 1620  
 QY 1621 TCTGAATCACTGACAGAGAAAGATTTTCTGTGAGCCACAGACACTATGTTGTAAT 1680  
 Db 1621 TCTGAATCACTGACAGAGAAAGATTTTCTGTGAGCCACAGACACTATGTTGTAAT 1680  
 QY 1681 ATCCCGAAATTTCAACCAATTTGCTGTGTTAAATGAACTCTTAAGATGAAGTA 1740  
 Db 1681 ATCCCGAAATTTCAACCAATTTGCTGTGTTAAATGAACTCTTAAGATGAAGTA 1740  
 QY 1741 GCTCAGATGTAATGCTTGTGTAAGATTTGGCTTCAATCAAGCTGAACAGGCTATAGAG 1800

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Db      1741 GCTCAGATGTAACGCTTGTTGTAAGAAAGATGGCCCTCCAACTCAACCCCTGAAACGGCTATGAG 1800
QY      1801 CTTTGGAGTCGAATTAACCCAGATCCTATGTTGAGAGTTTTCGTTGCGTCTTAGAA 1860
Db      1801 CTTTGGAGTCGAATTAACCCAGATCCTATGTTGAGAGTTTTCGTTGCGTCTTAGAA 1860
QY      1861 AATATTTAAGATGACAAACCTTTCTCAGTACCTTAATTAAGTATGACAGTACTTAAA 1920
Db      1861 AATATTTAAGATGACAAACCTTTCTCAGTACCTTAATTAAGTATGACAGTACTTAAA 1920
QY      1921 TATGAACAGTATTTGATTAACCTGTTGAGATTTTAACTCAAAAAGGTTAACTAAT 1980
Db      1921 TATGAACAGTATTTGATTAACCTGTTGAGATTTTAACTCAAAAAGGTTAACTAAT 1980
QY      1981 CAAGAGTGGTCACCTTTTCTTTGGCATTTTAAATCTGAGATGACAAATAAAGATT 2040
Db      1981 CAAGAGTGGTCACCTTTTCTTTGGCATTTTAAATCTGAGATGACAAATAAAGATT 2040
QY      2041 AGTCAGAGTTTGGCTGCTTTGGAGTCTATATGCGTCATGTGGAGATGTAATCTGAAG 2100
Db      2041 AGTCAGAGTTTGGCTGCTTTGGAGTCTATATGCGTCATGTGGAGATGTAATCTGAAG 2100
QY      2101 CACCTTAATAGGCAAGTTGAGGCTATGAAAAGCTAATTAAGTGAAGTCAATCTCAAA 2160
Db      2101 CACCTTAATAGGCAAGTTGAGGCTATGAAAAGCTAATTAAGTGAAGTCAATCTCAAA 2160
QY      2161 CAAGAGAGAGAGATGAAAACAAAGAGTACAGATAGTTTAACTGAGCAATGCGG 2220
Db      2161 CAAGAGAGAGAGATGAAAACAAAGAGTACAGATAGTTTAACTGAGCAATGCGG 2220
QY      2221 CGACCAAGATTTTATGATGCTCTCCAGGGCTTTCTGCTCTCTTAAACCTGCTCAG 2280
Db      2221 CGACCAAGATTTTATGATGCTCTCCAGGGCTTTCTGCTCTCTTAAACCTGCTCAG 2280
QY      2281 CTGGGAAATCTCAGGCTTGAAGAGTGTGCAATTAATGCTCTTCCGAAAAGGCGACG 2340
Db      2281 CTGGGAAATCTCAGGCTTGAAGAGTGTGCAATTAATGCTCTTCCGAAAAGGCGACG 2340
QY      2341 TTGAATTGGGAGACCCAGACATCATATGTCAGATTAATCTTTTCAAGAACATAGATCATC 2400
Db      2341 TTGAATTGGGAGACCCAGACATCATATGTCAGATTAATCTTTTCAAGAACATAGATCATC 2400
QY      2401 TTTAAAAATGGGAGATTTACGCGAAGATATGCTAACCTTCAAGTATTTGCAATTATG 2460
Db      2401 TTTAAAAATGGGAGATTTACGCGAAGATATGCTAACCTTCAAGTATTTGCAATTATG 2460
QY      2461 GAAAAATATGCGCAAAATCAAGGCTCTTGAATCTTCAAGCACTTCACTCATCACTGAG 2520
Db      2461 GAAAAATATGCGCAAAATCAAGGCTCTTGAATCTTCAAGCACTTCACTCATCACTGAG 2520
QY      2521 ATCGGTGACTGTGTGGGACTTATCGAGGTGTGAGAAATTTCCACACTATTAATGAGATT 2580
Db      2521 ATCGGTGACTGTGTGGGACTTATCGAGGTGTGAGAAATTTCCACACTATTAATGAGATT 2580
QY      2581 CAGTGTAAAGAGGCTCTGAAGGTCACAGTTTAAACAGCACACACTCCATCAGTGG 2640
Db      2581 CAGTGTAAAGAGGCTCTGAAGGTCACAGTTTAAACAGCACACACTCCATCAGTGG 2640
QY      2641 CTCAAGACAAGAAACAAGGGGAAATATATGATGCGGCGCATGATTTGTTTACAGATCA 2700
Db      2641 CTCAAGACAAGAAACAAGGGGAAATATATGATGCGGCGCATGATTTGTTTACAGATCA 2700
QY      2701 TGTGCTGATATTTGTGTGCCACTTCAATTTTGGGAATTTGAGATGTCACAATGTAT 2760
Db      2701 TGTGCTGATATTTGTGTGCCACTTCAATTTTGGGAATTTGAGATGTCACAATGTAT 2760
QY      2761 ATCATGTGTTAAAGATGACAACTGTTTCAATATGATTTTGAACACTTTTGGATCAC 2820
Db      2761 ATCATGTGTTAAAGATGACAACTGTTTCAATATGATTTTGAACACTTTTGGATCAC 2820
QY      2821 AAGAAAGAAAAATTTGGTTATTAAGAGAGCGCGCTTGTGTTGACACAAATTTTC 2880
Db      2821 AAGAAAGAAAAATTTGGTTATTAAGAGAGCGCGCTTGTGTTGACACAAATTTTC 2880

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QY      2881 TTAATAGTATTAAGTAAAGAGCCCAAGATGACAAAGACAAAGATTTGAGAGTTT 2940
Db      2881 TTAATAGTATTAAGTAAAGAGCCCAAGATGACAAAGACAAAGATTTGAGAGTTT 2940
QY      2941 CAGGAGATGTGTTACAGGCTTATCTAGTATTTGGCAGCATGCCAATCTTTCATTAAT 3000
Db      2941 CAGGAGATGTGTTACAGGCTTATCTAGTATTTGGCAGCATGCCAATCTTTCATTAAT 3000
QY      3001 CTTTCTCATATAGTGTGGCTGTGGAATGCCAAGCTGCAATCTTTGATGATATGCA 3060
Db      3001 CTTTCTCATATAGTGTGGCTGTGGAATGCCAAGCTGCAATCTTTGATGATATGCA 3060
QY      3061 TACATTGGAAGACCTTACCTTTAGATTAACCTGAGCAAGAGCTTTGGATTTTCATG 3120
Db      3061 TACATTGGAAGACCTTACCTTTAGATTAACCTGAGCAAGAGCTTTGGATTTTCATG 3120
QY      3121 AAACAAATGATGATGACACCATGTGGCTGGACAAACAAATGATTTGATCTTCCAC 3180
Db      3121 AAACAAATGATGATGACACCATGTGGCTGGACAAACAAATGATTTGATCTTCCAC 3180
QY      3181 ACAATTAAGCAGCATGCTTTGAACCTGA 3207
Db      3181 ACAATTAAGCAGCATGCTTTGAACCTGA 3207

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RESULT 3
AA051156
ID AA051156 standard; cDNA; 3412 BP.
XX
XX AA051156;
AC
XX
XX 25-MAR-2003 (updated)
DT 12-APR-1994 (first entry)
XX
XX Human p110 cDNA.
DE
XX
KW Phosphoinositide kinase; PI; p85 subunit; screening; agonist;
KW antiproliferative; cell proliferation; inhibition; prophylaxis; therapy;
KW platelets; neutrophil activity; 3-phosphorylated phosphoinositides;
KW de.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..3207
FT CDS /*tag= a
FT /note= "PI3- kinase p110"
XX
XX W09321328-A1.
PN
XX
XX 28-OCT-1993.
PD
XX
XX 13-APR-1993; 93WO-GB00761.
PF
XX
XX 13-APR-1992; 92GB-0008135.
PR
XX
XX (LUDM-) LUDMIG INST CANCER RES.
PA
XX
XX Hiles ID, Fry MJ, Dhand R, Waterfield MD, Parker PJ, Otsu M;
PI Panayotou G, Volinia S, Gout I;
XX
XX WPI. 1993-351736/44.
DR P-PSDB; ABR43342.
XX
XX Recombinant polypeptide(s) - with phosphoinositide-3 kinase
PT activity, useful for controlling cell proliferation
XX
XX Claim 7; Fig 16; 146pp; English.
XX
XX Southern blot analysis was performed using a bovine cDNA probe contg.
CC a fragment of a PI3-kinase-encoding sequence and human cDNA isolated
CC from a cDNA library constructed from mRNA isolated from the human

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QY	1	ATGGCTCCAAAGCCATCATCGAGTGAACCTGGGCGCATCCCATGTAATGCCCAAGATC	60
Db	1	ATGGCTCCAAAGCCATCATCGAGTGAACCTGGGCGCATCCCATGTAATGCCCAAGATC	60
QY	61	CTAGTAGAATGTTTACTACCAATGGAGTGAATGACTTTAGAAATGCCCTCCGAGGGCT	120
Db	61	CTAGTAGAATGTTTACTACCAATGGAGTGAATGACTTTAGAAATGCCCTCCGAGGGCT	120
QY	121	ACGTTAATTAACGATAAAGCATGAATCTATTTTAAAGAAAGCAATAAAATACCCCTCCATCAA	180
Db	121	ACGTTAATTAACGATAAAGCATGAATCTATTTTAAAGAAAGCAATAAAATACCCCTCCATCAA	180
QY	181	CTTCTTCAAGATGAATCTCTTCAACATTTTCGTAGTGTTACCAAGAAAGCAAGAAAGGAA	240
Db	181	CTTCTTCAAGATGAATCTCTTCAACATTTTCGTAGTGTTACCAAGAAAGCAAGAAAGGAA	240
QY	241	GAAATTTTGGATGAACAGAGCAAGCTTTGTGACTTCCTGGCTTTTCAACCCCTTTTAA	300
Db	241	GAAATTTTGGATGAACAGAGCAAGCTTTGTGACTTCCTGGCTTTTCAACCCCTTTTAA	300
QY	301	GTAATTGAACCAAGTAGGCAACCGTGAAGAAAGATCTCAATCGAATAATGGTTTGTCT	360
Db	301	GTAATTGAACCAAGTAGGCAACCGTGAAGAAAGATCTCAATCGAATAATGGTTTGTCT	360
QY	361	ATCGGCATGCCAGTGTGTGAATTCGATATGTTTAAAGATCCGAAGTACAGGACTTCGGA	420
Db	361	ATCGGCATGCCAGTGTGTGAATTCGATATGTTTAAAGATCCGAAGTACAGGACTTCGGA	420
QY	421	AGAAATATTCCTCAATGTTTGTAAAGAAAGCTGTGCATCTTAGGGATCTTAATTCACCTCAT	480
Db	421	AGAAATATTCCTCAATGTTTGTAAAGAAAGCTGTGCATCTTAGGGATCTTAATTCACCTCAT	480
QY	481	AGTAGAGCAATGTATGTTTATTCCTCCAAATGTGAATCTTCACAGAACTGCCAAAGCAC	540
Db	481	AGTAGAGCAATGTATGTTTATTCCTCCAAATGTGAATCTTCACAGAACTGCCAAAGCAC	540
QY	541	ATATATTAATAATGGATGAATGAAGGCAATAATAGTGTGATTTGGTATATAGTTTCTCCA	600
Db	541	ATATATTAATAATGGATGAATGAAGGCAATAATAGTGTGATTTGGTATATAGTTTCTCCA	600
QY	601	AATAATGCAAAACAGAACTATCTGTGAATAACAACATGACTGTGTGCCAGAAACAAGTA	660
Db	601	AATAATGCAAAACAGAACTATCTGTGAATAACAACATGACTGTGTGCCAGAAACAAGTA	660
QY	661	ATTGCTGAAGCAATCAGAAAAAACTGCAAGTATGTTGCTATCATCTGAAACAATTAAAA	720
Db	661	ATTGCTGAAGCAATCAGAAAAAACTGCAAGTATGTTGCTATCATCTGAAACAATTAAAA	720
QY	721	CTCTGTGTTTAGAATATCAGGGCAAGTATTTTAAAGGTGTGATGATGATATAC	780
Db	721	CTCTGTGTTTAGAATATCAGGGCAAGTATTTTAAAGGTGTGATGATGATATAC	780
QY	781	TTTCCTAGAAAAATATCTCTGTGATCAAGTATATATTAAGAAAGCTGTATATATCTTGGG	840
Db	781	TTTCCTAGAAAAATATCTCTGTGATCAAGTATATATTAAGAAAGCTGTATATATCTTGGG	840

Db 781 TTCCAGAAAAATATCTCTGAGTCAGTATAGTATATPAGAGCTGTATATGCTGGG 840

Qy 841 AGAGTGGCCAAATTGATGCTGATGCTAAAGAAAGCCTCTATTTCTCAACTGCCAATGAC 900

Db 841 AGGATGCCCAATTTGAAAGTGAATGGCTAAAGAAAGCCTTATTTCTCAACTGCCAATGAC 900

Qy 901 TGTTTTAAATGCGCCATCATATTTCCAGAGCATCTCCACAGCTACGCTAATATPAGTAAATGGG 960

Db 901 TGTTTTAAATGCGCCATCATATTTCCAGAGCATCTCCACAGCTACGCTAATATPAGTAAATGGG 960

Qy 961 GAAACATCTACAAAATCCCTTTGGGTTATPAAATAGAGCTCAGAAATPAAAATTTCTTGT 1020

Db 961 GAAACATCTACAAAATCCCTTTGGGTTATPAAATAGAGCTCAGAAATPAAAATTTCTTGT 1020

Qy 1021 GGAACCTATGTAATGTAATATTTCCAGACATTTGACAAATTTATGTTCGACAGATATC 1080

Db 1021 GGAACCTATGTAATGTAATATTTCCAGACATTTGACAAATTTATGTTCGACAGATATC 1080

Qy 1081 TACCATGAGAGAAACCTTATGTGTATATGTGAACATCTCAAGAGTACCTTGTCCAAAT 1140

Db 1081 TACCATGAGAGAAACCTTATGTGTATATGTGAACATCTCAAGAGTACCTTGTCCAAAT 1140

Qy 1141 CCCAGGTGGAATGAATGGCTGAATTAACGATATATPACATTTCTCTCGTCTGCT 1200

Db 1141 CCCAGGTGGAATGAATGGCTGAATTAACGATATATPACATTTCTCTCGTCTGCT 1200

Qy 1201 CGACTTTGCTTTCAATTTGTTCTGTATTAAGGCGAAAGGGTGTCTAAGAGAAACATGT 1260

Db 1201 CGACTTTGCTTTCAATTTGTTCTGTATTAAGGCGAAAGGGTGTCTAAGAGAAACATGT 1260

Qy 1261 CCATTTGGCTGGGAAATATPAACTTGTGATTTACACAGATACTCTAGTATCTGGAAAA 1320

Db 1261 CCATTTGGCATGGGAAATATPAACTTGTGATTTACACAGACACTCTAGTATCTGGAAAA 1320

Qy 1321 ATGGCTTTGAATCTTTGGCCAGTACCTCAATGAGCTAGAGAAATTTGCTGAAACCTTATGGT 1380

Db 1321 ATGGCTTTGAATCTTTGGCCAGTACCTCAATGAGCTAGAGAAATTTGCTGAAACCTTATGGT 1380

Qy 1381 GTTACTGGATCAATCCAAATPAAAGAAATCCATGTTTGAAGTTGAGTTGACTGTGTTTC 1440

Db 1381 GTTACTGGATCAATCCAAATPAAAGAAATCCATGTTTGAAGTTGAGTTGACTGTGTTTC 1440

Qy 1441 AGCAGTGTGTAAAGTTTCCAGATATGTCAAGTATGTAAGAGCANTGCCAATTTGGTCTGTA 1500

Db 1441 AGCAGTGTGTAAAGTTTCCAGATATGTCAAGTATGTAAGAGCANTGCCAATTTGGTCTGTA 1500

Qy 1501 TCCCGTGAAGCAGATTTAGTTATTTCCCATGAGAGACTGAGTAPACAGACTAGCTAGAGAC 1560

Db 1501 TCCCGTGAAGCAGGATTTAGCTATTTCCCATGAGAGACTGAGTAPACAGACTAGCTAGAGAC 1560

Qy 1561 AATGAATTTAAGAGAAATGATTAAGAAACAGCTCCGAGCAATTTGTACACGAGATCCTCTA 1620

Db 1561 AATGAATTTAAGAGAAATGATTAAGAAACAGCTCCGAGCAATTTGTACACGAGATCCTCTC 1620

Qy 1621 TCTGAATCACTGAGCCAGAGAAAGATTTTCTGTGTGAGGCCACAGACATTTGTGTACT 1680

Db 1621 TCTGAATCACTGAGCCAGAGAAAGATTTTCTGTGTGAGGCCACAGACATTTGTGTACT 1680

Qy 1681 ATCCCCGAAATTTCTACCCCAAATTTGCTTGTGTGTTAAATGAACTCTAGAGATGAAGTA 1740

Db 1681 ATCCCCGAAATTTCTACCCCAAATTTGCTTGTGTGTTAAATGAACTCTAGAGATGAAGTA 1740

Qy 1741 GGTCAATGATCACTGTTGTAAAGAAATTTGGCTCCATCAATCAAGCTGAAACAGGCTATGGAG 1800

Db 1741 GGTCAATGATCACTGTTGTAAAGAAATTTGGCTCCATCAATCAAGCTGAAACAGGCTATGGAG 1800

Qy 1801 CTTCGTGACTGCAATTAACCCAGATCCTATGTCTGAGGTTTCTGTGCTGGTCTTGAAG 1860

Db 1801 CTTCGTGACTGCAATTAACCCAGATCCTATGTCTGAGGTTTCTGTGCTGGTCTTGAAG 1860

Qy 1861 AAATATTTAACAATGACAAATTTCTCACTACCTAATTCAGCTAGTACAGGTACTAAA 1920

Db 1861 AAATATTTAACAATGACAAATTTCTCACTACCTAATTCAGCTAGTACAGGTACTAAA 1920

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Db      1861 AATATTTAACAAGATGACAAACTTCTCAGTATTTAATTCAGTACTAGTACAGTCTCTAAAA 1920
Qy      1921 TATGAACAGTATTTGGATAAACCCTGTTGTGAGATTTTAACTCAAAAAAGCGTTAACTAAT 1980
Db      1921 TATGAACAGTATTTGGATAAACCCTGTTGTGAGATTTTAACTCAAAAAAGCGTTAACTAAT 1980
Qy      1981 CAAAGATGTGTACCTTTTCTTTGGCATTTTAAATCTGAGATGCAATAAACAGTT 2040
Db      1981 CAAAGATGTGTACCTTTTCTTTGGCATTTTAAATCTGAGATGCAATAAACAGTT 2040
Qy      2041 ACTCAGAGTTGGCGCTTTTGGAGTCTATTCGCGTCGATGGGATGTAATCGAAG 2100
Db      2041 ACCCAGAGTTGGCGCTTTTGGAGTCTATTCGCGTCGATGGGATGTAATCGAAG 2100
Qy      2101 CACCTTAATAGGCAAGTTGAGGCTATGAAAGGCTATTAACTTGACTGACATCTCAAA 2160
Db      2101 CACCTTAATAGGCAAGTTGAGGCTATGAAAGGCTATTAACTTGACTGACATCTCAAA 2160
Qy      2161 CAAAGAGAGAGATGAAAACAAAAAGTACAGATGAAGTTTAACTTGAGCAAAATGCGG 2220
Db      2161 CAGGAGAGAGAGATGAAAACAAAAAGTACAGATGAAGTTTAACTTGAGCAAAATGAGG 2220
Qy      2221 CGACGAGATTTGATGAGTCTCTCCAGGGCTTCTCTCTCTAAACCTGCTCATCG 2280
Db      2221 CGACGAGATTTGATGAGTCTCTCCAGGGCTTCTCTCTCTAAACCTGCTCATCA 2280
Qy      2281 CTGGGAAATCTCAGGCTTGAAGAGTGTCCGATTTATGCTTTCGCAAAAAAGGCGACGTGG 2340
Db      2281 CTAGGAAACCTCAGGCTTGAAGAGTGTCCGATTTATGCTTTCGCAAAAAAGGCGACGTGG 2340
Qy      2341 TTGAATTTGGAGAACCCGACATCATGTGAGATTAATCTTTTCAAGAACATAGATCATC 2400
Db      2341 TTGAATTTGGAGAACCCGACATCATGTGAGATTAATCTTTTCAAGAACATAGATCATC 2400
Qy      2401 TTTAAAAATGGGAGATTTTACGGCAAGTATGCGCAAAATTAATTTGATTTAAG 2460
Db      2401 TTTAAAAATGGGAGATTTTACGGCAAGTATGCGCAAAATTAATTTGATTTAAG 2460
Qy      2461 GAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAAATGTTACCTTATGAGTGTGTA 2520
Db      2461 GAAAAATATCTGGCAAAATCAAGGTCTTGATCTTCGAAATGTTACCTTATGAGTGTGTA 2520
Qy      2521 ATCGGTGACTGTGGGACTTATCGAGTGTGAGAAATTTCTACACTATAATGAGAT 2580
Db      2521 ATCGGTGACTGTGGGACTTATCGAGTGTGAGAAATTTCTACACTATAATGAGAT 2580
Qy      2581 CAGTGTAAAGAGGCGCTGAAAGTGTGACAGTTTAAAGCCACACACTCATAGTGG 2640
Db      2581 CAGTGTAAAGAGGCGCTGAAAGTGTGACAGTTTAAAGCCACACACTCATAGTGG 2640
Qy      2641 CTCAAGACAAAGAACAGGGGGAATATATGATGCGGCGCATGATTTGTTTACAGATCA 2700
Db      2641 CTCAAGACAAAGAACAGGGGGAATATATGATGCGGCGCATGATTTGTTTACAGATCA 2700
Qy      2701 TGTGCTGATATTTGTGTCACCTTCAATTTTGGAAATTTGAGATGTCACAAATAGTAT 2760
Db      2701 TGTGCTGATATTTGTGTCACCTTCAATTTTGGAAATTTGAGATGTCACAAATAGTAT 2760
Qy      2761 ATCATGTGTTAAGATGAGACAACTGTTTCAATATGATTTTGGACACTTTTGGATAC 2820
Db      2761 ATCATGTGTTAAGATGAGACAACTGTTTCAATATGATTTTGGACACTTTTGGATAC 2820
Qy      2821 AAGAAAGAAAAATTTGTTATTAACGAGAGGCGCGGTTTGTGTTTACCAAAATTTTC 2880
Db      2821 AAGAAAGAAAAATTTGTTATTAACGAGAGGCGCGGTTTGTGTTTACCAAAATTTTC 2880
Qy      2881 TTAATAGTATTAAGTAAAGAGCCCAAGATGCAAAAAGACAAAGAAATTTGAGAGTTT 2940
Db      2881 TTAATAGTATTAAGTAAAGAGCCCAAGATGCAAAAAGACAAAGAAATTTGAGAGTTT 2940
Qy      2941 CAGGAGATGTGTACAAAGCTTATCTAGCTATTTGGCGAGCATGCCAATCTCTCTAAT 3000
Db      2941 CAGGAGATGTGTACAAAGCTTATCTAGCTATTTGGCGAGCATGCCAATCTCTCTAAT 3000

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Qy      3001 CTTTCTCAATGATGTTGGCTCTGGAATGCCAGATGCAATCTTTGATGATATGCA 3060
Db      3001 CTTTCTCAATGATGTTGGCTCTGGAATGCCAGATGCAATCTTTGATGATATGCA 3060
Qy      3061 TACATTGGAAGACCTTACCTTTAGATTAACCTGACAGAGGCTTTGGAGTATTTGATG 3120
Db      3061 TACATTGGAAGACCTTACCTTTAGATTAACCTGACAGAGGCTTTGGAGTATTTGATG 3120
Qy      3121 AAACAAATGAATGATGACACCATGCTGTGACAAACAAATGATTTGATCTTCAC 3180
Db      3121 AAACAAATGAATGATGACACCATGCTGTGACAAACAAATGATTTGATCTTCAC 3180
Qy      3181 ACAATTAAGCAGCATGCTTTGAACTGA 3207
Db      3181 ACAATTAAGCAGCATGCTTTGAACTGA 3207

RESULT 4
ABL59523
ID ABL59523 standard; cDNA, 3424 BP.
XX
AC ABL59523;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human phosphatidylinositol-3-kinase catalytic alpha cDNA SEQ ID NO:23.
XX
KW Human; phosphatidylinositol-3-kinase catalytic alpha; enzyme;
KW tumour; lipid associated gene; lipid metabolism; lipid synthesis;
KW chromosome 3q26.3; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200227028-A1.
PD
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-US30366.
XX
PR 28-SEP-2000; 2000US-0676052.
XX
PA (ATAT-) ATRIRGIN TECHNOLOGIES INC.
XX
PI Skinner MK, Paton JL, Chaudhary J;
XX
DR WPI; 2002-402054/43.
XX
PT Identifying tumor characteristics in a tissue sample taken from a
PT patient, involves determining the copy number or expression level of
PT genes associated with lipid metabolism, synthesis or action
XX
PS Example 1; Page 82-83; 113pp; English.
XX
CC The present invention describes a method for identifying tumour
CC characteristics, comprising measuring a copy number or expression level
CC of at least two genes associated with lipid metabolism, synthesis, or
CC action in cells from a patient tissue sample, and comparing the results
CC with a copy number or expression level of the genes in a normal cell.
CC Also described is an array of nucleic acid polymers immobilised on a
CC solid support, comprising a solid support, at least two different nucleic
CC acid polymers which are each specific for a different gene associated
CC with lipid metabolism, synthesis or action, where each nucleic acid
CC polymer is located at a predetermined position on the solid support, and
CC the array comprises nucleic acid polymers which are specific for less
CC than 100 genes other than the selected genes. The method is useful for
CC determining tumour characteristics in a tissue sample taken from a
CC patient. The present sequence represents a human lipid-associated gene
CC related cDNA sequence, which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 other;

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Db 2113 CACTGATATAGGCAATCGAGGCAATGAAAGCTATTAACTTAATGACATCTTCAAA 2172  
 Qy 2161 CAGAGAGAGAGATGAAACACAAAAGGTAAGATGAGTTTGTAGTGAACAATGCGG 2220  
 Db 2173 CAGGAGAGAGAGATGAAACACAAAAGGTAAGATGAGTTTGTAGTGAACAATGCGG 2232  
 Qy 2221 CGACCGAGATTTTCAATGATGCTCTCCAGGGCTTTCTGTCTCTCTAACCCTGCTATCAG 2280  
 Db 2233 CGACCGAGATTTTCAATGATGATGCTCTCCAGGGCTTTCTGTCTCTCTAACCCTGCTATCAG 2292  
 Qy 2281 CTGGGAAATCTCAGGCTTAAAGAGTGCATTAATATCTCTTCCAAAAGGCCACTGTGG 2340  
 Db 2293 CTAGGAAACCTCAGGCTTAAAGAGTGCATTAATATCTCTTCCAAAAGGCCACTGTGG 2352  
 Qy 2341 TTGAATTGGAGAACCCAGACATCATGTGAGATTACTCTTCCAGAACATGAGATCATC 2400  
 Db 2353 TTGAATTGGAGAACCCAGACATCATGTGAGATTACTCTTCCAGAACATGAGATCATC 2412  
 Qy 2401 TTTAAAAATGGGAGATTTTACGGCAAGATATGCTAACCCCTTCAGATTATTCGCATTATG 2460  
 Db 2413 TTTAAAAATGGGAGATTTTACGGCAAGATATGCTAACCCCTTCAGATTATTCGCATTATG 2472  
 Qy 2461 GAAAAATATCGCAAAATCAAGTCTTGAATCTTCCAAATGTTACCTATGAGATGCTGTGA 2520  
 Db 2473 GAAAAATATCGCAAAATCAAGTCTTGAATCTTCCAAATGTTACCTATGAGATGCTGTGA 2532  
 Qy 2521 ATCGGTGACTGTGTGGGACTTATCGAGTGTGAGAAATTTCCACACTATAATGAGATTT 2580  
 Db 2533 ATCGGTGACTGTGTGGGACTTATGAGTGTGAGAAATTTCCACACTATAATGAGATTT 2592  
 Qy 2581 CAGTGTAAAGAGGCCCTGAAAGGTGACTGAGTTTAAACAGCACACACTCCATCAGTGG 2640  
 Db 2593 CAGTGTAAAGAGGCCCTGAAAGGTGACTGAGTTTAAACAGCACACACTCCATCAGTGG 2652  
 Qy 2641 CTCAAAGACAAGAGAGGAGGAAATATATGATGCGGCGCATGATTTGTTTACAGATCA 2700  
 Db 2653 CTCAAAGACAAGAGAGGAGGAAATATATGATGCGGCGCATGATTTGTTTACAGATCA 2712  
 Qy 2701 TGTGTGATATTTGTGTGTCACCTTCAATTTTGGGAATGAGATCGTACAAATGATAT 2760  
 Db 2713 TGTGTGATATTTGTGTGTCACCTTCAATTTTGGGAATGAGATCGTACAAATGATAT 2772  
 Qy 2761 ATCATGTGTTAAAGATGAGACAACTGTTTCAATATAGATTTTGGACACTTTTGGATCAC 2820  
 Db 2773 ATCATGTGTTAAAGATGAGACAACTGTTTCAATATAGATTTTGGACACTTTTGGATCAC 2832  
 Qy 2821 AAGAAGAAAAATTTGTTTATTAACGAGAGCGCGTGGCTTTGTTTGAACACAGATTTT 2880  
 Db 2833 AAGAAGAAAAATTTGTTTATTAACGAGAGCGCGTGGCTTTGTTTGAACACAGATTTT 2892  
 Qy 2881 TTAATAGTATTAAGTAAGAGAGCCCAAGATGCAAAAAGACAGAAATTTGAGAGGTTT 2940  
 Db 2893 TTAATAGTATTAAGTAAGAGAGCCCAAGATGCAAAAAGACAGAAATTTGAGAGGTTT 2952  
 Qy 2941 CAGGAGATGTGTTTACAGGCTTATCTATCTATTCGAGACATGCCATCTCTTCAATAAT 3000  
 Db 2953 CAGGAGATGTGTTTACAGGCTTATCTATCTATTCGAGACATGCCATCTCTTCAATAAT 3012  
 Qy 3001 CTTTTTCTAAATGATGCTGGCTCTGGAATGCCAGAACTGCAATCTTTTGAATGATTTGCA 3060  
 Db 3013 CTTTTTCTAAATGATGCTGGCTCTGGAATGCCAGAACTGCAATCTTTTGAATGATTTGCA 3072  
 Qy 3061 TACATTCGAAAGACCCCTAGCTTTAGATAAACTGGAAGAGGCTTGGAGATTTGATG 3120  
 Db 3073 TACATTCGAAAGACCCCTAGCTTTAGATAAACTGGAAGAGGCTTGGAGATTTGATG 3132  
 Qy 3121 AAACAAATGAATGATGCAACCATGCTGTGCAACAACAAATGATGATCTTCCAC 3180  
 Db 3133 AAACAAATGAATGATGCAACCATGCTGTGCAACAACAAATGATGATCTTCCAC 3192  
 Qy 3181 ACAATTAAGCAGCATGCTTTGAATGCA 3207  
 Db 3193 ACAATTAAGCAGCATGCAATGCAATGCA 3219

RESULT 5  
 AAS14365  
 ID AAS14365 standard; cDNA; 3424 BP.  
 XX  
 AC AAS14365;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE cDNA encoding human p110alpha isoform of PI3-kinase.  
 XX  
 KW Human; phosphatidylinositol 3-kinase; PI3K; p110alpha isoform;  
 KW Lasp-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;  
 KW autoimmune disease; inflammatory bowel disease; bacterial pneumonia;  
 KW Type I diabetes mellitus; cytostatic; immunosuppressive; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 13..3219  
 FT /tag=a  
 FT /product="p110alpha isoform of PI3-kinase"  
 PN WO200185986-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 10-MAY-2001; 2001WO-US15065.  
 XX  
 PR 10-MAY-2000; 2000US-203346P.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX  
 PI Sadhu C;  
 XX  
 WP1; 2002-075252/10.  
 DR P-PSDB; AAU09687.  
 XX  
 PT Identifying a modulator of p110delta polypeptide binding to SH3  
 PT domain-containing polypeptides e.g. Lasp-1, comprising allowing the  
 PT binding partners to interact in the presence and absence of a test  
 PT compound  
 XX  
 PS Example 1; Page 55-60; 85dp; English.  
 XX  
 CC The present invention relates to identifying a modulator of the  
 CC phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to  
 CC the catalytic subunit via a SH3 domain-containing polypeptide such as  
 CC Lasp-1. Also described are methods of assaying the specific binding  
 CC affinity of the PI3-kinase binding partner. Such modulators are useful  
 CC for the treatment of diseases characterised by the undesirable or  
 CC excessive activity of PI3Kdelta. For example the modulators can be used  
 CC for inhibiting the growth or proliferation of cancer cells  
 CC (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,  
 CC Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid  
 CC arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),  
 CC autoimmune diseases (e.g. systemic lupus erythematosus), inflammatory  
 CC bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory  
 CC dermatoses (e.g. contact dermatitis), central or peripheral nervous  
 CC system inflammatory disorders (e.g. meningitis), bacterial pneumonia,  
 CC and Type I diabetes mellitus. The present sequence encodes for human  
 CC p110alpha isoform of PI3K.  
 XX  
 SQ Sequence 3424 BP; 1134 A; 618 C; 709 G; 963 T; 0 other;  
 Query Match 93.8%; Score 3008.6; DB 24; Length 3424;  
 Best Local Similarity 96.1%; Pred. No. 0;  
 Matches 3083; Conservative 0; Mismatches 124; Indels 0; Gaps 0;  
 Qy 1 ATGCTCCAGAACCATCATCATGAGTGAACCTGTGGGCAATCATTGATGATCCCCCAAGATC 60  
 Db 13 ATGCTCCAGAACCATCATCATGAGTGAACCTGTGGGCAATCATTGATGATCCCCCAAGATC 72







Db 2233 CGACCGAATTTTCATGAGATGCCCCCTACAGGGCTTGCTGTCCTCTTAACCCCTGCTCATCAA 2292  
QY 2281 CTGGGAATCTCAGGCTTGAAGAGTGTGCAATTTATGTCCTTCGCAAAAAGGCCACTGTGG 2340  
Db 2293 CTAGGAACCTCAGGCTTAAAGAGTGTGCAATTTATGTCCTTCGCAAAAAGGCCACTGTGG 2352  
QY 2341 TTGAATTTGGAGAACCCAGACATCATGTCAAGATTACTCTTCAGAACATGAGATCATC 2400  
Db 2353 TTGAATTTGGAGAACCCAGACATCATGTCAAGATTACTCTTCAGAACATGAGATCATC 2412  
QY 2401 TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACCCCTTCAGATTATTGGCAATTATG 2460  
Db 2413 TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACCCCTTCAGATTATTGGCAATTATG 2472  
QY 2461 GAAATATCTGGCAAAATCAAGGTCTTGATCTTGAATGTTAACCTTATGAGATGCTGTCA 2520  
Db 2473 GAAATATCTGGCAAAATCAAGGTCTTGATCTTGAATGTTAACCTTATGAGATGCTGTCA 2532  
QY 2521 ATCGGTGACTGTGTGGGACTTATCGAGGTGTGAGAAAATTCACACATATATGAGAT 2580  
Db 2533 ATCGGTGACTGTGTGGGACTTATGAGGTGTGAGAAAATTCACACATATATGAGAT 2592  
QY 2581 CAGGTAAAGAGGCTTGAAGAGTGTGACTGCAATTAAACAGCCACACACTCCATCATGTG 2640  
Db 2593 CAGGTAAAGAGGCTTGAAGAGTGTGACTGCAATTAAACAGCCACACACTCATCATGTG 2652  
QY 2641 CTCAAGCAAGAACAGGGGGAAATATATGATGGGCACTGATTTGTTTACACATCA 2700  
Db 2653 CTCAAGCAAGAACAGGGAAATATATGATGAGCACTGATTTGTTTACACATCA 2712  
QY 2701 TGTGCTGATATTTGTGTGCTCCACTTCAATTTGGGAAATTTGAGATTCGACAAATAGTAAT 2760  
Db 2713 TGTGCTGATATTTGTGTGCTCCACTTCAATTTGGGAAATTTGAGATTCGACAAATAGTAAT 2772  
QY 2761 ATCATGTTAAAGATGATGACAACTGTTTCAATATGATTTTGGACACTTTTGGATCAC 2820  
Db 2773 ATCATGTTAAAGATGATGACAACTGTTTCAATATGATTTTGGACACTTTTGGATCAC 2832  
QY 2821 AAGAAGAAAAAATTTGTTTAAACGAGGCGGTGCGCTTGTGTTTGAACCAAGATTTTC 2880  
Db 2833 AAGAAGAAAAAATTTGTTTAAACGAGGCGGTGCGCTTGTGTTTGAACCAAGATTTTC 2892  
QY 2881 TTAATAGTATTAAGTAAGAGCCCAAGAAATGACAAAGACAGAGATTTGAGAGGTTT 2940  
Db 2893 TTAATAGTATTAAGTAAGAGCCCAAGAAATGACAAAGACAGAGATTTGAGAGGTTT 2952  
QY 2941 CAGAGATGTGTTTCAAGGCTTATCTAGCTAATTTGGGAGCATGCGCAATCTCTTCAATAAT 3000  
Db 2953 CAGAGATGTGTTTCAAGGCTTATCTAGCTAATTTGGGAGCATGCGCAATCTCTTCAATAAT 3012  
QY 3001 CTTTTCCTCAATGATGCTGCTGCGGAAATGCGCAAACTGCAATCTTTTGAATGATTTGCA 3060  
Db 3013 CTTTTCCTCAATGATGCTGCTGCGGAAATGCGCAAACTGCAATCTTTTGAATGATTTGCA 3072  
QY 3061 TACATTCGAAAGACCTTAGCTTTAGATTAATACTGAGCAAGAGGCTTTGAGATTTGATG 3120  
Db 3073 TACATTCGAAAGACCTTAGCTTTAGATTAATACTGAGCAAGAGGCTTTGAGATTTGATG 3132  
QY 3121 AAAACAATGAATGATGACACCATGCTGTGCAACAACAAAATGATGGATCTTCCAC 3180  
Db 3133 AAAACAATGAATGATGACACCATGCTGTGCAACAACAAAATGATGGATCTTCCAC 3192  
QY 3181 ACAATTAAGCAGATGCTTTGAACTGA 3207  
Db 3193 ACAATTAAGCAGATGCTTTGAACTGA 3219

RESULT 6  
AAA02190  
ID AAA02190 standard; cDNA; 741 BP.  
XX  
AC AAA02190;

XX 19-MAY-2000 (first entry)  
DT Human colon cancer cell line polynucleotide sequence SEQ ID NO:2181.  
XX  
DE Human; colon cancer; tumour; diagnosis; gene expression product;  
XX probe; detection; cancerous state; metastasis; identification;  
XX breast cancer; oestrogen receptor-positive breast cancer; therapy;  
XX oestrogen receptor-negative breast cancer; lung cancer; ss.  
OS Homo sapiens.  
XX  
XX WO958675-A2.  
XX  
XX 18-NOV-1999.  
XX  
XX 13-MAY-1999; 99WO-US10602.  
XX  
XX 14-MAY-1998; 98US-0085426.  
XX 15-MAY-1998; 98US-0085537.  
XX 15-MAY-1998; 98US-0085636.  
XX 21-OCT-1998; 98US-0105234.  
XX 27-OCT-1998; 98US-0105877.  
XX  
XX (CHIR ) CHIRON CORP.  
XX (HYSE-) HYSEQ INC.  
XX  
XX Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J,  
XX Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;  
XX Larson G, Drmanac R, Cirvenjakov R, Dickson M, Drmanac S, Labat I,  
XX Leshkowitz D, Kita D, Garcia V, Jones LW, Steche-Crain B;  
XX WPI: 2000-126369/11.  
XX  
XX Polynucleotide library used to determine cancerous states of mammalian  
XX cells -  
XX  
XX Claim 1; Page 850; 1097pp; English.  
XX  
XX AAA0010 to AAA02716 represent polynucleotides isolated from cDNA  
XX libraries constructed from human colon cancer cell lines. The present  
XX invention also describes a method of detecting differentially expressed  
XX genes correlated with a cancerous state of a mammalian cell, comprising  
XX detecting at least one differentially expressed gene product in a test  
XX sample derived from a cell suspected of being cancerous, where detection  
XX of the differentially expressed gene product is correlated with a  
XX cancerous state of the cell from which the test sample was derived.  
XX The polynucleotide sequences can be used in a method for detecting  
XX differentially expressed genes correlated with a cancerous state of a  
XX mammalian cell. The polynucleotides can also be used as probes for  
XX detecting and mapping related genes. They can be used in diagnosis and  
XX prognosis of diseases and disorders (e.g. identification of  
XX pre-metastatic or metastatic cancerous states, stages of cancer, or  
XX responsiveness of cancer to therapy). This is particularly for breast  
XX cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-  
XX negative breast cancer, lung cancer, and colon cancer.  
XX  
XX Sequence 741 BP; 221 A; 137 C; 154 G; 208 T; 21 other;  
SQ  
Query Match 16.2%; Score 519.2; DB 21; Length 741;  
Best Local Similarity 89.0%; Pred. No. 6.3e-134;  
Matches 633; Conservative 0; Mismatches 69; Indels 9; Gaps 7;  
QY 2182 CAAAAGTACAGATGAAGTTTATGTTGAGCAATGCGGACACAG-ATTTCATGATGC 2240  
Db 18 CAANAGTACAGATGAAGTTTATGTTGAGCCATGAGGAGACACAAATTTATGATGC 77  
QY 2241 TCTCCAGGGCTTTC-TGTCTCTCTTAAACCTGCTCATAGCTGGGAAATCTAGGCTTG 2299  
Db 78 TCTACAGGGCTTCTTCTCTCTTAACCTGCTCATCACTAGGAAACCTCAGGCTTG 137  
QY 2300 AAGAGTGCATATATGATCTTCTGCAAAAAGGCCACTGTGTTGAATTTGGAGAACCCAG 2359

	138	AAGAGTGTGCAATTATGTCCTCTGCGAAAAGGCCACGTGTGGTTGAATTGGGAAACCAG	197
YY	2360	ACATCATGTCCGAATTACTCTTTTGAGAACAATGAGATCATCTTTAAAAATGGGGATGATT	2419
YY	198	ACATCATGTCCGAGTACTGTTCTTGCAAGAACATGAGATCATCTTTAAAAATGGGGATGATT	257
YY	2420	TACGGCAAGATATGCTTAACCCCTTCAGATTAATTCGATTATGGAAAAATATCTGGCAAAATC	2479
bB	258	TACGGCAAGATATGCTTAACCTTCAAATTAATTCGATTATGGAAAAATATCTGGCAAAATC	317
YY	2480	AAGCTCTTGATCTTGGAAATGTTAAGTTAAGTCTTAAAGTCTCAATCGGTGACTGTGGAGC	2539
Dd	318	AAGCTCTTGATCTTGGAAATGTTAAGTCTTAAAGTCTTCAATCGGTGACTGTGGAGC	377
OY	2540	TTATTCGAGGTGTGGAATAATTCACACTATATATGCAGATTTCAGTGTAAAGAGGCTCTA	2599
Dd	378	TTATTCGAGGTGTGGAATAATTCACACTATATATGCAGAAATTCAGTGTAAAGAGGCTCTA	437
OY	2600	AAGGTSCATCTGCAGTTTAAACGCCACACACTCCATCATGTGGCTCAAGACAAAGAC-AA	2658
Dd	438	AAGGTTC-CTGCAGTTCAACAGCACACACTTAATCATGTGGCTCAAGACAAAGAC-AA	496
OY	2659	GCGGAATATATATGATCGCGGCATCGATTTGTTACA-CGATCATGTGCTGATATTGTCT	2717
Dd	497	GGAGAATATATATGATCGNNCCATTCAGCTGTTTACACCGTTCAATGTGCTGATATTGTGT	556
OY	2718	TGCGACCTTATTTTGG-GAATTGGAGATGCTCAATAGTATATCATGGTTAAAGATG	2776
Dd	557	AGCTACCTTCAATTTTGGCGAATTGGAGATGCTCAATAGTATATCATGGTTAAAGATG	616
OY	2777	ATGCACAACCTGTTTCATATAGATTTTGGACACTTTTGGATCACAGAGAAAAATTTG	2838
Dd	617	ATGCACAACCTGTTTCATATAGATTTTGNACACTTTTGGATCNCAGAAAAATTTT	676
OY	2837	GTTATMAACGAGAGCGCGTG---CCGTTGTTTTGACACAAATTTCTTAA	2884
Dd	677	GGTATMAACGAGAAACNTGTGCCATTTTGTTTGACACNGAATTCCTTA	727
	RESULT 7		
XX	AAC65690		
XX	ID AAC65690 standard; DNA; 3213 BP.		
XX	AAC65690;		
XX	16-FEB-2001 (first entry)		
XX	Human P13 kinase.PI10beta DNA..		
XX	Human: PI3 kinase PI10 beta; antisense inhibition; primer; cytosstatic;		
XX	antiflammatory; antiinfective; ds.		
XX	Homo sapiens.		
OS	US613032-A.		
XX	PN 17-OCT-2000.		
XX	PD 09-SEP-1999; 99US-0392350.		
PF	PR 09-SEP-1999; 99US-0392350.		
XX	(ISIS-) ISIS PHARM INC.		
PA	Monia BP, Cowser LM;		
PI	WPI; 2000-686014/67.		
XX	P-PSDB; AAB11124.		
DR	Antisense compound 8-30 nucleobases in length targeted to a start codon		
XX	of the coding region of human p13 kinase pi10beta, useful for		
PT	inhibiting the expression of the human polynucleotide -		
FT			
XX			

QY 838 GGGAGATGCCCAATTTGATGCT-----GATGCTAAAGAAAGCCCTCTATTTCTCAACTGC 892  
Db 826 AAGGCCCTCCCATTTTATCTTGGAATCTGCAAGATCAAGAAAATGATGAACA 885  
QY 893 CAATGAGCTGTTTACAAATGCCATCATATTTCCAGAGCAATCTCCAGAGCTAGCCCATATA 952  
Db 886 GAAATGATTCCTTAAGAGCTGCCATTAATCGAAATTCATCTAATCTTCCCTTCATTA 945  
QY 953 TGAATGAGAAAATCTACAAAATCCCTTTGGGTTTAAATAGTCAGTCAGAAATATAAAA 1012  
Db 946 CCACCAAGAAAACAGAAATATTTCTCATGTTGGGAAAATACAAACCTTTCCAAATT 1005  
QY 1013 TTCTTTTGCGAACCTATGTAATGTAATTAATTTGAGACATGCAAGATTTATGTTGAA 1072  
Db 1006 GTCTTGTTAAGGGAATTAACCTTAACAGAGGAAAC--TGTAAAGTTCAATGTCAAGG 1063  
QY 1073 CAGGTATCTACATGAGAGAAACCTTATGTGATATATGTGAACACTCAAGAGTACCTT 1132  
Db 1064 CTGGCTTTTTCATGCTAGCTGAGCTCTGTGTAACCATCGTAAGCTCAGAGTATCAG 1123  
QY 1133 GTTCCA--ATCCAGGTGAAATGAATGGCTGAATTAACATATATCATTTCCGATCTTC 1189  
Db 1124 GGAATAATATCATATTTGGAATGAACCACTGGAATTTGATATTAATTTGTGACTTAC 1183  
QY 1190 CTGCTGCTGCTGACTTTCCTTTCATTT-----GTCTGTTAAAGCCGAAAGGCTGC 1244  
Db 1184 CAGAAATGCGCTATATGTTTGTGTTATGACAGTTTGGATAAAGTAAACGAAAGA 1243  
QY 1245 TAAAGGAACCTGTCAT-----TGCCCTGGGGAATATATAAATTGTTTG 1291  
Db 1244 AATCAACGAAACATATTAATCCCTTAATATCAGACCATCAGGAAAGCTGAAAAGTGC 1303  
QY 1292 ATTACACAGATATCTGATATCTGAAAATAGGCTTTGAATCTTTGGCCAGTACCTCATG 1351  
Db 1304 ATTATCTGTAGCGTGGTAATAGATGCTTTTGAATTTAAGAGCAATTTGAGACTG 1363  
QY 1352 GACTGAGAGATTTCTGAAACCTTATGTTGTTGTTGATCTGATCAATCCAAATTAAGAAATC 1411  
Db 1364 GAGACATATATTTACACAGCTGCTTTCATTTCTGATGAACTCGAAGAAATGTTGAATC 1423  
QY 1412 CATGTTTAAAGTTGAGTTGACTGTTGACGAGTGTGTAAAGTTTCCAGATATGTCG 1471  
Db 1424 CAATGGGAACCTGTCCAAACAAATCATATATGMAAATGCCAACGTTTGCATGTTAAAT 1483  
QY 1472 TGAATGAAGAGCATGCAATTTGATCTGATCCCGTGAACAGAGATTTAGTTATCCCATG 1531  
Db 1484 TTCCAGAGAAATAAAAACAACCTTATTTATACCTCCCTTCATTAAGATTTGAAAAG 1543  
QY 1532 CAGGACTGAGTAACAGACTAGCTAGACATGAATTAAGAGAAAATGATAAGAACAGC 1591  
Db 1544 CAGCTGAGATTCAGAGCAGTGAATGCTAATGTCTCAAGTGAAGTGAAGAAAAGTTTC 1603  
QY 1592 TCC-----GAGCAATTTGTACACGATCTCTATCTGAAATCACTGAGCAAGAGA 1642  
Db 1604 TTCTGTATGGAAGAAATCTTGAACAGGATCCCTGTCTCAAGCTGTGTGAAAATGAAA 1663  
QY 1643 AAGATTTCTGTGAGCCACAGAC--ACTATTTGTAACTATCCCGAAATTTCAACCA 1699  
Db 1664 TGGATCTTATTTGACTTTTGCAACAAGACTGCCGAGAGATTTTCCACATATCATGCCAA 1723  
QY 1700 AATTCCTTCTGTCTTAAATGAACTTAAGATGAATAGCTAGATGATCTGCTTGG 1759  
Db 1724 AATTACTGCTGTCAATCAAGTGAATTAACCTTAGAGAGTGTCTCAAGCTTCAGGGGCTGC 1783  
QY 1760 TAAAGATTTGGCTTCAATCAAGCTGAAACAGGCTATGAGCTTCTGGACTGCAATTAC 1819  
Db 1784 TTCAATTTGGCTTAAACCTGCCCGGAGGCTCAGAGCTTCTGGAATTTCAACTATC 1843  
QY 1820 CAGATCTATGCTGAGGTTTGTGCTGCTGCTGAGTAAATATTTAAACAGATGACA 1879  
Db 1844 CAGACAGATGCTTGAAGATATGCTGTAAGCTGCT--GCGACAGATGATGATGAAG 1900  
QY 1880 AACTTTCTCACTAATTTCAAGTAGTACAGTACTAAATATATGAACAGTATTTTGATA 1939

Db 1901 AACTTTCTCAATATCTTTTACAACTGTGCAAGTGTAAATATATAGACCTTTCTTGATTT 1960  
QY 1940 AACTGCTGTGAGATTTTACTCAAAAAAGCGTTAACTATCAAGAGATCGGTCACTTT 1999  
Db 1961 GTGCCCTCTCTAGATTTCTATTAGAAAGGCACTGTGTAATGTGAGAGATAGGGCAGTTTC 2020  
QY 2000 TCTTTTGGCATTTAAATCTGATGACACATTAATAACAGTTAGTCAGAGCTTTGGCCTGC 2059  
Db 2021 TATTTTGGATCTTAGTCAAGATGACATTTCTGCTGTCTCATGATCAATTTGGTGTCA 2080  
QY 2060 TTTTGGAGTCTTATTTGCCGTGATGTGGAGTATCTGAAGCACCTTATAGCAAGTTG 2119  
Db 2081 TCTTGAAGCATACGTCCGGGAGAGTGGGCAATGAAAGTGTCTTTTAAGAGGTTG 2140  
QY 2120 AGGCTATGGAAGAGCTCATTAATCTGACATCTCTCAACAGAAAGAAAGATGAAA 2179  
Db 2141 AGCACTCAATTAAGTTAAACCTTTAAATAGTTATCAAACTGAAATGCCGTAAGTTAA 2200  
QY 2180 CACAAAGGTAAGATGAAGTTTATAGTGAACAATGGCGGACCAAGTTTCATGATG 2239  
Db 2201 ACAGAGCCAAAGGAGAGAGGCCATGATCCTGTTTAAACAGAGTCTTACCGGAAAG 2260  
QY 2240 CTCTCCAGGCTTTCTGTCTCTCTTAACCCCTGCTCATCAGCTGGGAAATCTCAGGCTTG 2299  
Db 2261 CCCTCTGACCTGCAAGTCAACCCCTGMAACCATGTTATCTCTCAAGACTCTATGTTG 2320  
QY 2300 AAGATGTGCAATTAATGCTTTGTGCAAAAAGGCCACTGTGTTGAATGGGAAACCCAG 2359  
Db 2321 AAAAGTGCAATTAATGATATCCAAATGAAGCCCTTTGGCTGTGATATCAATTAACAG 2380  
QY 2360 ACATCATGTCAAGATTAATCTCTTGAACCAATGAGATCATCTTTAAATGGGAGTGAAT 2419  
Db 2381 TATTTGGAGGATTCAGT-----TGAGTGAATTTTAAATAGTGTGAATTT 2428  
QY 2420 TAAGGCAAGATATGCTAAACCTTCAGATTAATGCAATTAAGAAAATCTGGCAAAATC 2479  
Db 2429 TACGACAGATATGTTGAACATCCAAATGTTGCCCTTATGATTTTACTGGAAGAAAG 2488  
QY 2480 AAGCTTGTGATTTGAAATGTTTACTTAATGATGCTGTCAATCGGTGACTGTGGGAC 2539  
Db 2489 CTGATTTGATCTTGGATGATGTTGCTTATGCTGTATGTCGAAACAGAGATGCTCTGCC 2548  
QY 2540 TTATGAGGTGTGGAATTTCTCACTATTAATGACATTAATGAGTAAAGAGGC---C 2596  
Db 2549 TCATTTAAAGTTGTGACCTCTGAAACAAATGCTGACATTAAGTGAACAGTATCAATG 2608  
QY 2597 TGAAGGTGCACTGCACTTTTAAACAGCCACACACTCCATCAGTGCCTCAAGACAGAAACA 2656  
Db 2609 TGGCTGTGACAGACGCTTCAACAAAGATGCTTCTGAACTGGCTTTAAAGAAATCAACT 2668  
QY 2657 AAGGGAAATATATGATTCGGCCATCGATTTGTTTACACGATCATGTCTGTGATTTGTG 2716  
Db 2669 CTGGGATGACCTGGAACCGACAGCATTTAGGAATTTACATCTGCTGTGCTGCTACTGTG 2728  
QY 2717 TTGCACCTTCAATTTGGGAATTTGAGATGCTCAATAGTAATATGTTTAAAGATG 2776  
Db 2729 TAGCTTCTTATGCTCTTGGATGTTGTCACAGACATAGACATCAATGCTCAAAAAAA 2788  
QY 2777 ATGACAACTGTTTCATATATGATTTTGGACACTTTTGGATCACAAGAAAAAATTTG 2836  
Db 2789 CTGGCAGACTCTTCAACATTAATTTGACATATTTCTTGGAAATTTCAAAATCTAAGTTTG 2848  
QY 2837 GTTATTAACGAGAGCGCTGCCGTTGTTTGAACAAGATTTCTTAATAGTATTAATA 2896  
Db 2849 GCATTTAAAGGAGAGAGATGCTTTTATTTTACTATATGATTTATCATCATCATTTCAAC 2908  
QY 2897 AAGAGCCCAAGAAATGACAAAGACAAGAGAAATTTGAGAGTTTCAGAGATGTTTCA 2956  
Db 2909 AAGGAAAAACGG-----AAATACAGAAAGTTTGGCGGTTTCGCGAGTGTGTGAGG 2962  
QY 2957 AAGCTTATCTAGCTATTTGGGAGATGCAATCTCTTCAATAATCTTTTCAATGATGC 3016

Db 2963 ATGCATATCTGATTTTACGACGGCATGGGAATCTTCTTCACTCTCTTTGGCTGATGT 3022  
 OY 3017 TTGGCTCGAATGCGCAGAACTGCATCTTTTATGATATTTGCATPACATTCGAAAGACCC 3076  
 Db 3023 TGACTGCAAGGCTTCTGTAACATCAGATCAGTCAAGATATTAAGATTAAGACTCTC 3082  
 OY 3077 TAGCTTTAGATTAATACTGACAGAGGCTTTGGAGTATTTTCATGAAACAAATGAATGATG 3136  
 Db 3083 TTGCATTTAGGAAAGACTGAAAGAAAGCACTCAACAGTTTAAGCAAAAATTTGATGAGG 3142  
 OY 3137 CACACCATGTGCTGCTGACACAAACAAATGATTTGATCTTCCACACATTTAAGCA 3191  
 Db 3143 CGCTCAGGGAAGAGCTGACTTAAGTGAAGTGAAGTGGCCCAAGAGTTCCGAA 3197  
 RESULT 8  
 ABV78026  
 ID ABV78026 standard; DNA; 3213 BP.  
 XX  
 AC ABV78026;  
 XX  
 DT 12-NOV-2002 (first entry)  
 XX  
 DE Hypoxia-regulated protein coding sequence #46.  
 XX  
 KM Cytostatic; vasoregic; tranquilliser; antiatherosclerotic; gene therapy;  
 KM antiinflammatory; vulnery; gynecological; ophthalmological; vaccine;  
 KM hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;  
 KM ischaemic condition; reperfusion injury; retinopathy; neonatal stress;  
 KM preecclapmia; atherosclerosis; inflammatory condition; wound healing;  
 KM inflammation; erythropoiesis; hair loss; human; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO200246465-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 10-DEC-2001; 2001MO-GB05458.  
 XX  
 PR 08-DEC-2000; 2000GB-0030076.  
 PR 08-FEB-2001; 2001GB-0003156.  
 PR 25-OCT-2001; 2001GB-0025666.  
 XX  
 PA (OXFORD BIOMEDICA UK LTD.  
 PI white J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;  
 PI Rayner WN;  
 XX  
 DR WPI: 2002-627238/67.  
 XX  
 PS Claim 37; Page 363-364; 538pp; English.  
 XX  
 CC The present invention relates to methods for identifying genes and  
 CC proteins that are implicated in a specific disease or physiological  
 CC condition. The method comprises comparing the transcriptome/protome of a  
 CC specialised cell type implicated in a disease or condition with that of a  
 CC second specialised cell type, under two experimental conditions, and  
 CC identifying a gene that is differentially regulated in the two  
 CC specialised cell types under experimental conditions. ABV7873-ABV78116  
 CC and ABP65061-ABP65257 were identified using the methods of the invention.  
 CC The coding sequences and proteins are useful for treating hypoxia-regulated  
 CC patient, for manufacture of a medicament for treating hypoxia-regulated  
 CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,  
 CC pathological response to hypoxia conditions, or hypoxic-associated  
 CC pathology in a patient. The coding sequences and proteins are also useful  
 CC for monitoring the therapeutic treatment of a disease or physiological  
 CC condition, such as cancer, ischaemic conditions, reperfusion injury,

CC retinopathy, neonatal stress, preecclapmia, atherosclerosis, inflammatory  
 CC conditions, wound healing, inflammation, erythropoiesis or hair loss.  
 XX  
 SQ Sequence 3213 BP; 979 A; 612 C; 704 G; 918 T; 0 other;  
 Query Match 14.0%; Score 448.2; DB 24; Length 3213;  
 Best local Similarity 50.1%; Pred. No. 8.3e-114;  
 Matches 1591; Conservative 0; Mismatches 1478; Indels 106; Gaps 15;  
 OY 58 ATCTAGTAGAATGTTTACTACCAATGGATGATGACTTTGAAATGCTCCGTAG 117  
 Db 88 ATACTGTGATTTCTTCTTTGGCCACTGGATTTATTCAGTTGAGATACCTGGGAA 147  
 OY 118 GCTACGTTAATACATAAAGCATGAACTATTTAAGAGCAAGAAATACCTCCAT 177  
 Db 148 GCTACCATTTCTTAATATTAAGAGATGTTATGAAAGCAAGTTACAAATTAACCAATGTT 207  
 OY 178 CAATCTTTCAAGATGAATCTTACATTTTCTTAAGTGTATACCCAGAGCAAGAGG 237  
 Db 208 AACCTCTTAATGATATTTGACTCTATATGTTTGCATGTGTGAATCAGACTGTAAT 267  
 OY 238 GAAGAAATTTTGTAGTAAACAAAGACGCTTGTGACCTTGGCTTTTCAACCTTTTA 297  
 Db 268 GAGAGCTTGAAGATGAACAAAGACGCTGATGTGACGCTTTTCTTCCAGTTCTC 327  
 OY 298 AAGTAATTAAGACCACTAGGCAACCGTGAAAGAAATCCTCAATGAGAAATGTTG 357  
 Db 328 AATTTAGTGCAAGAAAGTTGTGACCCAGGGGAAA--ATTAGATCTCAAAATTTGAGTC 384  
 OY 358 GCTATGGCGATGCGACATGTGTGAATTCGATATGTTTAAAGATCCAGAGTACAGACTTC 417  
 Db 385 CTATAGGAAAGAGCTGTGATGAATTTGATCTTGAAGATCTCGAATTAATGAATTT 444  
 OY 418 CGAAGAAATATTCATATGTTTGTAAAGAGCTGTGATTTAGGATCTTAATCACT 477  
 Db 445 CGAAGAAATATTCGCAAAATTCAGGA-----GGAAAAATCTGTCA 486  
 OY 478 CATATAGACCAATGATATGTTTATCTCCAAATGTAGAAATCTTCCAGCAAGTCCAAAG 537  
 Db 487 CTGTGGGAATTTGCTTGATGATGAGCTGTAAACAAATATCCACAGAGCATGAACCA 546  
 OY 538 CACATATATTAATTAATGATTAAGGCAAAATATAGTGTGATTTGGTAAATGATTTCT 597  
 Db 547 TCCATCCCTGAATCTTAAGAGATTAATTTATGGGGAAGAGCTGATGTTGAT 606  
 OY 598 CCAATATATGACAAACAGAAATATCTGAAAATCAACATGCTGTGTCCAGAACAA 657  
 Db 607 TTGAAAACCTCCAGAGAGTGTAGCTTCAAGTGTCTCTTAATATGAATCTATCAAA 666  
 OY 658 GTAATTTGTAAGCAATGAGAAAAAACTCGAAGTATGTTGATATCATCTGAACAACATA 717  
 Db 667 GTAATTTGATTTGGCAATC---CAAAAAGTTTGAATTTATTCAGGAGAGAAATGAAATT 723  
 OY 718 AAATCTGTGTTTGAATATCAGGCAAGTATATTTAAAGTGTGTGATGATGAA 777  
 Db 724 AGCCCTATG-----ATATGTTTGAAGTCAAGGAGGAGATAGAA 765  
 OY 778 TACTTCCTGAAGAAATATCTCTGAGTCAATTAAGTATTAAGAACTGTATATGCTT 837  
 Db 766 TATGTTTGTGATGATCATCACTAATTCAGTTCCAGTATATCCGAACTGTGTGATGAAC 825  
 OY 838 GGGAGAGTCCCAATTTGATGCT-----GATGCTAAAGAAAGCCTATTTCTCAACTGC 892  
 Db 826 AGAGCCCTCCCATTTTACTTGTGTGATCTGCAAGATCAAGAAATGATATGAACAA 885  
 OY 893 CAATGACCTTTTACAAATGCAATATTTCCAGAGCATCTCAAGCTAGCCATATA 952  
 Db 886 GAATATTTGCAATTAAGGCTGCAATTAATTCGAAATTTCTATTTCTCTTCATTA 945  
 OY 953 TGAATGAGAAACATCTAAGAAATCTTTGGTGTATTAATGATGACTCAGAAATAAAA 1012  
 Db 946 CCACCAAGAAACAGAAATTAATTTCTCATGTTTGGGAAATTAACAACTTTTCAAAATT 1005

QY 1013 TTCTTTGTGCACTTATGCAATGTAAATATTCAGACATTGACAAAGATTATGTCGAA 1072  
DB 1006 GTCTTGTGTTAAGGAATAAATTAACACAGAGGAAAC--TGTAAAGATTCAATGTCAGGG 1063  
QY 1073 CAGGTATCAACATGGAGGAAACCTTATGATATATGTGAACCTCCAAAGATACCTT 1132  
DB 1064 CTGGTCTTTTTCATGTGATGAGCTCCTGTGTAAACCATGTGAAGTCGAGAGTATCAG 1123  
QY 1133 GTTCCA--ATCCAGGTGGAATGAAATGGCTGAATTACGATATATCATCTGATCTTCG 1189  
DB 1124 GGAAAAATGATCATATTTGGAAATGAACCACTGGAATTTGATATTAATTTTGTGACTTAC 1183  
QY 1190 CTGTGCTGTGACCTTTGCTTTCCATTT--GTTCTGTAAAGCCGAAAGGGTGC 1244  
DB 1184 CAGGAATGGCTCATATGTTTGTCTGTATGACGTTTGTGATTAAGTAAACCAAG 1243  
QY 1245 TAAAGAGAACACTGTCCAT-----TGGCCTGGGAAATATATACTTGTTCG 1291  
DB 1244 AATCAACGAAATTAATTAATCCCTTAATATCAGACCATCAGGAAAGCTGAAAGTGC 1303  
QY 1292 ATTACACAGATACCTAGTATCTGAAAAATGGCTTTGAATCTTGGCCAGTACTCATG 1351  
DB 1304 ATTATCTGTAGCGTGGTAAATAGATGCTTTTGACTTTAAAGCAATTGAGAACTG 1363  
QY 1352 GACTAGAGATTTGCTGAACCTTATGTTGTTACTGATCAAAATCCAAATTAAGAACTC 1411  
DB 1364 GAGACATATATATTAACACAGCTGGTCTTCAATTCCTGATGAATCGAAGAAATGTGAATC 1423  
QY 1412 CATGTTTAAGTTGAGTTTGAAGTGTTCAGCAGTGTGTAAGTTTCCAGATATGTGAG 1471  
DB 1424 CAATGGAACTGTTCAACAAATCCATATACGAAATGCAACAGCTTTGCAATGTTAAAT 1483  
QY 1472 TGATTGAAGAGATGCGCAATTTGGTCTGTATCCCGTAGAGAGATTAGTATTTCCATG 1531  
DB 1484 TTCCAGAGAAATAAAAACAACCTTATTAATTAACCTCCCTTCGATGAATTAATGAAAAG 1543  
QY 1532 CAGGACTGATACAGACTAGCTAGACAAATGAATTAAGAGAAATGAATAAGAACAGC 1591  
DB 1544 CAGCTGAGATTCAGACAGATGATAGTCTAATGTGTCAAGTGAAGTGAAGAAATTTTC 1603  
QY 1592 TCC-----GAGCAATTTGTACACAGATCTCTATCTGAATCACTGACCAAGAGA 1642  
DB 1604 TTCTGTATTTGAAAGAAATCTTGGACAGGAGATCCCTGTCTCAACGTGTGAAATGAAGA 1663  
QY 1643 AAGATTTCTGTGAGCCACAGAC--ACTATGTGTAACTATCCCGAAATTTCTACCA 1699  
DB 1664 TGGATCTTATTTGGACTTTGCGACAAAGCTGCCGAGAGATTTTCCCAATATCAGTCCAA 1723  
QY 1700 AATGCTTCTGTCTGTAAATGGAATCTAGAGATGAATAGTCAATGATGATCTGCTTG 1759  
DB 1724 AATTAAGTGTCTCAATCAAGTGAATTAACCTTAGAGATGTTGCTCAGCTTCAAGGCGCTGC 1783  
QY 1760 TAAAGATTTGGCTCCAAATCAAGCTGGAACAGGCTATGAGCTTCTGGAATGCAATTAAC 1819  
DB 1784 TTCAATTTGGCTTAAACCTGCCCCCGGAGAGCCCTAGAGCTTCTGGAATTTCACTATC 1843  
QY 1820 CAGATCTATGTTGAGGTTTGTGCTGTTCCGGTCTTAAGAAAATTTTAACAGATGACA 1879  
DB 1844 CAGACAGACGATCTTGAGAAATATGCTGTAGGCTGCT--GCGACAGATGAGTGAAG 1900  
QY 1880 AACTTTCTAGTACCTTAATTCAGTATGACAGTACTAATAATATGAACAGATTTTGGATA 1939  
DB 1901 AACTTTCTCAATATCTTTTACAACTGTGTCAAGTGTAAATATGAGCTTTTCTTGAT 1960  
QY 1940 AACTGCTGTGAGATTTTACTCAAAAAAGCGTTAACTATCAAAAGATGCGTCACTTTT 1999  
DB 1961 GTGCGCTCTCTAGATTCCTATTAGAAAGCACTTGTGAATCGAGGATAGGCGATTTTC 2020  
QY 2000 TCTTTTGGCATTTAAATCTGAGATGACAAATAAACAGTTAGTCAAGAGTTTGGCGTGC 2059  
DB 2021 TATTTTGGCATTTAGTGAAGTGAACATCTTCTGCTGTCTCAAGTCAATTTTGGTGTCA 2080  
QY 2060 TTTTGAAGTCTTATTTGCGGTGATGTGGATGTATCTGAAGCACTTAATAGCAAGTTG 2119

DB 2081 TCCTTGAAGCATCTCCGGGAAAGTGGGGCAGATGAAGTCTTCTTAAGCAGGTTG 2140  
QY 2120 AGGCTATGAAAAAGCTCATTTAACTTACTGACATTTCTCAACAGAGAAAGAGATGAAA 2179  
DB 2141 AAGCACTCAATAAATTTAAACCTTTAAATATTAATCAAACTGAATGCCGTGAAGTTTA 2200  
QY 2180 CACAAAAGGTACAGATGAAGTTTATGTTGAGCAAAATGGGGGACCAAGATTCATGATG 2239  
DB 2201 ACGAGCCAAAGGAAGAGGCGCATATCCTGTTTAAACAGAGTCTTACCGGAAG 2260  
QY 2240 CTCTCGAGGCTTTCTGTCTCTTAACCTGTCTCATCAGCTGGGAAATCTCAGGCTTG 2299  
DB 2261 CCTCTCTGACCTGACAGTCAACCCCTGAACCAATGTGTATTCCTCAGAACTGTATGTTG 2320  
QY 2300 AAGAGTGTGAATTAATGTTCTTCTGCAAAAAAGCCACTGTGTGTAATGGAGAACCCAG 2359  
DB 2321 AAAAGTGAATAACATGAGATTCGAAATGAAGCTTTGTGGCTGTATCAATTAACAAAG 2380  
QY 2360 ACATCATGTCAATTAATCTTTCAAGAACATGAGATCATCTTTAAAAATGGGATGAT 2419  
DB 2381 TATTTGTGAGATTCAGT-----TGAAGTATTTTAAATAATGGTATGAT 2428  
QY 2420 TACGCGAAGATATGCTAACCTTCAGATTAATTCGATTAAGAAAAATATCTGGCAAAATC 2479  
DB 2429 TACGACAGATATATGTTGACATCCAAATGTGGCTTATGATTAATCTCTGGAAGAAAG 2488  
QY 2480 AAGGCTTATCTTGAATGTTTAACTTATGATGTCTGCAATCGGTGACTGTGGGAC 2539  
DB 2489 CTGTTTGTGATCTTGGATGTTGCTTATGCTTATGCTTATACCAAGAGATTCCTCTGGCC 2548  
QY 2540 TTATCGAGTGTGAGAAATTCACACATTAATGAGATTAGGTAAAGAGGC--C 2596  
DB 2549 TCAITGAATTTGTGACACCTTGAAACATTTGCTGACATTCAGCTGAACAGTACGATG 2608  
QY 2597 TGAAGGTGCACTGAGTTTAAAGCCACACACTCCATCAGTGGCTCAAGACAAAGACA 2656  
DB 2609 TGGCTGTGACAGAGCTTCAACAAAGATGCCCTTCTGAACTGGCTTAAGATTAACAAT 2668  
QY 2657 AAGGGGAATATATATGATGCGGCATGATTTGTTTACACGATCATGTCTGATATTGTG 2716  
DB 2669 CTGGGATGACCTGACCGAGCATTTGAGGAATTAACATGCTGTGTGCTGCTACTGTG 2728  
QY 2717 TTGCCACTTCAATTTTGGAAATGAGATGTGCACAAATAGTAATATCAGTAAAGATG 2776  
DB 2729 TAGCTTCTTATGTCTCTGGATTTGTGACAGACATATGACAAATCATGATGTCAAAAA 2788  
QY 2777 ATGCAACTGTTCATATAGATTTTGGACACTTTTGGATCACAAGAAAGAAAAATTTG 2836  
DB 2789 CTGGCAGCTCTTCCACATGATGCTTTGACATATCTTGGAATTTCAATCTAAGTTG 2848  
QY 2837 GTTATTAACGAGAGCGCGTCCGTTGTTTGAACAAGATTTCTTAATAGTATTAAGTA 2896  
DB 2849 GCATTAAAGGAGAGAGAGCTTTTATTTACTTAAGTATTAATCAATGTCATTAAC 2908  
QY 2897 AAGGAGCCCAAAATGCAAAAGACAAGAAATTTGAGAGGTTTCAGAGATGTGTTACA 2956  
DB 2909 AAGGAAAAACAG-----AATTAACGAAATTTTGGCGGTTGCGCAAGTGTGTGAG 2962  
QY 2957 AAGCTTATCTAGCTATTTGGGACATGCAATCTCTTAATAATCTTTCTCAATGATGC 3016  
DB 2963 AAGCATATCTGATTTTACGAGCGGATGGGAATCTTTATCATCCTCTTTTGGCTGATGT 3022  
QY 3017 TTGGCTCTGGAATGCCAAGCTGCAATCTTTTGAATATGATGATATTCGAAAGACC 3076  
DB 3023 TGACTGACAGGCTTCTCAATCAATCAGTCAAGATATACAGATCTTAAGACTCTC 3082  
QY 3077 TAGCTTATGATTAATCTAGCAAGAGGCTTTGAGATTTTATTAAGAAACAAATGATGATG 3136  
DB 3083 TTGCAATTTAGGAGAGTGAAGAGAGACATCAAAAGATTAAGAAAAATTTGATGAGG 3142  
QY 3137 CACACCATGTGTGCTGACAAACAAAATGATGGATCTTCACACAAATTAAGCA 3191

Db 3143 CGCTCAGGAGGAGCTGACTACTAAAGTGAAGTGGATGGCCACACAGTTGGGAA 3197

RESULT 9

AA514366

ID AA514366 standard; cDNA: 3213 BP.

XX

AC AA514366;

XX

DT 12-MAR-2002 (first entry)

XX

DE cDNA encoding human p110delta isoform of PI3-kinase.

XX

XX Human; phosphatidylinositol 3-kinase; PI3K; p110delta isoform;

KW LAMP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;

KW autoimmune disease; inflammatory bowel disease; bacterial pneumonia;

KW Type I diabetes mellitus; cytostatic; immunosuppressive; ss.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 1..3213

FT /tag= a

FT /product= "p110delta isoform of PI3-kinase"

XX

PN MO200185986-A2.

XX

PD 15-NOV-2001.

XX

PF 10-MAY-2001; 2001WO-US15065.

XX

PR 10-MAY-2000; 2000US-203346P.

XX

XX (ICOS-) ICOS CORP.

PA

PI Sadhu C;

XX

DR WPI: 2002-075252/10.

XX

DR P-PSDB; AAU09688.

XX

PT Identifying a modulator of p110delta polypeptide binding to SH3

PT domain-containing polypeptides e.g. LAMP-1, comprising allowing the

PT binding partners to interact in the presence and absence of a test

PT compound

XX

PS Example 1: Page 63-68; 85pp; English.

XX

XX The present invention relates to identifying a modulator of the

XX phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to

XX the catalytic subunit via a SH3 domain-containing polypeptide such as

XX LAMP-1. Also described are methods of assaying the specific binding

XX affinity of the PI3-kinase binding partner. Such modulators are useful

XX for the treatment of diseases characterized by the undesirable or

XX excessive activity of PI3Kdelta. For example of cancer cells

XX for inhibiting the growth or proliferation of cancer cells

XX (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,

XX Hodgkin's lymphoma, leukemias), inflammatory diseases (e.g. rheumatoid

XX arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),

XX autoimmune diseases (e.g. systemic lupus erythematosus), inflammatory

XX bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory

XX dermatoses (e.g. contact dermatitis; central or peripheral nervous

XX system inflammatory disorders (e.g. meningitis), bacterial pneumonia,

XX and Type I diabetes mellitus. The present sequence encodes for human

XX p110delta isoform of PI3K.

XX

SQ Sequence 3213 BP; 979 A; 612 C; 704 G; 918 T; 0 other;

XX

Query Match 14.0%; Score 448.2; DB 24; Length 3213;

Best Local Similarity 50.1%; Pred. No. 8.3e-114;

Matches 1591; Conservative 0; Mismatches 1478; Indels 106; Gaps 15;

XX

58 ATCTCTAGTAATGTTTACTACCAAAATGGGATGATAGTACTTTAGATGCTCCGTGAG 117

Db 88 ATACCTGTGATTTCTTTTGGCCACTGGATTTATATCCAGTTGAGATCTCGGAA 147

Qy 118 GCTACGTTATATACGATTAAGCATGAACTATTTAAGAGCAAGAAAATACCTCTCCAT 177

Db 148 GCTACCATTTCTTATATTAAGCAGATGTTATGGAAGCAAGTTCACTATACCAATGTTCT 207

Qy 178 CACTTTCTTCAAGATGAATCTTTTACATTTTCTGTAAGTGTATACCAAGCAAGAAAG 237

Db 208 AACCTCTTATGGAATATGACTCTTATATGTTTGTGATGTGATACAGACTGCTGTATAT 267

Qy 238 GAGATTTTGTGATGAACAAGACGACTTGTGACCTTGGCTTTTCAACCTTTTAA 297

Db 268 GAGAGCTTGAAGATGAACAGAAAGACTGTGATGTGACGCTTTCTTCCAGTTCTC 327

Qy 298 AAAGTAAATGAAACGATAGCAACCGTGAAGAAAAGATCCTAATCGGAATGTTT 357

Db 328 AATATGATACAAAGAGTTGTGACCCAGGGGAAAA--ATTAGACTCAAAAATGAGTTC 384

Qy 358 GCTATCGCATGCCAGTGTGTGATTCGATATGTTAAGATCCAGAGTAGACGACTTC 417

Db 385 CTATATGGAAGAAAGTGTGATGAATTTGATCTTGAAGATCTGAAATATGAATTT 444

Qy 418 CGAAGAAATATTTCTCAATGTTGTAAAGAGCTGTGATCTTAGGATCTTAATTCCT 477

Db 445 CGAAGAAATATGCGCAAAATTCAGCGA-----GGAAAAATCTGTGCA 486

Qy 478 CATATGAGCAATGATATGTTATCTTCCAAATGTGAATCTTACAGAGTCCCAAG 537

Db 487 CTGTGGGATTTCTTGATGAGCTGCTGCTAAACAAATATCCAGAGCATGAACCA 546

Qy 538 CACATATATTAATTAATTTGATTAAGGCAAAATATAGTGTGATTTGGTAAATAGTTCT 597

Db 547 TCCATCCCTGAAAACTTGAAGATTAACCTTATAGGGGAAAGCTCATCGTAGCTTCAT 606

Qy 598 CCAATATATGACAAACGAGATATCTGTAATAATCAACATGACTGTGCCAGAACAA 657

Db 607 TTTGAAAATCTGCCAGAGCGTGTAGCTTCAAGTGTCTCTAATATGAATCTTATCAA 666

Qy 658 GTAATGCTGAGCAATCAGAAAAAACTCGAAGTATGTTGCTATCATCTGAACAACTA 717

Db 667 GTAAATGAATGGCAATC---CAAAAAGTTGACTATTCATGCGAAGAAAGATGAATTT 723

Qy 718 AACTCTGTGTTTGAATATCAGGCAAGATATTTTAAAGTGTGATGTGATGA 777

Db 724 AGCCCTATG-----ATTATGTGTCAGAGTCACGCGGAGATGA 765

Qy 778 TACTTCCAGAAAATATCTCTGAGTCAGTATAGTATATAGAAAGCTGTATATGCTT 837

Db 766 TATGTTTGGTATCATCTCACTAATTCAGTTCCAGTATATCCGAACTGTGTATGAAC 825

Qy 838 GGGAGATGCCCAATTTGATGCT---GATGCTAAAGAAAGCCTTATCTCAACTGC 892

Db 826 AGAGCCGCGCCCAATTTATCTTGTGAAATGCTGCAGAAATCAAGAAATGTATGACAA 885

Qy 893 CAATGACTGTTTACATATGCATCATATTCACAGCGCATCTCCACAGCTACGCCATATA 952

Db 886 GAAATGATGGCCATAGAGGCTGCCATTAATGCAAAATTAATCTTAATCTTCTTCCATTA 945

Qy 953 TGAATGGAACATCTCAAAATCCCTTTGGGTATTAATATGCTCACTCAGAAATAAA 1012

Db 946 CCAACCAAAAGAAACAGAAATTTTCTCATGTTTGGAAAAATTAACAACCTTTCCAAAT 1005

Qy 1013 TTTCTTTGCAACCTATGTGAATGTAAATATTCGAGACATTCACAAAGATTTATGTTGCA 1072

Db 1006 GTCTTGTTAAGGAAATTAACCTTAACAAGAGGAAC--TGTAAAGTTCAATGTACGG 1063

Qy 1073 CAGTATCTACATGAGAGAAACCTTATGATATATGTAACACTCAAGATACCTT 1132

Db 1064 CTGTCTCTTTTCTTATGATGAGCTCTGTGTAACATCTGTAAGCTCAGAGTATCAG 1123

Qy 1133 GTTCCA--ATCCAGAGTGAATGAATGCTGATTAATGATATATATCTCTGATCTTC 1189

Db 1124 GAAAAATGATCATATTTGAAATGAACCACTGGAATTTGATATATATTTGACTTAC 1183

OY	1190	CTCGTGCCTGCTGACTTTGGCTTTCCATT-----GTTCTGTTAAAGCCGAAAGGTCG	1244
Db	1184	CAAGATGGCTCGATTATGTTTTGGCTTTATGCACTTTGGATTAAGTAAAAAGAA	1243
OY	1245	TAAAGGGAACCTGTCAT-----TGGCCCTGGGGAATATTAACCTTGTTG	1291
Db	1244	AATCAACGAAACCTTAATCCCTCTAAATATACAGACATCAGAAAGCTGAAAAAGTC	1303
OY	1232	ATTACACAGATACCTGTAGTATCGAAAAAATGGCTTTGATCTTTGGCAGATCCTCAG	1351
Db	1304	ATTATCTGTACCGGGGTAATACAGATGGTTTTTGACTTTAAAGACAAATTGGAACCTG	1362
OY	1352	GACTGAAAGATTTGCTGAACCCCTATTTGGTACTAGATCAAAATCAATTAAGAAATC	1411
Db	1364	GAGACATATATTAACACAGCTGGTCTCATTTCTGATGAATCCAGAAATGTTGAATC	1423
OY	1412	CATGTTTAGAGTGGAGTTTGTCTGGTTCAGACAGTGTGTAAAGTTCCAGATATGTAG	1471
Db	1424	CAATGGGAACCTGTTCAACCAATTCATATACGAAATAGCAACGCTTTGATGTTAAT	1483
OY	1472	TGATTGAAGAGCATGCCAATTTGTCGTATCCCGGAAGCAGAGATTTATGTTATCCAGT	1511
Db	1484	TTCCAGAGAAATAAAAACAACCTTATTATTACCTCCCTTGATATAGTTTATGAAAAAG	1543
OY	1532	CAGACTGATTAACAGACTAGCTAGACAAATGAATTAAGAAATATATAAGAACAGC	1591
Db	1544	CAGCTGAAGATTGCAGCAGTGATGTAGCTAATGTGTCAAGTCAGAGTGGAAAAAGTTT	1603
OY	1592	TCC-----GAGCAATTTGTACAGAGATCCTTATCTGAAATCACTAGACAAAGA	1642
Db	1604	TTCTGTATGAAAMAAAATCTTGGACAGAGGATCCCTGTCTCACTGTGTAAAAATGAA	1653
OY	1643	AAGATTTTCTGNGAGCCACAGAC--ACTATTTGTAACTATCCCGAAATTTCTACCA	1699
Db	1664	TGATCTTATTTGACTTTGGCACAAGCTGCCAGAGATTTTCCCAATCACTCTGCCAA	1723
OY	1700	AATTGCTTCTGTCTGTTAAATGGAACCTAGAGATGAATGAGTCACTGACTCTGG	1759
Db	1724	AATTACTCTGTCAATCAAGTGAATTAACTTGAGAGATGTTGCTGACTGAGCGCTGC	1783
OY	1760	TAAAGATTTGGCTTCCAATCAAGCTGAACAGGCTATGAGCTTCTGACTGCATTAAC	1819
Db	1784	TTCAATTTTGGCTTAAACCTGCCCCCGGAGGCGCTGAGCTCTTGATTTCAACTATC	1843
OY	1820	CAGATCCTATGGTTGAGGTTTTGCTGTGCTGCTTAGAAAAAATTTAACATAGACA	1879
Db	1844	CAGACCACTAGCTTGGAAATATGTCTGAGCTGCT--CGCAAGATGTATATAG	1900
OY	1880	AACCTTTCAGTACCTAATTCAGCTAGTACAGTAACTAAATATAGAACAGATTTTGATA	1939
Db	1901	AACCTTTCATATCTTTTACACCTGGTGCAGAGTGTAAATATAGAGCTTTTCTTGATT	1960
OY	1940	ACCTGCTTGTAGATTTTACTCAAAAAGCGTTAATCAATCAAAAGATCGGTCACTTT	1999
Db	1961	GTGCCCTCTAGATTCTTATTAGAAAGCACTTGTATCGAGAGATAGGCAAGTTTC	2020
OY	2000	TCTTTGGCATTTAAATCTGATGACCAATTAATAACGTTATGTACAGAGTTTGGCTGC	2059
Db	2021	TATTTTGGCATTTAGGTCAAAAGTGCAATTTCTGTCTCAGTACAAATTTTGTGTCA	2080
OY	2060	TTTTGAGTCTTATTTGCGGTGATGTGATGTAATCGAAGCACCTTAATATGGAAGTGG	2119
Db	2081	TCTTTGAAGCATCTCGCCGGGAAATGTGGGACATAGAAAGTGTCTTTTGAAGAGTTG	2140
OY	2120	AGGCTATGAAAAGCTCATTAATTGACTGACATTTCTCAAACAAGAGAAAGATGAAA	2179
Db	2141	AAGCACTCAATTAAGTTAAAACTTTAAATATGTTTATCAAACTGAATGCCGTGAAGTTAA	2200
OY	2180	CACAAAAGGTACAGATGAAGTTTTTATGTGAGCAAAATCCGGGACACAGATTTTATGATG	2239
Db	2201	ACAGAGCCAAAGGAAGAGCCATGCAATCTGTTTAAACAGAGTCTTACCGGGAAG	2260

QY	2240	CTCTCCAGAGGCTTCTGTCTCTCTTAAACCTTGCTCATCAGCTGGAAATCTCAGGCTTG	2239
Db	2261	CCCTCTCGACCTGCAAGCACCCCTGAAACCATGTTATCTCTCAAACTCTATGTTG	2320
QY	2300	AAGAGTCTCGAATTAATGCTCTCTGCAAAAAGGCCACCTGCTGTAAATTGGAGAACCCAG	2359
Db	2321	AAAGTGCMAATACATGATGATTCCAAAATGAAAGCTTTGTGCTGTATACATTAACAAG	2380
QY	2360	ACATCATGTCAGAATTACTCTTTCAGAACATGAGATCATCTTTAAAAATGGGATGATT	2419
Db	2381	TATTGTGAGAGATTCAGT-----TGGAGTGATTTTAAAAATGCTATGATT	2428
QY	2420	TACGCCAAGATATGTCTAAACCTTCAGATTAATTCGATTAATGGAATAATCTCGCAAAATC	2479
Db	2429	TACGCAAGAGATATGTTGCACTCCAAATGTTGCCCTTGATGGAATTAATCTCGGAAACAG	2488
QY	2480	AAGGCTTGATCTTCGAAATGTTACCTTAATGGAATGCTCAATGGAGACGTGTGGAGC	2539
Db	2489	CTGGTTTGGATCTTCGGATGTTGCTTATGCTGTTTATGCAACAGGAGATGCTCTGACC	2548
QY	2540	TTATTCAGSTGTGAGAAATTTCTCACTATATATGCAATTCAGTGTAAAGAGAGC--C	2596
Db	2549	TCATTGAAGTTGTGAGACCTCTGAAACAAATTCGTGACATTCAGCTGAACAGTAGCATG	2608
QY	2557	TGAAAGGTGCCTGCACTGATTTAACGACCAACACATCTCCATCAGTGGCTCAAAAGACAAGACA	2656
Db	2609	TGGCTGCTGCAGACGACCTTCAACAAAGATGCCCTTCTGAACTGGCTTAAAGAAATACACT	2668
QY	2657	AGGGGAGAAATATATGATTCGGGCGCATTCGATTTGTTTACACATCATGTGCGAATATGTG	2716
Db	2669	CTGGGGAATGACCTTGGACCGAGCCATTGAGGAATTTAACCTGTCTGTGCTGGCTACTGTG	2728
QY	2717	TTGCCACCTTCATTTTGGGAATTTGAGATGCTCAATAGTAATATCATGTTAAAGATG	2776
Db	2729	TAGCTTCTTATGTCCTTGGGATTTGTTGTGACAGACATAGTGAACAATCATGTTGCAAAAAA	2788
QY	2777	ATGCAACAATCTTTCATATATAGATTTTGGACACTTTTGGATCACAGAAAGAAAAATTTG	2836
Db	2789	CTGGCGAGCTTTCACATATGACTTTGGACATATTTCTTGAAATTTCCAAATCTTAAGTTTG	2848
QY	2837	GTTATTAACAGAGACGCGGTGCGGTTGTTTGTGACACAAGAATTTCTTAATATGATTTAGTA	2896
Db	2849	GCATTTAAAGGAGCGAGTGCCTTTTATTTCTTACCTATGATTTTCATCATGTCAATTAAC	2908
QY	2897	AAGAGCCCAAGAAATGCAAAAAGACAAGAGATTTTGAAGGTTTCAGAGATGTTTACA	2956
Db	2909	AAGAAAAAACAGS-----AAATACAAAAAGTTTGGCGGTTCCGCAAGTGTGTAGG	2962
QY	2957	AGGCTTATCTTAAGCTATTTCCGAGAGATGCCAATCTCTTCATTAATCTTTTCTCATATGTC	3016
Db	2963	ATGATATATCTGATTTTAAGACGAGATGGGAATCTTTTCATCACCTCTCTTGGCGCTGATGT	3022
QY	3017	TTGGCTCTGGAATCCAGAACTGCAATCTTTTGTATGATTTTGCAATCATTCGAAAGAGCC	3076
Db	3023	TGACTGCAAGGCTTCTCGAACTCATCATCACTCAAAAGATATACAGTATCTTAAAGACCTTC	3082
QY	3077	TAGCTTTAGATTAAACTGAGCAAGAGGCTTTGGAGTATTTTCATGAACAATAGATGATG	3136
Db	3083	TTGCATTAGGAGAGAGTGAAGAAAGAACACTCAAAACAGTTTAAGCAAAAATTTGATGAGG	3142
QY	3137	CACACCAATGTGTGTGACAACAAAAATGATTTGATCTTTCACACACAATTTAAGCA	3191
Db	3143	CGCTCAGGGAAGCTTGACCTTACTAAATGTGAATCGGATGGCCACACAGTTCGGAA	3197

```
RESULT 10
ABX37274
ID ABX37274 standard; cDNA; 412 BP
XX
XX ABX37274;
AC
XX
XX 20-FEB-2003 (first entry)
XX
```







standards immunoassays. These assays are particularly used for diagnosing and predicting motility/invasiveness of metastatic cancer cells. The protein can be used in human or veterinary medicine for controlling motility of cells, where the protein increases motility while antiense sequences are used to reduce it.

Sequence 3387 BP; 711 A; 1044 C; 1001 G; 631 T; 0 other;

Query Match	10.5%	Score 336.2;	DB 19;	Length 3387;
Best Local Similarity	53.5%;	Pred. No. 1.3e-82;		
Matches 804; Conservative	0;	Mismatches 678;	Indels 21;	Gaps 4;

QY	1682	TCGCCGAATTCACCCAAATTGCTTCTGTCTGTTAAATGGAACCTCTAGAGTAGAGTAG	1747
Db	1625	TCCCGAGGGCGCTAGCCCGGCTGTCTGTGTACCAACAGTGGAAACAAGCATGAGGATGTCTGG	1684
QY	1742	CTCAGATGTACTGTCTGGTAAAGAATGGCGCTCCCAATCAACCTCGMAACAGGCTATGAGGC	1801
Db	1685	CCCGAGATGCTTACCTGTGTGTCTCTGGCCGAGACTGCCCCGTCTTGAGCCCTCTGGAGC	1744
QY	1802	TTCTGACCTGCAATTACCCAGATCTCTATGTTGAGGTTTTGTCTGTGTGGGTCTTAGAA	1861
Db	1745	TGCTAGACTTCAGCTTCCCGATTTGCCAGATGAGGCTCCTTTGGCATTCAAGTCGCTCGCGA	1804
QY	1862	AATTTTAAACAGATGACAAACTTTTCTCAGTACCTTAATTCACTAGTACAGGTACTAAAT	1921
Db	1805	AAC--TGACGGAGGATGAGAGCTGTATCCAGTACCTGTGCACTGTGTGAGGTGTCTCAAGT	1861
QY	1922	ATGACAGTATTGTTGGATTAACCTGTGTGATTTTAACTTAACCTAAAMAAGCGTTAACTATC	1981
Db	1862	ACGAGTCTTACCTTGACCTGCGAGCTGACCAAATTCCTGTGTGAGCCGGGCTCTGGACCAAC	1921
QY	1982	AAAGATCGGTCACTTTTCTTTTGGGATTTAAATCTGAGATGCACAAATATAACAGTTA	2041
Db	1922	GCAAGATCGGCACTTCTCTTTCTGTGCACTCCGCTCCGAGATGACGCTGCCCTCGGTGG	1981
QY	2042	GTCAAGGTTTGGCTGCTTTTGGAGTCTTATGTCCTGATGTGAGTGTATCTGAAGC	2101
Db	1982	CCCTGCGCTTCGGCTCATCTCTGAGGCGCTACTCAGAGGGCAGAGACCCACACATGAAGG	2041
QY	2102	ACCTTAATAGGCAAGTTGAGGCTTATGGAAGAAGCTCATTAACCTTGAATGACATTTCTCAAC	2161
Db	2042	TGCTGATGAACAGGGGGAAGCACTGAGCAAACTGAAGGCCCTTAATGATCTGTCAAGC	2101
QY	2162	AAGAGAAGAAAGATGGAACAACAAGAAGTACAGATGAAGTTTTTATGTTAGCAATTTGGCGC	2221
Db	2102	TGAGCTCTCAGAAAGACCCCAAGCCCAAGACCAAGAGAGCTGATGACTTGTGCAATGGCGC	2161
QY	2222	GACCAAGTTTCATGATGATGCTCTCCAGGGCTTTCTGTCTCTTAAACCTTGCTCATGAGC	2281
Db	2162	AGGAGGCTTACTTAAAGGCCCTCTCCACCACTGACAGTCCCACTCGAATCCCAAGCACCTCGC	2221
QY	2282	TGGGAATCTCAGGCTTGAAAGAGTGTGGAATTATGTCTTCTGCAAAAAGCCACTGTGGT	2341
Db	2222	TGCTGAAAGTCTGCTGAGACAGTGCACCTTCATGAGACTCCAGATGAAGCCCCCTGTGGGA	2281
QY	2342	TGATTTGGGAAACCCAGACATCATGTCAGAATTAATCTTTCAAGACATGAGATCACTT	2401
Db	2282	TCATGTACACCAACGAGGAG-----GACGACACGGCGGCGAAGCTGGGCATCATCT	2332
QY	2402	TTAAAAATGGGAGTATTTACGGGACAGATATGCTAACCTTCAGATTTATTCGACTTAGG	2461
Db	2333	TTTAAAGAACGGGAGATGACCTCCGGCAGGACATGTGACCTCTGACAGATGCACAGCTATGG	2392
QY	2462	AAATATCTGGCAAAATCAAGGCTTTGATCTTGGATGTTAATCTTATGATGTGTGTCAA	2521
Db	2393	ACGTCTCTGTGAAAGACAGAGAGGGCTGTGACCTTGAGATGAAACCCCTTATGGCTCTCCCA	2452
QY	2522	TGCGTGACTGTGGGACTTATCGAGGTGTGGAGAAATTCACACATATATGCAATTC	2581
Db	2453	CCGGGACCGCACAGGCTCATTTGAGGTGTATCTCCGTTACAGACATGCCCCAATCC	2512
QY	2582	A---GTGTAAAGAGCGCTGAAGGTGCACTGCAGTTTAAACGACACACATCCATCAGT	2638

[illegible]

PR 19-JUL-1999; 99US-0357070.  
XX (ISIS-) ISIS PHARM INC.  
XX Monia BP, Cowsett LM;  
XX WPI; 2000-282691/24.  
DR P-PSDB; AAY8372.  
PT New antisense compounds targeting nucleic acids encoding human p13  
PT Kinase p110 delta useful for treating a disease or condition associated  
PT with p13 Kinase p110 delta expression, e.g. rheumatoid arthritis.  
PT asthma  
XX  
XX Example 13; Column 45-52; 35bp; English.  
XX This sequence represents a nucleotide sequence encoding the delta  
XX catalytic subunit of human phosphatidylinositol 3 Kinase. Phosphatidylinositol 3 Kinases (PI3K) act as downstream effectors of hormone and growth factor receptors, and have been implicated in growth factor mediated cell transformation, mitogenesis, protein trafficking, cell survival and proliferation, and many other cellular activities. PI3K is a heterodimer, consisting of a 110KD catalytic subunit (p110), and an 85KD regulatory subunit (p85). The invention relates to antisense oligonucleotides which target the p110 delta mRNA of PI3K. The antisense oligonucleotides specifically hybridise with various regions of the PI3K mRNA sequence, and inhibit the expression of PI3K. The antisense oligonucleotides may be used to treat an animal, particularly human, oligonucleotides may be used to treat a disease or condition associated with the expression of PI3K, e.g. rheumatoid arthritis or asthma. The treatment works through the modulation (preferably inhibition) of the expression of PI3K. The antisense oligonucleotides may also be used for research and diagnostics, in pharmaceutical compositions and formulations, in the preparation of kits for detecting the level of PI3K in a sample, and as prophylaxis, e.g. to prevent or delay infection, inflammation or tumour formation. Antisense oligonucleotides, which are able to inhibit gene expression specifically, are used to elucidate the function of particular genes, and to distinguish between functions of various members of a biological pathway.  
XX  
XX Sequence 3868 BP, 800 A; 1190 C; 1141 G; 737 T; 0 other;  
SQ  
Query Match 10.5%; Score 336.2; DB 21; Length 3868;  
Best Local Similarity 53.5%; Pred. No. 1.4e-82;  
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;  
QY 1682 TCCCGGAATTCTACCCAAATTGCTTGTCTGTTAAATGAAGACTCTAGATGAGTAG 1741  
DB 1821 TCCCGAGGCGGTAGCCCGGCTGCTGTGTGTACCAAGAGAAACAAGCATGAGATGTGG 1880  
QY 1742 CTCAGATGACTGCTTGTAAGATATGCGCTTCACATCAAGCCTGAACGGCTATGAGAC 1801  
DB 1881 CCCAGATGCTTACCTGCTGTGTCTGTGCGGAGCTGCCGTCCTGAGCGCCCTGAGAC 1940  
QY 1802 TTCTGACTGCAATTACCAAGATCTATGCTTGAAGTTTGTGTGTGCTTGAAGA 1861  
DB 1941 TGTACACTTACAGCTTCCCGATTTGCGAGTACGCTCTTGGCAATCAAGTGTGCGGA 2000  
QY 1862 AATATTTAACATGACAAACTTTCAGTACCTAATTCAGTAGTACAGTACTAAAT 1921  
DB 2001 AAC---TGACGGAGCATGAGCTGTCCAGTACCTGCTGACGCTGTGTGAGTGTCAAGT 2057  
QY 2001 AATACAGATTTTGGATTAACCTGCTGTGTGAGATTTTACTCAAAAAAGCCTTAATTC 1981  
DB 1922 ATGACAGATTTTGGATTAACCTGCTGTGTGAGATTTTACTCAAAAAAGCCTTAATTC 2017  
QY 2058 ACAGATCTTACCTGAGTGTGAGCTGACCAATTTCCGTGTGACCGGGCCCTGGCCAAAC 2117  
DB 1982 AAGAGATCGGTCACTTTTCTTTGGCATTTAAATTTGAGATGACAAATTAACAGTTA 2041  
QY 2118 GCAAGATCGGCACTTCTTTTCTGGACCTCCGCTCCGAGATGACAGTGTGCGGTGG 2177  
QY 2042 GTACAGAGTTTGGCTGTCTTTTGGAGTCTATTTGCGGTGAGTGTGATGTGAGC 2101  
DB 2178 TCCCTGCTTGTGCGCTCATCTGTGAGGCTTACCTGAGGCGACGACCAACCATGTAAGG 2237

QY 2102 ACCTTAATGAGCAAGTTGAGGCTATGGAAGAGCTCAATTAAGTGTGACATCTCAAC 2161  
DB 2238 TGCTGATGAGCAGAGGGGAGACCTGAGCAACATGGAAGCCCTGATATCTTGTCAAGC 2297  
QY 2162 AAGAGAAAGAGATGAAACACAAAAAGTACAGATGAAGTTTATGTTAGCAAAATCGCCG 2221  
DB 2298 TGAGCTTCAGAAAGACCCCAAGCCCAAGACCAAGAGACGTATGACTTGTGATGCGGC 2357  
QY 2222 GACCAAGATTTTCAATGATGATCTCTCCAGGCTTTCTGTCTCTCTTAAACCTGTATGACG 2281  
DB 2358 AGAGAGCTTACTTACAGGCTCTCTCCACCTGCACTGTCCCACTGACCCAGACCTTGC 2417  
QY 2282 TGGGAATCTCAGGCTTGAAGGTGTCAATTATGCTTGTGCAAAAAAGCCACTGTGGT 2341  
DB 2418 TGGCTGAAGTCTGCTGTGAGGAGTCACTTGTATGACTTCAAGATGAAGAGCCCTGTGGA 2477  
QY 2342 TGAATTTGGAGAACCCAGACATCATGTGCAATTAATCTCTTTTCAAAATGAGATCAT 2401  
DB 2478 TCAATGACAGCAACGAGGAG-----GACAGCAGGGGGGCAAGCGGCATCATCT 2528  
QY 2402 TTAATAATGGGATGATTTTACCGCAAGATATGCTAACCTTCAATTAATTCGATATGAG 2461  
DB 2529 TTAAGAACGGGATGACCTCCGCAAGACATGCTGACCTGCAAGATCCAGCTCATGG 2588  
QY 2462 AAAATATCTGGCAAAATCAAGGCTTGAATCTTGAATGTTACCTTATGATGATCTGTCAA 2521  
DB 2589 ACCTCTGTGGAAGCAGAGGGGCTGACCTGAGATGACCCCTTATGTGCTGTCCCA 2648  
QY 2522 TCGGTACCTGTGTGAGGACTTATGAGAGTGTGAATTTCTCACTATATGACAGATT 2581  
DB 2649 CCGGGAGCCGACAGGCTTATGAGTGTATCTCGGTGACACATGCGCAATCC 2708  
QY 2582 A---GTGTAAAGAGGCTGAAAGGTGACCTGCACTTTAAACAGCACACCTCCATCAGT 2638  
DB 2709 AATCAACAAAGAGCAATGAGCAGCCAGCCCTTCAACAAAGATCCCTCTCACT 2768  
QY 2639 GGCTCAAAAGACAAAGACAGGGGAAATATATATGAGGCGCATGATTTTATACAGAT 2698  
DB 2769 GGCTGAAGTCCAAAGAACCGGGGAGGCGCTGATGACGACATTTGAGAGATTCACTCT 2828  
QY 2699 CATGTCTGATATATGTTGTTGCCACTTCAATTTTGGAAATTTGAGATGCTCAATATGTA 2758  
DB 2829 CCTGTGCTGATATGTTGTTGCCACTTCAATTTTGGAAATTTGAGATGCTCAATATGTA 2888  
QY 2759 AATCATGTTTAAAGATGATGACCACTGTTTCAATATGATTTTGGACATTTTGGATC 2818  
DB 2889 ACATCATGATCCGAGAGGTGGCAGCTGTTCCACATTTGATTTGGCCACTTCTGGGGA 2948  
QY 2819 ACAAGAGAAAAAATTTTGTATTAACGAGAGCGCGCTTGTGTTTGAACAGATT 2878  
DB 2949 AATTCAAAGCAAGTTTGTGAATCAACCGCGAGCGTGTCCATTCCTCACATGACAT 3008  
QY 2879 TCTTAATGATATGTAAGAGAGGCCCAAGATGACAAAGACAAAGAAATTTGAGAGT 2938  
DB 3009 TTGTCCATGTGATTAAGCAGG-----GAGACTAATATATGTAAGAAATTTGAACGCT 3062  
QY 2939 TTCAGAGATGTTTAAAGGCTTATCTAGCTATTTGGAGAGATGCAATCTTCTTCAATA 2998  
DB 3063 TCCGGGGCTACTGTGAAGGGCTTACACATCTCGGCGCCACGGGCTTCTTCTCTCC 3122  
QY 2999 ATCTTTTCAATGATGCTTGTGCTGTGCAATGCCAAGACTGCAATCTTTTGAATGATTG 3058  
DB 3123 ACTCTTTTCCCTGATGCGGGGCGGAGGCGTCTGTGAGTCTGAGTCTTCAAAAGACATCC 3182  
QY 3059 CATACATTGGAAGACCCCTAGCTTTAGATTAATGAGCAAGAGGCTTTGAGATTTTGA 3118  
DB 3183 AGTATCTCAAGACTTCTCTGGAATGAGGAAAAAGAGAGAGGACACTGAAGCACTTCC 3242  
QY 3119 TGAACAAATGAATGATGACACATGATGTGCTGCAACAAATATGATTTGATCTTCC 3178  
DB 3243 GAGTGAAGTTTAAGCAAGGCTTCTGTGAGAGCTGGAAGAAACAAAGTGAACCTGTGGCC 3302

QY 3179 ACA 3181  
 DB 3303 ACA 3305  
 RESULT 13  
 ABR84750  
 ID ABR84750 standard; cDNA, 3868 BP.  
 AC ABR84750;  
 XX  
 DT 14-AUG-2002 (first entry)  
 DE Human cDNA differentially expressed in granulocytic cells #1321.  
 XX  
 DE Human; ss; granulocytic cell; DNA chip; bacterial infection;  
 KM viral infection; parasitic infection; protozoal infection;  
 KM fungal infection; sterile inflammatory disease; psoriasis;  
 KM rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
 KM cardiac reperfusion injury; renal reperfusion injury; ARDS;  
 KM adult respiratory distress syndrome; inflammatory bowel disease;  
 KM Crohn's disease; ulcerative colitis; periodontal disease;  
 KM granulocyte activation; chronic inflammation; allergy.  
 XX Homo sapiens.  
 OS  
 PN WO200228999-A2.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 03-OCT-2001; 2001WO-US30821.  
 XX  
 PR 03-OCT-2000; 2000US-237189P.  
 XX  
 PA (GENE-) GENE LOGIC INC.  
 PI Beazer-Barclay Y, Weiseman SM, Yamaga S, Vockley J;  
 DR WPI; 2002-435328/46.  
 XX  
 PT Detecting granulocyte activation by detecting differential expression  
 PT of genes associated with granulocyte activation, which serves as  
 PT diagnostic markers that is useful for monitoring disease states and  
 PT drug toxicity -  
 PS  
 XX Claim 1; SEQ ID No 1321; 114pp: English.  
 CC The invention relates to detecting (M1) granulocyte (GC) activation  
 CC (GCA), by detecting the level of expression of gene(s) identified by  
 CC DNA chip analysis as given in the specification, and comparing  
 CC the expression level to an expression level in an unactivated  
 CC GC, where differential expression of Gs is indicative of GCA.  
 CC Also included are modulating (M2) GA by contacting GC with an agent  
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)  
 CC for an agent capable of modulating GCA or an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease using the  
 CC gene expression profile; (3) detecting (M4) an inflammation (especially  
 CC chronic) in a tissue, an allergic response in a subject, exposure of a  
 CC subject to a pathogen or sterile inflammatory disease, by detecting the  
 CC level of expression in a sample of the tissue of gene(s) from Gs, where  
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,  
 CC an allergic response in a subject, exposure of a subject to a pathogen  
 CC or sterile inflammatory disease, by contacting a tissue having  
 CC inflammation with an agent that modulates the expression of gene(s)  
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for  
 CC modulating Gs; M3 is useful for screening an agent capable of modulating  
 CC GCA preferably in an inflammation (especially chronic) in a tissue; M4 is useful for  
 CC detecting an inflammation (especially chronic) in a tissue, an allergic  
 CC response in a subject, exposure of a subject to a pathogen or sterile  
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,  
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal

CC reperfusion injury, ARDS, adult respiratory distress syndrome,  
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
 CC periodontal disease, also bacterial infection, viral infection,  
 CC parasitic infection, protozoal infection, fungal infection and M5 is  
 CC useful for treating one of the above conditions. The present  
 CC sequence represents a gene differentially expressed in granulocytes.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 3868 BP, 800 A; 1190 C; 1141 G; 737 T; 0 other;  
 Query Match 10.5%; Score 336.2; DB 24; Length 3868;  
 Query Local Similarity 53.5%; Pred. No. 1,4e-82;  
 Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;  
 QY 1682 TCCCGGAATTTCTACCCCAATTTGCTTCTGTTAAATGGAACCTAGATGAAGTAG 1741  
 DB 1821 TCCCGGAGCGCTAGCCGGCTGCTGCTGTCACCAATGGAACAGATAGATGTGG 1880  
 QY 1742 CTCAGATCTACTGCTTGTAAAGATTGGCTCCCAATCAAGCTGAAACAGCTATGAGC 1801  
 DB 1881 CCCAGATCTCTACCTGCTGTGCTCTGCGCGAGCTGCCGTCTAGCGCCCTGAGC 1940  
 QY 1802 TTCTGAGTGAATTAACCAATCTATGTTTCCAGATTTTGGTGTGCTTGA 1861  
 DB 1941 TGCTAGACTTACGCTCCCGATTTGCCACGATGCTCCCTTGCATCAAGTGTGCGGA 2000  
 QY 1862 AATATTTACAGATGACAACTTCTCAGTACTTATTCAGTCTAGTACAGTACTAAAT 1921  
 DB 2001 AAC---TGACGGAAGATGAGCTGTTCCAGTACTCTGCTGACGTGAGGTCTCAAGT 2057  
 QY 1922 ATGAACGATATTTGATTAACCTGCTTGTGATTTTAACTCAAAAACGTTAACTATC 1981  
 DB 2058 ACGAGTCTTACCTGAGCTGCGAGCTGACCAATTTCTGTGAGCCGGCCCTGGCAAC 2117  
 QY 1982 AAAGATCGGCTACTTTTCTTTGGCATTTAAATCTGAGATGACATTAACAGTTA 2041  
 DB 2118 GCAGATCGGCACTTCTTTTCTGCACTCCGCTCCGAGATACAGTGTGCGGTGG 2177  
 QY 2042 GTCAGAGTTTGGCTCTTTTGGAGTCTTATGCGCGCATGNGGATGATGTGAAGC 2101  
 DB 2178 CCTGCGCTTGGCTCTATCTGAGGCTTACTGACGGGAGGACCCACATGAAAGG 2237  
 QY 2102 ACCTTAATAGGCAAGTTAGGCTATGAAAAAGCTCATTAACCTGACTGACATTTCTAAAC 2161  
 DB 2238 TGCTGATGAGACGAGGGGAGCACTGAGCAAACTGAAAGGCCCTGAATGACTTGTCAAGC 2297  
 QY 2162 AAGAGAAAGATGAAACACAAAAGGTACAGATGAAGTTTATGTTAGGCAAAATGCGGC 2221  
 DB 2298 TGAAGCTCTGAGAAACCCCAAGCCCAAGCAAGGAGCTGATGCACTTGTGATGCGGC 2357  
 QY 2222 GACCAAGTTTCATGAGATGCTCTCCAGGCTTTGTCTCTTAAACCCGCTCATAGC 2281  
 DB 2358 AGAAGGCTTACCTTGAAGGCTCTTCCCACTGCAAGTCCCACTGACCCACGACACCTTGC 2417  
 QY 2282 TGGGAAATCTCAGGCTTGAAGATGCAATTAATGTTCTTGTGCAAAAAGGCCACTGTGT 2341  
 DB 2418 TGCGTGAAGTCTGGTGTGAGCAAGTCACTTATGAGCTCAGATGAACCCCTGTGGA 2477  
 QY 2342 TGAATTTGGGAAACCCGACATATGTCAGAAATTAATCTTTTCAAGAACATGAGATCTT 2401  
 DB 2478 TCAATGTACAGCAACGAGAG-----GCAGGACGCGCGGACGCTGGGATCATCT 2528  
 QY 2402 TTAATAATGGGAGATGATTTACGGGAAGATATGCTAACCCCTTCAGATTAATTCGATTAAG 2461  
 DB 2529 TTAAGAAAGGAGATGACTTCCGACAGACATGCTGACCTTGCAGATGATCACTCATGG 2588  
 QY 2462 AAAATATCTGGCAAAATCAAGATCTTGAATCTTGAATGTTACCTTATGATGTCTGTCA 2521  
 DB 2589 ACGTCTGTGAGAGCAGAGAGGCTGACCTGAGATGACCCCTTATGCTGCTCCCA 2648

QY 2522 TCGGTGACTGTGTGGACCTTATGAGGTGGTGAATAATCTCTACATATATGACATTC 2581  
DB 2649 CCGGGGAGCCGACAGGCTCATTTAGGTGTGTAATCTCCGTTGAGACCATGCGCAACATCC 2708  
QY 2582 A---GTGTAAGAGGCGCTGAAAGTGACATGACGTTTAAACAGCCACACATCTCATAGT 2638  
DB 2709 AACTCAACAGAGCAACATGCGACGACGCGCTTCAACAGAGATGCGCTGTCAACT 2768  
QY 2639 GGCTCAAGACAGACAGAGGCGGAATATATATGATGCGGCGCATGATTTTTCACAGAT 2698  
DB 2769 GGCTGAAGTCCAGAGAACCGGGGAGGCGCTGATGAGCCATTGAGAGATTCACCTCT 2828  
QY 2699 CATGTGCTGATATTTGCTTGGCACCTTCATTTTGGAAATGGAGATGTCACAACTACTA 2758  
DB 2829 CCGTGGCTGGCTATTTGTGTGTGACATATGTCTGGGATGGGATGGGACACAGCACA 2888  
QY 2759 ATATGATGTTAAAGATGAGACACTGTTTCATATGATTTTGGACACTTTTGGATC 2818  
DB 2889 ACATCATGATCCGAGAGAGTGGGACGCTGTTCCACATGATTTTGGCCACTTTTGGGGA 2948  
QY 2819 ACAGAGAGAAAAATTTGGTTATTAACAGAGCGCGCTGCTTTTTCACACAAGATT 2878  
DB 2949 ATTCAAGACCAAGTTTGAATCAACCGGAGCGTGTCCATTCTCTACCTACGACT 3008  
QY 2879 TCTTAATAGTATTAAGAGAGCCCAAGATGACAAAGACAGAGAAATTTGAGAGGT 2938  
DB 3009 TTGTCCATGTGATTCAGCAGG-----GAGACTAATTAATGTAATTTGAACGGT 3062  
QY 2939 TTCAGAGATGTGTCAAGAGCTTATCTAGCTATTTGGGACGATGCCAATCTTTCATAA 2998  
DB 3063 TCCGGGCTACTGTGAAGGGCTCAACCACTGCGGCGCCACGCGCTTCTTCTCTCC 3122  
QY 2999 ATCTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTGCAATCTTTGATGATATG 3058  
DB 3123 ACCTCTTGGCTGATCGGGGCGGACGCGCTGCTGAGCTGAGTCTCCAAAGACATCC 3182  
QY 3059 CATACATTCAGAAAGACCTTACTTATGATTAATACTGACAGAGGCTTTGAGATTTCA 3118  
DB 3183 AGTATCTCAAGACTCCCTGCGACTGGGAGAAACAGAGAGAGGCACTGAAGCACTTCC 3242  
QY 3119 TGAAGCAATGATGATGACACCATGTGTGCTGAGACAAATAATGATTTGATCTTCC 3178  
DB 3243 GAGTGAAGTTTAAGAGAGCCCTCCGTGAGACTGGAATAACCAAGTGAATGGCTGCGCC 3302  
QY 3179 ACA 3181  
DB 3303 ACA 3305

PD 15-NOV-2001.  
PF 10-MAY-2001; 2001WO-US15065.  
PR 10-MAY-2000; 2000US-203346P.  
PA (ICOS-) ICOS CORP.  
PI Sadhu C;  
XX WPI: 2002-075252/10.  
DR P-PSDB; AAU09685.  
PT Identifying a modulator of p110delta polypeptide binding to SH3  
PT domain-containing polypeptides e.g. Lasp-1, comprising allowing the  
PT binding partners to interact in the presence and absence of a test  
PT compound -  
PS Example 1; Page 43-48; 85pp; English.  
XX The present invention relates to identifying a modulator of the  
XX phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to  
XX the catalytic subunit via a SH3 domain-containing polypeptide such as  
XX Lasp-1. Also described are methods of assaying the specific binding  
XX affinity of the PI3-kinase binding partner. Such modulators are useful  
XX for the treatment of diseases characterized by the undesirable or  
XX excessive activity of PI3Kdelta. For example the modulators can be used  
XX for inhibiting the growth or proliferation of cancer cells  
XX (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,  
XX Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid  
XX arthritis), opthalmic disorders (e.g. allergic conjunctivitis),  
XX autoimmune diseases (e.g. systemic lupus erythematosus), inflammatory  
XX bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory  
XX dermatoses (e.g. contact dermatitis; central or peripheral pneumonia,  
XX system inflammatory disorders (e.g. meningitis), bacterial pneumonia,  
XX and Type I diabetes mellitus. The present sequence encodes for human  
XX p110delta isoform of PI3K.  
SQ Sequence 3868 BP; 800 A; 1190 C; 1141 G; 737 T; 0 other;  
Query Match 10.5%; Score 336.2; DB 24; Length 3868;  
Best Local Similarity 53.5%; Pred. No. 1.4e-82;  
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;  
QY 1682 TCCCGCAATTTACCAAAATGCTTCTGTCTTAATGAACTGAGAGATGAGTAG 1741  
DB 1821 TCCCGAGGCGCTTAGCCGCGCTGCTGTCAACAAAGTGAACAGCATGAGATGCG 1880  
QY 1742 CTCAGATGTACTGCTGTGTAAGATTGGCTCCATCAACAGCGCTATGAGAGC 1801  
DB 1881 CCCAGATGCTTACTGCTGTGCTCTGCGCGAGAGCTGCCCTCTAGAGCCCTTGAGAGC 1940  
QY 1802 TTCTGAGTGCATTTACCCGATCTATGTTGAGAGTTTGTCTGTTGGCTTAGAAA 1861  
DB 1941 TGCTAGACTTACGCTTCCCATTTGCCAGTAGAGCTCCTTGCCATCAAGTCGTCGCA 2000  
QY 1862 AATATTTAAGATGACAAATTTCTCTAGTACTTAATTCAGTACTAGTACTTAAT 1921  
DB 2001 AAC---TAGCGAGCATGAGCTGTCCAGTACTGCTCACTGTGTGAGAGTCTCAAGT 2057  
QY 1922 ATGAACAGATTTGATTAACCTGCTTGTGAGATTTTACTCAAAAACGTTAATAATC 1981  
DB 2058 ACGAGTCTTACTGAGCTGCGAGCTGACCAATTTCTGTGACCGGCGCTGCGCAAC 2117  
QY 1982 AAAGATGCTGACTTTTCTTTTGGCAATTAATTTGAATGCAATAAACAGTTA 2041  
DB 2118 GCAAGATGCGCACTTCTTTTGGCACTTCCGCTCGAAGATGACGCGCTGCTG 2177  
QY 2042 GTCAGAGTTTGGCGCTTTTGGAGTCTTATGCTGCTGATGAGATGATCTGAAC 2101  
DB 2178 CCTGCGCTTGGCTTCACTCTGAGAGCTTACGAGGCGGAGAGCCACCACTCAAG 2237  
QY 2102 ACCTTAATGAGCAAGTTGAGGCTATGAAAAGCTCATTAATTGACTGACATTTCAAC 2161

RESULT 14  
AAS14363  
ID AAS14363 standard; cDNA; 3868 BP.  
XX AAS14363;  
AC AAS14363;  
XX  
DT  
XX  
DE cDNA encoding human p110delta isoform of PI3-kinase.  
XX  
XX Human; phosphatidylinositol 3-kinase; PI3K; p110delta isoform;  
XX Lasp-1; cancer; inflammatory disease; opthalmic disorder; SH3 domain;  
XX autoimmune disease; inflammatory bowel disease; bacterial pneumonia;  
XX Type I diabetes mellitus; cytosolic; immunosuppressive; ss.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX FT 197..3331  
XX FT CDS /'tag= a  
XX FT /product= "p110delta isoform of PI3-kinase"  
XX  
XX PN W02C0185986-A2.

```

Db      2238 TCGTGAAGAAAGCAGGGGAGCACTGAGCAAACTGAAGGCCCTTAATGACTTCCTCAAGC 2297
QY      2162 AAGAGAAAGAGATGAAACACAAAGGTAACAGATGAATTTTATGAGCAAAATGCGGC 2221
Db      2298 TGAAGCTCAGAAAGACCCCAAGCCCAAGACCAAGAGCTGATCACTTGCAATGCGGC 2357
QY      2222 GACCAAGATTTTCATGATGCTCTCCAGGGCTTCTGCTCTCTTAACCCCTGCTCATGAC 2281
Db      2358 AGGAGGCTTACCTAGAGGCCCTCTCCACCTGCGATCCCACTGACCCCAAGCCTGCG 2417
QY      2282 TGGGAATCTCAGGCTTGAAGAGTGTGGAATATGCTCTTCTGCAAAAAGCCACTGTGT 2341
Db      2418 TGGCTGAAGTCTGCTGAGAGAGTGACCTTCATGGACTCCAGAGTAAAGCCCTGTGGA 2477
QY      2342 TGAATGGAGAAACCCAGACATCTGCAGAAATTAATCTTTCAGACAAATGAGATCACT 2401
Db      2478 TCAATGTCAGACAGAGAGAG-----GAGGACAGGGGGGCGCTGGGCACTATCT 2528
QY      2402 TTAATAATGGGAGATTTTACGGCAGATATGCTAACCTTCAGATTTATGCAATATG 2461
Db      2529 TTAAGAAAGGGGATGACCTCCGGCAGAGATGCTGACCTGCAAGATGATCCAGCTCATGG 2588
QY      2462 AAAATATCTGGCAAAATCAAGGCTTATGATCTTGAATGTTAATCTTATGATGTCTCAA 2521
Db      2589 ACCTCTGTGAAAGCAGAGAGGGGTGACCTGAGGATGACCCCTATGCTGCTCCCA 2648
QY      2522 TCGGTGACTGTGGGACTTATCGAGGTGGTGAATAATTCACACATATATAGAGATTC 2581
Db      2649 CCGGGAGCCGACAGGCTTATGAGTGTGATCCCTTCAGACACCATGCCAACAATCC 2708
QY      2582 A---GTGTAAGAGAGGCTTGAAGGTGACATGACATTAACAGCAACACACTCCATAGT 2638
Db      2709 AACTCAACAAGAGACATGAGCAGCCACACCCGCTTCAACAAGATGCCCTGCTCACT 2768
QY      2639 GGCTCAAGACAGAACAGAGGGGAAATATATATGTCGGCCATGCTTTTATTAACAGAT 2698
Db      2769 GGCTGAAGTCCAAAGAACCCGGGGAGGCTTCGATCGACATTCAGAGATTCACCTCT 2828
QY      2699 CATGTCTGATATTTGTTGTTGCCACCTTCATTTTGGGAATTTGACAAATATGTA 2758
Db      2829 CCTGTCTGCTATTTGTTGTTGCCACATATGCTGCTGGCATTTGGCAGATGGCAGAC 2888
QY      2759 AATATCATGTTAAAGATGATGACAACTGTTTATATAGATTTTGCACATTTTGGATC 2818
Db      2889 ACATCATGATCCGAGAGAGTGGGAGCTGTTCCAAATGATTTTGGCCATTTCTGGGGA 2948
QY      2819 ACAAGAAAGAAAAATTTGTTATTAACGAGAGCGCTGCGTTGTTTGAACAAGATT 2878
Db      2949 ATTTCAGACCAAGTTTGGATCAACCGGAGCGTGTCCATTCATCTCAGCTACGACT 3008
QY      2879 TCTTATATGATGATTAAGAGAGCCCAAGATATGCAAAAGACAAAGATTTGAAGGT 2938
Db      3009 TTGTTCATGATGATTCAGCAGG-----GAGAAGCTAATATATGAGAAATTTGAACGGT 3062
QY      2939 TTCAGAGATGTTGTTCAAGGCTTATCTAGCTATTCGGGAGAGTGCATCTCTTATTA 2998
Db      3063 TCCGGGCTACTGTGAAGGGCTTACACATCTGCGGGCCCAAGGGCTTCTTTCTCTC 3122
QY      2999 ATCTTTTTCATGATGCTTGTGCTCTGGAATGCGCAAGCTCAATCTTTTATGATATG 3058
Db      3123 ACCTCTTTTCCCTGATGCGGGCGGAGGCTGCTGAGCTCACTCTCCAAAGACATCC 3182
QY      3059 CATACATTTGAAAGACCTAGCTTTAGATTAACCTAGCAAGAGGCTTTGAGATATTTCA 3118
Db      3183 AGTATTCAGAGACTCCCTGCGACCTGGGAGAAACAAGAGGAGGACATGAACACTTCC 3242
QY      3119 TGAACCAATGATGATGACACATGATGCTGACCAACAAATATGATGATCTTCC 3178
Db      3243 GAGTGAAGTTTAAAGAGGCTCTCGAGAGCTGGAAGAAACAAAGTGAATGCTGCTGCC 3302
QY      3179 ACA 3181

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Db      3303 ACA 3305
RESULT 15
AAV31340
ID AAV31340 standard; cDNA; 5220 BP.
XX
AC AAV31340;
XX
DT 12-OCT-1998 (first entry)
XX
DE Human phosphatidylinositol 3-kinase p110 delta subunit cDNA.
XX
KW Phosphatidylinositol 3-kinase; p110 delta; human; immune system;
KM carcinogenesis; diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 196..330
FT /+tag= a
XX
PN W09823760-A1.
XX
PD 04-JUN-1998.
XX
PF 25-NOV-1997; 97MO-US21655.
XX
PR 25-NOV-1996; 96US-0777405.
XX
PA (ICOS-) ICOS CORP.
XX
PI Chantry DH, Hoekstra MF, Holtzman DA;
XX
DR MPI; 1998-322736/28.
XX
DR P-PSDB; AAW58570.
XX
PT New phosphatidylinositol 3-kinase catalytic subunit - used to
PT develop products for modulating kinase activity in immune system
PT signalling and in carcinogenesis
XX
PS Claim 4; Page 27-33; 53pp; English.
XX
XX
XX This full-length composite cDNA encodes the p110 delta catalytic
XX subunit (see AAW58570) of human phosphatidylinositol 3-kinase. It
XX was assembled from clone #249 obtained by PCR amplification (see
XX AAV31341-44) of human peripheral blood mononuclear cell cDNA, clone
XX #4928 obtained by screening a human macrophage cDNA library, and
XX further clones obtained by RACE and PCR (see AAV31345-50). The
XX following are claimed: (1) a purified and isolated polynucleotide
XX (PN) encoding p110 delta; (2) a vector comprising a DNA as in (1);
XX (3) a host cell stably transformed or transfected with a DNA as in
XX (1); (4) PN encoding a lipid kinase, and hybridizing to PN having
XX the 5220 bp sequence; (5) a purified and isolated p110 delta
XX polypeptide as in (4); (6) an antibody specifically immunoreactive
XX with p110 delta; (7) a hybridoma cell line (especially 208F
XX (HB 12200) producing a monoclonal antibody as in (6); and (8) a
XX humanized antibody as in (6). p110 delta has kinase activity and
XX may play a role in PI 3-kinase mediated signalling in the immune
XX system and in carcinogenesis. The products can be used to develop
XX agents that modulating p110 delta kinase activity and to develop
XX diagnostic reagents (claimed). They may also be used for detection
XX and diagnosis of p110 delta in a biological sample.
XX
SQ Sequence 5220 BP; 1120 A; 1525 C; 1483 G; 1092 T; 0 other;
Query Match 10.5%; Score 336.2; DB 19; Length 5220;
Best Local Similarity 53.5%; Pred No. 1,7e-82;
Matches 804; Conservative 0; Mismatches 678; Indels 21; Gaps 4;
QY 1682 TCCCGAATTTCTACCAATTTGCTCTGTTAAATGGAATCTTAGATGAAGTAG 1741
Db 1820 TCCGGAGGGCGCTAGCCGGCTGCTGTGTCACCAAGTGAACAAAGATGAGATGTGG 1879

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QY 1742 CTCAGATGACTGCTTGGTAAAGATTGGCTCCATCAAGCCTGAACAGGCTATGAGC 1801  
 DB 1880 CCCAGATGCTTACCTGCTGTGTCTCTGGCCGAGCTGCCCTCTGAGCCCTTGAGC 1939  
 QY 1802 TTCTGACAGCAATTAACCCAGATCTATGATTCGAGGTTTGTGTTCCGCTTAGAA 1861  
 DB 1940 TCGTAACTTCAAGCTTCCCGATTCGACGTAAGCTCTTCGCAATCAAGTGGCTCGGA 1999  
 QY 1862 AATATTAAAGATGAACAACCTTCTCACTACCTAATCACTAGTACAGGTAATTAAT 1921  
 DB 2000 AAC--TGACGAGCAATGAGCTGTTCAGTACCTGTGACGTGTGACAGTGTCAAGT 2056  
 QY 1922 ATGACAGATTTGGATTAACCTGCTGTGTGATTTTCTACCAAAAAGCTTAATATC 1981  
 DB 2057 ACAGATCTTACCTGACCTGACGCTGACCAATTTCCGTGACCCGGCCCTGCAACC 2116  
 QY 1982 AAGGATCGGTCTCTTTTGGCATTTAAATGTGATGCAACATMAAACAGTTA 2041  
 DB 2117 GCAGATCGGCACTTCTTTCTTGACCTCCGCTCCGAGATGCAAGTGCCTGGTGG 2176  
 QY 2042 GTCAGAGTTGGCTGCTTTTGGAGTCTATTGCTGCTGATGAGATGTATCTGAGC 2101  
 DB 2177 CCTGCGCTTCGGCTCATCTGAGGCTTACTCAGGGGACACCCACATGAAGG 2236  
 QY 2102 ACCTTAATAGCAAGTTGAGGCTATGAAAAGCTCATTAACCTTGAATCTCAAC 2161  
 DB 2237 TGTGATGAAGCAGGGGAGCACTGAGCAAACTGAAGGCCCTTAATGACTTCTCAAGC 2296  
 QY 2162 AAGGAAAGGATGAACAACAAGGATGAGATGAAATTTTATTGAGCAAAATGCGGC 2221  
 DB 2297 TGACCTCTCAAGAACCCCAAGCCCCAGACCAAGAGCTATGCACTTGTGATGCGGC 2356  
 QY 2222 GACCAGATTTGATGATGCTCTCAAGGCTTCTGTCTCTCTAAACCTCTCATAGC 2281  
 DB 2357 AGGAGGCTTACTAGAGGCCCTCTCCACCTGCACTGCCCACTGACCCCAAGCCTGTC 2416  
 QY 2382 TGGGAATCTGAGGCTTGAAGATGTCGAATATGTCTTCTGCAAAAAGGCCACTGTGGT 2341  
 DB 2417 TGGTGAAGTCTGCTGAGAGTGCACCTTCATGACTCCAAATGAAGCCCTGTGGA 2476  
 QY 2342 TGAATTTGGGAACCCAGACATCATGTCAAAATTAATCTCTTTCAGAAATGAGATCAT 2401  
 DB 2477 TCATGTACAGCAACGAGAG-----GCAGGACGCGCGGCGGCTGCTCATCT 2527  
 QY 2402 TTAATAATGGGATGATTTACGCAAGATATGTAACCTTCAATTAATGCAATATG 2461  
 DB 2528 TTAAGAACGGGATGACCTCCGAGGACATGCTGACCTGCAATGATCCAGCTCATGG 2587  
 QY 2462 AAAATATCTGGCAAAATCAAGTCTTGATCTTCGAATTTTACTTAATGATGCTGTCA 2521  
 DB 2588 ACGTCTGTGGAAGCAGAGGGGCTGACCTGAGATGACCCCTATGCTGCTGCCCA 2647  
 QY 2522 TGGGTACTGTGTGGACTTATCGAGGTGTGAATTTCTCACTATATGCAATTC 2581  
 DB 2648 CCGGGGACCGCACAGGCTCATTTGAGTGTACTCCGTTCAAGACCAATGCCAATCC 2707  
 QY 2582 A---GTGTAAGGAGGCTGAAAGTGAAGTGCATGCAATTTAACGCAACACTCCATCAGT 2638  
 DB 2708 AACTCAACAGACCAATGCGACGACGCGCTTCAACAGAGATGCCCTGCTCAACT 2767  
 QY 2639 GGCTCAAGACAAACAAAGGGGAAATATATATGATGCGGCAATGTTGTTTACAGAT 2698  
 DB 2768 GGTGAAGTCAAGAACCCGGGGAGGCCCTGATGAGGCAATGAGAGTTCACTCT 2827  
 QY 2699 CATGTCTGATATGTGTGTCCACCTTCAATTTTGGATTTGAGATGCTCAATATGTA 2758  
 DB 2828 CCGTGTCTGCTATTTGTGTGGCCCATATATGCTGGCAATTTGGCATGGCACAGGACA 2887  
 QY 2759 ATATCATGTTAAAGATGATGACAACTGTTTCAATATAGATTTGACACTTTTGGATC 2818  
 DB 2888 ACATCATGATCCGAGAGTGGGCACTGTTCCATTTGATTTTGGCACCTTCTGGGGA 2947

QY 2819 ACAAGAGAAAAATTGTTATTAACGAGAGCCGCTGCCGTTTGTTTGACACAGATT 2878  
 DB 2948 ATTCAAGACCAAGTTTGAATCAACCGGAGCGGTGTCATTCCTCACCTATGACT 3007  
 QY 2879 TCTTAATAGTATTAAGTAAGGAGCCAAAGATGCAAAAGACAAAGAAATTTGAGAGT 2938  
 DB 3008 TTGTCCATGTGATTCAGCAGGG-----GAAGACTAATATATAGTGAATAATTTGAACGT 3061  
 QY 2939 TTCAAGATGTGTTTCAAGGCTTATCTAGCTATTGGCAGCATGCAATCTCTTCAATTA 2998  
 DB 3062 TCCGGGGCTACTGTGAAGGGGCTTACACCATCTCGGGGCCACGGGCTTCTCTCTCC 3121  
 QY 2999 ATCTTTTCTCAATGATGCTTGTGCTCTGAGATGCCAGAACTGCAATCTTTGATGATTTG 3058  
 DB 3122 ACCCTTTGCCCTGATGCGGGGCGGACGCTGAGCTGAGCTGCTCAAAAGACATCC 3181  
 QY 3059 CATACATTTGAAAGACCTTAGCTTTAGATAAACTGAGCAAGAGCTTTGGATTTTCA 3118  
 DB 3182 AGTATCTCAAGACTCCCTGGCACTGGGAAAAACAGAGAGAGGACATGAAGCACTTCC 3241  
 QY 3119 TGAACAAATGAATGATGACACCATGCTGCTGCAACAAATGATGATGATCTTCC 3178  
 DB 3242 GAGTGAAGTTTAAGAGCCCTCCGTGAGAGCTGGAAGAACAAATGAACTGGCTGCCCC 3301  
 QY 3179 ACA 3181  
 DB 3302 ACA 3304

Search completed: November 7, 2003, 06:18:17  
 Job time : 556.733 secs

GenCore version 5.1.6  
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# OM nucleic - nucleic search, using sw model

Run on: November 7, 2003, 04:09:02 ; Search time 7715.41 Seconds

(without alignments)  
17004.573 Million cell updates/sec

Title: US-09-325-095-35

Perfect score: 3207

Sequence: 1 ATGCTTCACAGACCATCATC.....AGCAGCATGCTTGAACTGA 3207

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 segs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pln:\*

35: em\_htg\_rtd:\*

36: em\_htg\_mam:\*

37: em\_htg\_vrt:\*

38: em\_sy:\*

39: em\_htgo\_hum:\*

40: em\_htgo\_mus:\*

41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3207	100.0	3207	4 BOVPHOS3KN	M93252 Bovine phop
2	3207	100.0	3207	6 A75936	A75936 Sequence 36
3	3207	100.0	3207	6 AR048987	AR048987 Sequence
4	3207	100.0	3207	6 AR064288	AR064288 Sequence
5	3207	100.0	3207	6 AR164681	AR164681 Sequence
6	3205.6	100.0	3498	6 A37232	A37232 Sequence 1
7	3024.6	94.3	3207	9 HSU79143	U79143 Human phosp
8	3011.8	93.9	3240	6 AR048986	AR048986 Sequence
9	3011.8	93.9	3240	6 AR064287	AR064287 Sequence
10	3011.8	93.9	3240	6 AR164680	AR164680 Sequence
11	3008.6	93.8	3412	6 A75939	A75939 Sequence 39
12	3008.6	93.8	3412	6 AR048985	AR048985 Sequence
13	3008.6	93.8	3412	6 AR064286	AR064286 Sequence
14	3008.6	93.8	3412	6 AR164679	AR164679 Sequence
15	3008.6	93.8	3424	6 AX327651	AX327651 Sequence
16	3008.6	93.8	3424	9 HSPH13K	Z29090 H.sapiens m
17	2642.2	82.4	3207	10 MMU03279	U03279 Mus musculu
18	2528	78.4	225277	2 AC129863	AC129863 Rattus no
19	2512.8	78.4	222974	2 AC127178	AC127178 Rattus no
20	2459.8	75.7	3452	5 AF001076	AF001076 Gallus ga
21	2419.2	75.4	3389	14 AF001075	AF001075 Avian sar
22	1660.6	51.8	2556	5 AF204924	AF204924 Xenopus 1
23	827.2	25.8	250250	2 AC097304	AC097304 Rattus no
24	703.4	21.9	873	10 AF395897	AF395897 Rattus no
25	448.2	14.0	3213	6 AR116356	AR116356 Sequence
26	448.2	14.0	3213	6 AX327653	AX327653 Sequence
27	448.2	14.0	3213	9 S67334	S67334 phosphatidy
28	410.6	12.8	3213	10 RNDU12482	AJ012482 Rattus no
29	344.8	10.8	137113	9 AC076966	AC076966 Homo sapi
30	344.8	10.8	152484	2 AC067992	AC067992 Homo sapi
31	343	10.7	3132	10 MMU6587	U86587 Mus musculu
32	336.2	10.5	3387	6 AR255866	AR255866 Sequence
33	336.2	10.5	3868	6 AX327647	AX327647 Sequence
34	336.2	10.5	3868	9 HSPH10DEL	Y10055 H.sapiens m
35	336.2	10.5	5220	6 AR026868	AR026868 Sequence
36	336.2	10.5	5220	6 AR086499	AR086499 Sequence
37	336.2	10.5	5220	6 AR281257	AR281257 Sequence
38	336.2	10.5	5220	6 AX287052	AX287052 Sequence
39	336.2	10.5	5220	9 HSU86453	U86453 Human phosp
40	329.8	10.3	4933	10 BC035203	BC035203 Mus muscu
41	323.4	9.6	4713	3 HSU57843	U57843 Human phosp
42	309.2	9.6	1287	3 DDU23476	U23476 Dictyostel
43	308.6	9.6	1287	3 AK115578	AK115578 Ciona int
44	308	9.6	182777	2 AC110034	AC110034 Mus muscu
45	308	9.6	223296	2 AC130281	AC130281 Mus muscu

## ALIGNMENTS

RESULT 1

BOVPHOS3KN 3207 bp mRNA linear MAM 27-APR-1993

LOCUS Bovine phosphatidylinositol 3-kinase 110 kDa subunit mRNA, complete

DEFINITION

ACCESSION M93252

VERSION M93252.1 GI:163519

KEYWORDS phosphatidylinositol 3-kinase.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bos.

REFERENCE 1 (bases 1 to 3207)

AUTHORS Hiles,I.D., Oteu,M., Volintu,S., Fry,M.J., Gout,I., Dhan,R.,





QY	1501	TCCTGGTAAGCAGGATTTAGTATTTCCATGCGAGACTGAGTAAAGACTAGTAGAGAC	1560
Db	1501	TCCTGGTAAGCAGGATTTAGTATTTCCATGCGAGACTGAGTAAAGACTAGTAGAGAC	1560
QY	1561	AATGAATTAAGGAAATAGATTAAGAAACAGCTCCGAGCAATTTGTATACAGATCTCTTA	1620
Db	1561	AATGAATTAAGGAAATAGATTAAGAAACAGCTCCGAGCAATTTGTATACAGATCTCTTA	1620
QY	1621	TCTGAATTCATCTGAGCAAGAGAAAGATTTCTGTGAGCCACAGCACTATTTGTATACT	1680
Db	1621	TCTGAATTCATCTGAGCAAGAGAAAGATTTCTGTGAGCCACAGCACTATTTGTATACT	1680
QY	1661	ATCCCCGAAATTCATCCCAAAATTCGTCTGTCTGTAAATGGAATCTTAGATGAAGTA	1740
Db	1661	ATCCCCGAAATTCATCCCAAAATTCGTCTGTCTGTAAATGGAATCTTAGATGAAGTA	1740
QY	1741	GCTCAGATGTACTGCTGTGTAAAGATTTGGGCTCCAAATCAAGCCGTGAACAGAGTAAGAG	1800
Db	1741	GCTCAGATGTACTGCTGTGTAAAGATTTGGGCTCCAAATCAAGCCGTGAACAGAGTAAGAG	1800
QY	1801	CTTTCGACTGCAATTAACCCAGATCCATATGAGTTGGCTGTTGGCTGCTTAA	1860
Db	1801	CTTTCGACTGCAATTAACCCAGATCCATATGAGTTGGCTGTTGGCTGCTTAA	1860
QY	1861	AAATTTTAAACAGATGACAAACTTTCTCAGTACCTAATTCAGTGTATCAGGTACTAAA	1920
Db	1861	AAATTTTAAACAGATGACAAACTTTCTCAGTACCTAATTCAGTGTATCAGGTACTAAA	1920
QY	1921	TATGAAACGTATTTGGATTAACCTGCTGTGAGATTTTAACTCAAAAAGCGTTAACTAAT	1980
Db	1921	TATGAAACGTATTTGGATTAACCTGCTGTGAGATTTTAACTCAAAAAGCGTTAACTAAT	1980
QY	1981	CAAGGATCGGTCACTTTTCTTTTGGCATTTAAATCTGAGATGCACAATTAACAAGTT	2040
Db	1981	CAAGGATCGGTCACTTTTCTTTTGGCATTTAAATCTGAGATGCACAATTAACAAGTT	2040
QY	2041	AGTCAGAGGTTGGCTCTCTTTGGAGTCTTAATTCGCGTGCATGTGGAGTATCTGAAG	2100
Db	2041	AGTCAGAGGTTGGCTCTCTTTGGAGTCTTAATTCGCGTGCATGTGGAGTATCTGAAG	2100
QY	2101	CACCTTAATTAGGCAAGTTGAGGCTATGGAAGAGCTCAATTAACCTGACTGACTTCTCAA	2160
Db	2101	CACCTTAATTAGGCAAGTTGAGGCTATGGAAGAGCTCAATTAACCTGACTGACTTCTCAA	2160
QY	2161	CAGAAGAAAGAGATGAAACACAACAAAGGTACAGATGAAAGTTTATGTTGAGCAATCGG	2220
Db	2161	CAGAAGAAAGAGATGAAACACAACAAAGGTACAGATGAAAGTTTATGTTGAGCAATCGG	2220
QY	2221	CGACCAAGATTTCAATGATGCTCTCCAGGCTTTCTGTCTCCCTTAAACCTGCTCATCAG	2280
Db	2221	CGACCAAGATTTCAATGATGCTCTCCAGGCTTTCTGTCTCCCTTAAACCTGCTCATCAG	2280
QY	2281	CTGGGAAATCTCAGGCTTTGAAAGAGTGTCTGAATTAATGTCTCTGCAAAAAGGCCACTGTGG	2340
Db	2281	CTGGGAAATCTCAGGCTTTGAAAGAGTGTCTGAATTAATGTCTCTGCAAAAAGGCCACTGTGG	2340
QY	2341	TTGGAATTTGGGAGAACCCAGACATCATGTCCAGAAATTAATCTTTTCAAGCAATGAGATATC	2400
Db	2341	TTGGAATTTGGGAGAACCCAGACATCATGTCCAGAAATTAATCTTTTCAAGCAATGAGATATC	2400
QY	2401	TTTAAAAATGGGGATGATTTACGGGCAAGATATGCTAACCCCTTCAGATTAATTCGATTATG	2460
Db	2401	TTTAAAAATGGGGATGATTTACGGGCAAGATATGCTAACCCCTTCAGATTAATTCGATTATG	2460
QY	2461	GAATAATATCTGGCAAAATCAAGGCTTGATCTTCGAAATGTTAACTTAATGATGTCTGTCA	2520
Db	2461	GAATAATATCTGGCAAAATCAAGGCTTGATCTTCGAAATGTTAACTTAATGATGTCTGTCA	2520
QY	2521	ATCGGTACTGTGTGGGACTTATGAGAGTGGTGAAGAAATTTCTCAACTATATATGCAGATT	2580
Db	2521	ATCGGTACTGTGTGGGACTTATGAGAGTGGTGAAGAAATTTCTCAACTATATATGCAGATT	2580
QY	2581	CAGTGTAAAGAGGCTTGAAAGGTGCACTGCAGTTTAAAGCCACAATCTCATCATGTG	2640

Dp	2591	CAGTGTAAAGGAGGCTTAAGAGTGCATCGACGTTTAAACCCACACCTCCATCAGTGG	2644
Qy	2641	CTCAAAAGCAGAAACAMGGGGGAAATATATGATGGCCATCGATTGTTTACACGATCA	2700
Dp	2641	CTCAAAAGCAGAAACAMGGGGGAAATATATGATGGCCATCGATTGTTTACACGATCA	2700
Qy	2701	TGTGCTGGATATTTGTTGTGCCACCTTCATTTTGGGAATTTGAGATTCGCACAAATGAT	2766
Dp	2701	TGTGCTGGATATTTGTTGTGCCACCTTCATTTTGGGAATTTGAGATTCGCACAAATGAT	2766
Qy	2761	ATCATGGTTAAAGATGATGACAACTGTTTCATATGATTTTGACACTTTTGGATCAC	2820
Dp	2761	ATCATGGTTAAAGATGATGACAACTGTTTCATATGATTTTGACACTTTTGGATCAC	2820
Qy	2821	AAGAGAGAAAAATTTGGTTATTAACAGAGGCGCGCTTGTTTGGACCAAGATTTC	2880
Dp	2821	AAGAGAGAAAAATTTGGTTATTAACAGAGGCGCGCTTGTTTGGACCAAGATTTC	2880
Qy	2881	TTAAATAGTATTTAGTAAAGAGCCCAAGATGACAAAGACMAGATTTTGAGAGTTT	2940
Dp	2881	TTAAATAGTATTTAGTAAAGAGCCCAAGATGACAAAGACMAGATTTTGAGAGTTT	2940
Qy	2941	CAGAGATGTGTTCAAGGCTTATCTGAGTATTTGGGACATGTCATCTTTATATAAT	3000
Dp	2941	CAGAGATGTGTTCAAGGCTTATCTGAGTATTTGGGACATGTCATCTTTATATAAT	3000
Qy	3001	CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACCTGCATCTTTTGATGATATTGCA	3060
Dp	3001	CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACCTGCATCTTTTGATGATATTGCA	3060
Qy	3061	TACATTGAAAGACCCCTGAGCTTTTGATATTAACCTGACAAAGGCTTTGGATATTTTATG	3120
Dp	3061	TACATTGAAAGACCCCTGAGCTTTTGATATTAACCTGACAAAGGCTTTGGATATTTTATG	3120
Qy	3121	AAACAAATGGAATGACACACCATGATGGCTGACACAAAAATGGAATTTGATCTTCAC	3180
Dp	3121	AAACAAATGGAATGACACACCATGATGGCTGACACAAAAATGGAATTTGATCTTCAC	3180
Qy	3181	ACAATTAGACGATGCTTTGAACATGA 3207	
Dp	3181	ACAATTAGACGATGCTTTGAACATGA 3207	

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	FEATURES
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AUTHORS	Hiles, I. D. and Fry, M. J.						
TITLE	POLYPEPTIDES HAVING KINASE ACTIVITY, THEIR PREPARATION AND USE						
JOURNAL	Patent: WO 93131328-A 36 28-OCT-1993.						
	LUDWIG INST CANCER RES (GB); HILES IAN D (GB)						
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[illegible]

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 ORGANISM Unknown.  
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 AUTHORS Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J.,  
 Otsu, M., Paneyoutou, G., Volinia, S. and Gout, I.,  
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DEFINITION Sequence 35 from patent US 5846824.  
ACCESSION AR064288  
VERSION AR064288.1 GI:5993596  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 3207)  
AUTHORS Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J.,  
Oesu, M., Parayoutou, G., Volinia, S. and Gout, I.  
TITLE Polypeptides having kinase activity, their preparation and use  
JOURNAL Patent: US 5846824-A 35 08-DEC-1998;  
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Source 1. 3207  
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BASE COUNT 1028 a 581 c 680 g 918 t  
ORIGIN

Query Match 100.0%; Score 3207; DB 6; Length 3207;  
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Matches 3207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 3207)  
AUTHORS Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J., Otsu, M., Panayotou, G., Volinia, S. and Gout, I.,  
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OR PROTEIN KINASE AND ASSAYS USING THEM
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 complete cds.  
 ACCESSION U79143

VERSION U79143.1 GI:1763625  
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 SOURCE Homo sapiens  
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 REFERENCE 1 (bases 1 to 3207)  
 Oliff, A. and Heimbrock, D.C.  
 Cloning and mutagenesis of the p110 alpha subunit of human phosphoinositide 3'-hydroxylase  
 Bioorg. Med. Chem. 5 (1), 65-74 (1997)  
 JOURNAL 97196568  
 MEDLINE 9043658  
 PUBMED 2 (bases 1 to 3207)  
 Stirdivant, S.M., Ahern, J., Conroy, R.R., Barnett, S.F., Ledder, L.M., Oliff, A. and Heimbrock, D.C.  
 REFERENCES  
 AUTHORS Direct Submission  
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Db      3121 AAACAAATGATATGATGACACCATGCTGTGAGCAACAAATATGATGATCTTCCAG 3180
Qy      3181 ACAATTTAGCAGATGCTTTGAATCTGA 3207
Db      3181 ACAATTTAGCAGATGCTTTGAATCTGA 3207

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RESULT 8
AR048986 3240 bp DNA linear PAT 29-SEP-1999
LOCUS AR048986
DEFINITION AR048986
ACCESSION AR048986
VERSION AR048986.1 GI:6005025
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 3240)
AUTHORS Hiles, I. D., Fry, M. J., Dhand, R., Waterfield, M. D., Parker, P. J.,
Osbu, M., Panayotou, G., Volinia, S. and Gout, I.
TITLE Polypeptides having kinase activity, their preparation and use
JOURNAL Patent: US 5824492-A 34 20-OCT-1998;
FEATURES Location/Qualifiers
Source 1. .3240

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BASE COUNT 1057 a 582 c 682 g 919 t
ORIGIN
Query Match 93.9%; Score 3011.8; DB 6; Length 3240;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 3085; Conservative 0; Mismatches 122; Indels 0; Gaps 0;
/organism="unknown"
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Db      1 ATGCTCCAAAGACCATCATCAGTGAACCTGTGGGGCATCCATGATGCCCCCAAGATC 60
Qy      61 CTAGTGAATGTTTACTTACCAATGAGATGATGATGATGATGATGATGATGATGATGATG 120
Db      61 CTAGTGAATGTTTACTTACCAATGAGATGATGATGATGATGATGATGATGATGATGATG 120
Qy      121 ACCTTAATACGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Db      121 ACCTTAATACGATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Qy      181 CTTCTTCAGATGATCTTCTTCACTTTTCTGATGATGATGATGATGATGATGATGATGAT 240
Db      181 CTTCTTCAGATGATCTTCTTCACTTTTCTGATGATGATGATGATGATGATGATGATGAT 240
Qy      241 GAAATTTTGTATGAACAAAGACGATTTGATGATGATGATGATGATGATGATGATGATG 300
Db      241 GAAATTTTGTATGAACAAAGACGATTTGATGATGATGATGATGATGATGATGATGATG 300
Qy      301 GTAATTGAACAGTAGGCAACCGTGAAGAAAGATCTCAATGAGAAATGTTGTTGCT 360
Db      301 GTAATTGAACAGTAGGCAACCGTGAAGAAAGATCTCAATGAGAAATGTTGTTGCT 360
Qy      361 ATGGGATGCGCATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db      361 ATGGGATGCGCATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Qy      421 AGAAATTTCTCAATGTTTGAAGAGAGCTGTGATGATGATGATGATGATGATGATGATG 480
Db      421 AGAAATTTCTTAAATGTTTGAAGAGAGCTGTGATGATGATGATGATGATGATGATGAT 480
Qy      481 AGTAGACCAATGATGTTTATCTCTCAATGATGATGATGATGATGATGATGATGATGATG 540
Db      481 AGTAGACCAATGATGTTTATCTCTCAATGATGATGATGATGATGATGATGATGATGATG 540
Qy      541 ATATATTAATTAATGATTAAGGCAATTAATAGTGTGATGATGATGATGATGATGATG 600
Db      541 ATATATTAATTAATGATTAAGGCAATTAATAGTGTGATGATGATGATGATGATGATG 600
Qy      601 AATATGACAAAGAGATGATCTGAAATCAACATGATGATGATGATGATGATGATGATG 660
Db      601 AATATGACAAAGAGATGATCTGAAATCAACATGATGATGATGATGATGATGATGATG 660
Qy      661 ATTGCTGAAGCATCAGAAAAAACTGAGATGATGATGATGATGATGATGATGATGATG 720
Db      661 ATTGCTGAAGCATCAGAAAAAACTGAGATGATGATGATGATGATGATGATGATGATG 720
Qy      721 CTGTGTGTTTGAATATCAGGCAAGTATTTTAAAGGTGTGATGATGATGATGATGATG 780
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Qy      781 TTCTTGAAGAAATATCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 840
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Qy      841 AGGATGCCCAATTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 900
Db      841 AGGATGCCCAATTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 900
Qy      901 TGTTTTAAACATCATATATCCAGAGCATCTCCAGCTACAGCTACAGCTACAGCTACAG 960
Db      901 TGTTTTAAACATCATATATCCAGAGCATCTCCAGCTACAGCTACAGCTACAGCTACAG 960
Qy      961 GAAACATCTACAAATTCCTTTGGTTATTAATGATGATGATGATGATGATGATGATGAT 1020

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D	961	GAACATCTACAAATCCCTTTGGGTTATTAATAGAGACTCAGATAAAAAATCTTTGCT	1020
Q	1021	GCAACCTATGTGAATGTAATATTCGAGACATTCGACAAGATTATATGTCGAA	1080
D	1021	GGAACCTATGTGAATGTAATATTCGAGACATTCGACAAGATTATATGTCGAA	1080
Q	1081	TACCATGAGAGAAACCTTATGTGATAATGTGAACACTCAAGAATACCTTTCCAT	1140
D	1081	TACCATGAGAGAAACCTTATGTGATAATGTGAACACTCAAGAATACCTTTCCAT	1140
Q	1141	CCGAGTGGAAATGAGTGTGAATACGATATATACATTCCTGATTTCTCTGCTGCT	1200
D	1141	CCGAGTGGAAATGAGTGTGAATACGATATATACATTCCTGATTTCTCTGCTGCT	1200
Q	1201	CGACTTGGCTTTCCATTGTTCTGTAAAGGCGGAAAGGAGTGTAAAGAGGACACTGT	1260
D	1201	CGACTTGGCTTTCCATTGTTCTGTAAAGGCGGAAAGGAGTGTAAAGAGGACACTGT	1260
Q	1261	CCATTGGCTGGGAAATATAAACCTTGTTGATTACAGAGACACTCTAGTATCTGAAAA	1320
D	1261	CCATTGGCATGGGAAATATAAACCTTGTTGATTACAGAGACACTCTAGTATCTGAAAA	1320
Q	1321	ATGGCTTGAATCTTTGGCCAGTACCTCATGAGACTAGAAAGATTGCTGAACCTTATGGT	1380
D	1321	ATGGCTTGAATCTTTGGCCAGTACCTCATGAGATTAGAAAGATTGCTGAACCTTATGGT	1380
Q	1381	GTATCTGATCAAAATCCAAATTAAGAACTCCATGTTTAAAGTTGAAAGTTGACGTGTC	1440
D	1381	GTATCTGATCAAAATCCAAATTAAGAACTCCATGTTTAAAGTTGAAAGTTGACGTGTC	1440
Q	1441	AGCAGTGTGTAAAGTTTCCAGATATGTCAGTATGGAAGCATGCCAATTGCTGTATA	1500
D	1441	AGCAGTGTGTAAAGTTTCCAGATATGTCAGTATGGAAGCATGCCAATTGCTGTATA	1500
Q	1501	TCCCGTGAAGAGATTATGTTATTCATGTCAGAGACTGAGTACAGACTAGCTAGAGAC	1560
D	1501	TCCCGTGAAGAGATTATGTTATTCATGTCAGAGACTGAGTACAGACTAGCTAGAGAC	1560
Q	1561	AATGATTTAAGAGAAATGATTAAGAACAGCTCCGAGCAATTTGTACACGAGATCTCTTA	1620
D	1561	AATGATTTAAGAGAAATGATTAAGAACAGCTCCGAGCAATTTGTACACGAGATCTCTTC	1620
Q	1621	TCTGAATCACTGACAGAGAAAGATTTCTGTGAGCCACAGACACTATTTGTGTAAT	1680
D	1621	TCTGAATCACTGACAGAGAAAGATTTCTATGSACTCACAGACACTATTTGTGTAAT	1680
Q	1681	ATCCCCGAAATTTTACCCAAATGCTGCTGTCTGTAAATGGAATCTTAGAGATGAAGTA	1740
D	1681	ATCCCCGAAATTTTACCCAAATGCTGCTGTCTGTAAATGGAATCTTAGAGATGAAGTA	1740
Q	1741	GCTCAGATGTACTGCTGGTAAAGATTGGGCTCCAAATCAAGCCCTGAAACAGGCTATGGAG	1800
D	1741	GCCCAAGATGTACTGCTGGTAAAGATTGGGCTCCAAATCAAGCCCTGAAACAGGCTATGGAA	1800
Q	1801	CTTCTGACATGCAATTAACCCAGATCTTATGAGTGTGGAGTTTGTCTGCTGCTGAGAA	1860
D	1801	CTTCTGACATGTAATTAACCCAGATCTTATGAGTGTGGAGTTTGTCTGCTGCTGAGAA	1860
Q	1861	AAATATTTTACAGATGACAACTTTCTCAGTACCTAATTCAGTATGACAGTACTAAA	1920
D	1861	AAATATTTTACAGATGACAACTTTCTCAGTATCTAATTCAGTATGACAGTACTAAA	1920
Q	1921	TATGACAGATTTGGATTAACCTGCTGTGAGATTTTAACTCAAAAAGCTTAACTAAT	1980
D	1921	TATGACAGATTTGGATTAACCTGCTGTGAGATTTTAACTCAAAAAGCTTAACTAAT	1980
Q	1981	CAAGGATCGGTCACTTTTCTTTGGCATTTAAATCTGAGATGACAAATTAACAGTT	2040
D	1981	CAAGGATTTGGGCACTTTTCTTTTGGCATTTAAATCTGAGATGACAAATTAACAGTT	2040
Q	2041	AGTGAAGGTTTGGCTGCTTTTGGAGTCTATTGGCCGTGATGTGGATGATCTGAAG	2100
D	2041	AGTGAAGGTTTGGCTGCTTTTGGAGTCTATTGGCCGTGATGTGGATGATCTGAAG	2100
D	2041	AGCCAGAGTTTGGCTGCTTTTGGAGTCTATTGTCGTGATGTGGAGTGAATTTGAAG	2100
Q	2101	CACCTTAATPAGGCAAGTTGAGGCTATGGAAGAAAGCTATTAATCTTACATGACATTTCCAAA	2160
D	2101	CACCTTAATPAGGCAAGTTGAGGCAATGGAAGAAAGCTATTAATCTTACATGACATTTCCAAA	2160
Q	2161	CAGAGAGAGAGATGAAACAAAGAGTACAGATGAAGTTTGTGAGCAAAATGGG	2220
D	2161	CAGAGAGAGAGATGAAACAAAGAGTACAGATGAAGTTTGTGAGCAAAATGGAG	2220
Q	2221	CGACCAATTTTCAAGATGCTCTCCAGGCTTTTCTGCTCCTTAAACCTGCTCATCAG	2280
D	2221	CGACCAATTTTCAAGATGATGAGGCTTACAGGCTTGTCTCTCTTAAACCTGCTCATCA	2280
Q	2281	CTGGGAATCTCAGGCTTGAAGAGTGTGAATTAATGCTTTCTGCAAAAAGGCCACTGGG	2340
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Q	2341	TTGAATTTGGAGAAACCCAGACATCATGTCAGAAATTAATCTTTTCAAGAACATGATCATC	2400
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D	2401	TTTAAAAATGGGATGATTTACGGCAAGATATGCTAACACTTCAAAATTAATCGATATATG	2460
Q	2461	GAAAAATCTGGCAAAATCAAGGCTTGTATCTTGAATGTTAATCTTATGATGATGTGTCA	2520
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D	2521	ATCGGTGACTGTGGGACTTATGAGGTGTGAGAAATTTCTCACATATATGACAGTT	2580
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Q	2641	CTCAAGACAAAGCAAGGAGGAAATATATATGTCGGCCATCGATTTGTTTACACGATCA	2700
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D	2701	TGCTGCTGATCTGTGTGTCACCTTCATTTTGGAAATTTGGAGATTCGCAATATGAT	2760
Q	2761	ATCATGTGTAAGATGATGACAACTGTTTCAATATGATTTTGGACAATTTTGGATCAC	2820
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D	2941	CAGGAGATGTTTAAAGAGCTTATCTAGCTATTTGGCAGATGCAATCTTTTCATTAAT	3000
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D	3001	CTTTTCTCAATGATGCTTGGCTCTGGAATCCAGAACTCAAAATCTTTTGTGATGATGCA	3060
Q	3061	TACATTTGAAAGACCTTAGCTTATGATTAATCTGAGCAAGAGCTTTGGAGTATTCATG	3120
D	3061	TACATTTGAAAGACCTTAGCTTATGATTAATCTGAGCAAGAGCTTTGGAGTATTCATG	3120
Q	3121	AAACCAATGAATGATGACATCATGTGTGCTGAGCAACAAAAATGATGATCTTCCAC	3180
D	3121	AAACCAATGAATGATGACATCATGTGTGCTGAGCAACAAAAATGATGATCTTCCAC	3180



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QY 1741 GCTCAGATGTAAGTCTTGGTAAAGATGGCTCCAAATCAAGCTGAACAGGCTATGAG 1800
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DB 1861 AAATATTTAAGATGACAAACTTCTCAGTACCTAATTCAGTACAGTAACTAAA 1920
QY 1921 TATGAACATATTTGGATTAACCTGCTTGTAGATTTTACTCAAAAAAGCGTTAACTAAT 1980
DB 1921 TATGAACATATTTGGATTAACCTGCTTGTAGATTTTACTCAAAAAAGCGTTAACTAAT 1980
QY 1981 CAAGAAGATGGTCACTTTTCTTTGGCATTAAATCTAGATGACCAATMAACAGTT 2040
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DB 2941 CAGAGATGTTTACAGAGGTTTATCTAGCTATTGCGGACAGATGCCAATCTTCAATAA 3000
QY 3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCCAAGCTGCAATCTTTGATGATATGCA 3060
DB 3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCCAAGCTGCAATCTTTGATGATATGCA 3060
QY 3061 TACATTCGAAGACCTTACCTTTAGTAAACTGACCAAGAGGCTTTGAGATTTTCATG 3120
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DB 3121 AAACAAATGAATGATGACACACATGGTGGCTGGACAAACAAATGGATGGATCTTCCAC 3180
QY 3181 ACAATTAACAGCATGCTTTGAACCTGA 3207
DB 3181 ACAATTAACAGCATGCTTTGAACCTGA 3207

RESULT 10
ARI64680 3240 bp DNA linear PART 17-OCT-2001
LOCUS ARI64680
DEFINITION Sequence 34 from patent US 6274327.
ACCESSION ARI64680
VERSION ARI64680.1 GI:16237790
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3240)
AUTHORS Hiles,I.D., Fry,M.J., Dhand,R., Waterfield,M.D., Parker,P.J.,
Otsu,M., Panayotou,G., Volinia,S. and Gout,I.
TITLE Polyepitides having kinase activity, their preparation and use
JOURNAL Patent: US 6274327-A 34 14-AUG-2001;
FEATURES
source 1..3240
location/Qualifiers
BASE COUNT 1057 a 582 c 682 g 919 t
ORIGIN
Query Match 93.9%; Score 3011.8; DB 6; Length 3240;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 3085; Conservative 0; Mismatches 122; Indels 0; Gaps 0;
QY 1 ATGCTCCCAAGACATCATCAGGTGAACGTGAGGCGATCCTTGATGCCCAAGATC 60
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DB 181 CTTCTCAAGATGATCTTCTTACATTTTCTGTAAGTTTACCAAGAGAGAAAGGGA 240
QY 241 GAATTTTGTGATGAACAAAGACGATTTGTGACCTTGGCTTTTCAACCTTTTAA 300
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QY 301 GTAAATTGAAACGATAGGCAACCGTGAAGAAAGATCTCAATCGAATAATGGTTTGGT 360  
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DB 421 AGAAATATTCCTCAATGTTTGTAAAGAGCTGTGATCTTAGGGATCTTAATTCACCTCAT 480  
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DB 1021 GCAACCTATGTAATGTAATAATTTGAGACATTTGACAGATTTATGTTGGAACAGGTATC 1080  
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DB 1141 CCCAGGTGAATGAATGCTGTAATTAAGATATATACATTTCTGATCTTCTGCTGCT 1200  
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DB 1201 CGACTTTGCTTTCCATTTGTTCTGTTAAAGGCTTAAAGGAACTG 1260  
QY 1261 CCATTGGCCTGGGAAATATAAATCTGTTGATTACACAGATCTCTAGTATCTGAAAA 1320  
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QY 1681 ATCCCGAAATTTCTACCAATTTGCTTGTCTGTTAAATGGAATCTGAGATGAGTA 1740  
DB 1681 ATCCCGAAATTTCTACCAATTTGCTTGTCTGTTAAATGGAATCTGAGATGAGTA 1740  
QY 1741 GCTCAGATGACTGCTTGTGTAAGAAATGAGCTCCCAATCAAGCTGAAGAGCTATGAG 1800  
DB 1741 GCTCAGATGACTGCTTGTGTAAGAAATGAGCTCCCAATCAAGCTGAAGAGCTATGAG 1800  
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AUTHORS Hiles,I.D. and Fry,M.J.  
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REFERENCE 1 (bases 1 to 3412)  
AUTHORS Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J.,  
Oseu, M., Panayotou, G., Volinia, S. and Gout, I.  
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## RESULT 13

AR064286

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

BASE COUNT

ORIGIN

Query Match

3412 bp DNA linear PAT 29-SEP-1999  
 Sequence 32 from patent US 5846824.

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Unknown.  
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Unclassified.  
 1 (bases 1 to 3412)

Hiles, I.D., Fry, M.J., Dhand, R., Waterfield, M.D., Parker, P.J.,  
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Polyepitopes having kinase activity, their preparation and use  
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Db 1693 ATCCCGCAAAATTTCTACCCAAATTTGCTGTCTGTAAATGGAATTTCTGAGATGAAGTA 1752  
Qy 1741 GCTCAGATGTACTGCTGTGTAAGATTTGGCCTCCAAATCAAGCTTGAAAGGCTATGAG 1800  
Db 1753 GCCCAGATGTAATGCTGTGTAAGATTTGGCCTCCAAATCAAGCTTGAAAGGCTATGAG 1812  
Qy 1801 CTTCTGGAAGTGAATTAACCCAGATCTTAAGTTGCGAGGTTTGTGCTGTGTAGAA 1860  
Db 1813 CTTCTGGAAGTGAATTAACCCAGATCTTAAGTTGCGAGGTTTGTGCTGTGTGTAGAA 1872  
Qy 1861 AAATATTTAAACAGATGACAACTTTCTCAGTACTAATCAGCTGATCAGGTAATCAAAA 1920  
Db 1873 AAATATTTAAACAGATGACAACTTTCTCAGTACTAATTTTATTTACAGCTGATCAGGTAAT 1932  
Qy 1921 TATGAACAGTATTTGATTAACCTGCTGTGTGAGATTTTATCTCAAAAAGCGTTAACTAAT 1980  
Db 1933 TATGAACAGTATTTGATTAACCTGCTGTGTGAGATTTTATCTCAAAAAGCATTTGACTAAT 1992  
Qy 1981 CAAAGAGATCGGCACTTTTCTTTTGGCAATTTAAATCTGAGATGCACAATTAACAGTT 2040  
Db 1993 CAAAGAGATTTGGCACTTTTCTTTTGGCAATTTAAATCTGAGATGCACAATTAACAGATT 2052  
Qy 2041 AGTCAGAGTTTGGCTGCTTTTGGAGTCTTAATGCTCCGTCAGTGGGAGTATCTGAAG 2100  
Db 2053 AGCCAGAGTTTGGCTGCTTTTGGAGTCTTAATTTGCTGCTGCTGGAGTATTTGAAG 2112  
Qy 2101 CACCTTAATAGGCAAGTTGAGGCTATGAAAAGCTCATTAACCTTGAAGTCAATTCCTCAA 2160  
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Db 2113 CACCTGAATAGGCAAGTCAGGCAATGGAAGAGCTCATTAACCTTAACATTTCTCAA 2172  
Qy 2161 CAGAGAAAGAGATGATAACCAAAAGGTATACAGATGAAGTTTATAGTGAAGAAATGCGG 2220  
Db 2173 CAGAGAGAGAGATGATAACCAAAAGGTATACAGATGAAGTTTATAGTGAAGAAATGAGG 2232  
Qy 2221 CGACCAATTTTCTGATGCTCTCCAGGCTTTCTGTCTCTCTAAACCTGCTCATCAG 2280  
Db 2233 CGACCAATTTTCTGATGATGCTCTCCAGGCTTTCTGTCTCTCTAAACCTGCTCATCAG 2292  
Qy 2281 CTGGGAATCTCAGGCTTGAAGATGTCGAATTTATGCTTCTGCAAAAAGGCCACTGTGG 2340  
Db 2293 CTAGGAACCTCAGGCTTAAAGATGTCGAATTTATGCTTCTGCAAAAAGGCCACTGTGG 2352  
Qy 2341 TTGAATTTGGAGAACCCCAACATCATGTGAATTACTCTTTCAGAACATGAGATCATC 2400  
Db 2353 TTGAATTTGGAGAACCCCAACATCATGTGAATTACTCTTTCAGAACATGAGATCATC 2412  
Qy 2401 TTTAAAAATGGGAGATTTTACGGCAAGATATGCTAACCCCTCAGATTAATTCGATTATG 2460  
Db 2413 TTTAAAAATGGGAGATTTTACGGCAAGATATGCTAACCTTCAATTTATGATTAATG 2472  
Qy 2461 GAAAAATCTGSCAAATCAAGCTCTGATCTTGAATGTTACCTTATGATGATGCTGTCA 2520  
Db 2473 GAAAAATCTGSCAAATCAAGCTCTGATCTTGAATGTTACCTTATGATGATGCTGTCA 2532  
Qy 2521 ATCCGATCTGTGTGGAATTTACAGTGTGTGAAGAAATTTCTCACATTAATGCAAT 2580  
Db 2533 ATCCGATCTGTGTGGAATTTACAGTGTGTGCAAAATTTCTCACATTAATGCAAT 2592  
Qy 2581 CAGTGTAAAGGAGGCTGAAAGTGCACTGCAAGTTTAAACGACACACACTCATGATGG 2640  
Db 2593 CAGTGTAAAGGAGGCTGAAAGTGCACTGCAAGTTTAAACGACACACACTCATGATGG 2652  
Qy 2641 CTCAAGACCAAGAGGAGGAAATATATGATGGGCAATGATTTGTTTCAAGATCA 2700  
Db 2653 CTCAAGACCAAGAGGAGGAAATATATGATGAGCATTGACCTGTTTCAAGATCA 2712  
Qy 2701 TGTGCTGATATTTGTTGCCACCTTCATTTGGGAATTTGAGATGCTCAATATGTAAT 2760  
Db 2713 TGTGCTGATATTTGTTGCCACCTTCATTTGGGAATTTGAGATGCTCAATATGTAAT 2772  
Qy 2761 ATCATGTTAAAGATGAGCAACATGTTTCAATATGATTTTGGACACTTTTGGATGAC 2820  
Db 2773 ATCATGTTAAAGATGAGCAACATGTTTCAATATGATTTTGGACACTTTTGGATGAC 2832  
Qy 2821 AAGAGAAAAAATTTGTTATTAACGAGAGCGCTGCCGTTGTTTGAACAAGATTTT 2880  
Db 2833 AAGAGAAAAAATTTGTTATTAACGAGAGCGTGCCGTTGTTTGAACAAGATTTT 2892  
Qy 2881 TTAATATGATTTAGTAAAGAGCCCAAGATGCAAAAGACAAAGAAATTTGAGAGGTTT 2940  
Db 2893 TTAATATGATTTAGTAAAGAGCCCAAGATGCAAAAGACAAAGAAATTTGAGAGGTTT 2952  
Qy 2941 CAGGAGATGTTTAAAGGCTTATCTAGCTATTCGCGAGATCCCAATCTCTTCAATAT 3000  
Db 2953 CAGGAGATGTTTAAAGGCTTATCTAGCTATTCGCGAGATCCCAATCTCTTCAATAT 3012  
Qy 3001 CTTTCTCAATGATGCTTGGCTGTGGAATGCGAGAACTGCAATCTTTGATGATTAATGCA 3060  
Db 3013 CTTTCTCAATGATGCTTGGCTGTGGAATGCGAGAACTGCAATCTTTGATGATTAATGCA 3072  
Qy 3073 TACATTTCAAAAGACCTTACCTTAGATTAACCTGCAAGAGGCTTTGAGATTTTCAATG 3132  
Db 3121 AAACCAATGAATGATGCAACACATGCTGGCAACCAAAAGATTTGATCTTCCAC 3180  
Qy 3133 AAACCAATGAATGATGCAACACATGCTGGCAACCAAAAGATTTGATCTTCCAC 3192  
Db 3181 ACAATTAAGCAGATGCTTTGAAGTGA 3207  
|||  
Db 3193 ACAATTAAGCAGATGCTTTGAAGTGA 3219  
|||

Wed Nov 12 14:55:42 2003

us-09-325-095-35.rge

Page 28

Search completed: November 7, 2003, 10:44:03  
Job time : 7725.91 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 6, 2003, 14:40:25 ; Search time 45 Seconds  
(without alignments)  
6130.183 million cell updates/sec

Title: US-09-325-095-37

Perfect score: 5709  
Sequence: 1 MPRPSSGELMGHLMPPRI.....GWTTKMDWIFHTIKOHALNX 1069

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: SPREMBL\_23:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*  
16: sp\_virus:\*  
17: sp\_bacteriophage:\*  
18: sp\_archaeophages:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	5545	97.1	1068	13	042391	042391 gallus gall
2	5443	95.3	1083	15	039483	039483 avian saeco
3	4104	71.9	852	13	09PTES	09PTES xenopus lae
4	1974	34.6	1064	11	08BT19	08BT19 mus musculu
5	1966	34.4	1043	11	08CU28	08CU28 mus musculu
6	1964.5	34.4	1037	11	08CI98	08CI98 mus musculu
7	1963	34.4	1047	11	08BS14	08BS14 mus musculu
8	1903.5	33.3	1068	4	000034	000034 mus musculu
9	1677.5	29.4	1088	5	P91634	000334 homo sapien
10	1527	26.7	291	11	Q91XL6	P91634 drosophila
11	1472.5	25.8	1102	4	Q9BEC8	Q91XL6 ractus norv
12	1472.5	25.8	1102	4	Q81V23	Q9BEC8 homo sapien
13	1467	25.7	1113	11	Q9EOL1	Q81V23 homo sapien
14	1049.5	18.4	1467	11	Q61182	Q9EOL1 mus musculu
15	1038.5	18.2	1509	11	Q61194	Q61182 mus musculu
16	1014.5	17.8	1686	4	000443	Q61194 mus musculu
						000443 homo sapien

17	859.5	15.1	318	11	Q9CTK7	Q9CTK7 mus musculu
18	859	15.0	1876	5	Q9VTN5	Q9VTN5 drosophila
19	804.5	14.1	286	4	Q9BFS4	Q9BFS4 homo sapien
20	751	13.2	1607	5	Q20187	Q20187 caenorhabdi
21	718	12.6	887	11	Q88763	Q88763 ractus norv
22	714	12.5	887	4	Q8NEB9	Q8NEB9 homo sapien
23	685	12.0	887	4	Q15134	Q15134 homo sapien
24	680.5	11.9	847	11	Q8R3S8	Q8R3S8 mus musculu
25	660	11.6	260	11	Q8CSQ7	Q8CSQ7 mus musculu
26	660	11.6	949	5	P91635	P91635 drosophila
27	657	11.5	949	5	Q9W1M7	Q9W1M7 drosophila
28	649	11.4	808	10	Q8GUA6	Q8GUA6 medicago tr
29	631.5	11.1	901	5	Q9TX17	Q9TX17 caenorhabdi
30	625.5	11.0	897	5	Q9XZRO	Q9XZRO caenorhabdi
31	624.5	10.9	813	10	Q8H1S8	Q8H1S8 brassica na
32	600	10.5	650	5	Q9TX16	Q9TX16 caenorhabdi
33	578.5	10.1	1016	3	Q9Y8E4	Q9Y8E4 picchia angu
34	554	9.7	499	10	Q8RXR0	Q8RXR0 arabidopsis
35	513	9.0	409	11	Q8CFP1	Q8CFP1 mus musculu
36	491.5	8.6	732	10	Q04269	Q04269 chlamydomon
37	478.5	8.4	1889	10	Q94H07	Q94H07 oryza sativ
38	477.5	8.4	273	5	Q9BLU5	Q9BLU5 leishmania
39	474	8.3	2051	10	Q9SCX1	Q9SCX1 arabidopsis
40	473	8.3	1308	5	Q8MYR7	Q8MYR7 drosophila
41	465	8.1	2160	5	Q9UIK8	Q9UIK8 drosophila
42	465	8.1	2178	5	Q9W4X4	Q9W4X4 drosophila
43	465	8.1	2178	5	Q9W4X4	Q9W4X4 oryza sativ
44	459.5	8.0	608	10	Q8LSD9	Q8LSD9 oryza sativ
45	442	7.7	1466	6	Q28925	Q28925 bos taurus

## ALIGNMENTS

RESULT 1  
042391 PRELIMINARY; PRT; 1068 AA.  
ID 042391  
AC 042391;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Phosphoinositide 3-kinase catalytic subunit.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=97334438; PubMed=9188528;  
RA Chang H.W., Aoki M., Fryman D., Auger K.R., Bellacosa A.,  
RA Tschilts P.N., Cantley L.C., Roberts T.M., Vogt P.K.;  
RT "Transformation of chicken cells by the gene encoding the catalytic  
RT subunit of PI 3-kinase."  
RL Science 276:1848-1850(1997).  
DR EMBL: AF001076; AB82534.1; --  
DR InterPro: IPR000008; C2.  
DR InterPro: IPR001263; PI3K.  
DR InterPro: IPR002420; PI3K\_C2.  
DR InterPro: IPR003113; PI3K\_p85B.  
DR InterPro: IPR000341; PI3K\_p85B.  
DR InterPro: IPR000403; PI3K\_p85B.  
DR InterPro: IPR000403; PI3K\_p85B.  
DR Pfam: PF00613; PI3K\_A; 1.  
DR Pfam: PF00792; PI3K\_C2; 1.  
DR Pfam: PF02192; PI3K\_p85B; 1.  
DR Pfam: PF00794; PI3K\_p85B; 1.  
DR Pfam: PF00454; PI3K\_p85B; 1.  
DR SMART: SM00239; C2; 1.  
DR SMART: SM00145; PI3K\_A; 1.  
DR SMART: SM00146; PI3K\_C2; 1.  
DR SMART: SM00147; PI3K\_C2; 1.  
DR SMART: SM00143; PI3K\_p85B; 1.

DR SMART; SM00144; PI3K\_rbd; 1.  
 DR PROSITE; PS00915; PI3\_4\_KINASE\_1; 1.  
 DR PROSITE; PS00916; PI3\_4\_KINASE\_2; 1.  
 DR PROSITE; PS50290; PI3\_4\_KINASE\_3; 1.  
 KM Kinase.  
 SQ SEQUENCE 1068 AA: 124287 MW: 9912A96B3397735E CRC64:

Query Match 97.1%; Score 5545; DB 13; Length 1068;  
 Best Local Similarity 96.4%; Pred. No. 0;  
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QY 1 MPPRPSGGLMGHMLMPRLIVLCLPNSMTVTECLREATLTITIKHELFKARKYPLDQ 60  
 DB 1 MPPRPSGGLMGHMLMPRLIVLCLPNSMTVTECLREATLTITIKHELFKARKYPLDQ 60  
 QY 61 LLODESSYIFVSVQAEAREEFDETRRLCDLRFQPLKVIIEPVGNREKILNREIGFA 120  
 DB 61 LLODESSYIFVSVQAEAREEFDETRRLCDLRFQPLKVIIEPVGNREKILNREIGFA 120  
 QY 121 IGMVCEFDWVCKDEVDFFRNILNVCKEAVDLRDLNSPHSRAMVYVYPNVSSPELPKH 180  
 DB 121 IGMVCEFDWVCKDEVDFFRNILNVCKEAVDLRDLNSPHSRAMVYVYPNVSSPELPKH 180  
 QY 181 IYNKLDKGOITIVYVWVSPNNDKOKYTLKINHCVPEQVIAEAIKKTRSEMLSSDQK 240  
 DB 181 IYNKLDKGOITIVYVWVSPNNDKOKYTLKINHCVPEQVIAEAIKKTRSEMLSSDQK 240  
 QY 241 LCVLEYOGKYLTKVCGDEYFLEKPLSQYKIRSCIMLGMPLMLMAKESLYSOLPMD 300  
 DB 241 LCVLEYOGKYLTKVCGDEYFLEKPLSQYKIRSCIMLGMPLMLMAKESLYSOLPMD 300  
 QY 301 CFIMPSSYRRIISTATPYMNGESTYKSLWVINSALRIKLCATYVNNIRIDIKIYRTGI 360  
 DB 301 CFIMPSSYRRIISTATPYMNGESTYKSLWVINSALRIKLCATYVNNIRIDIKIYRTGI 360  
 QY 361 YHGEPLCDNNTQVRVPCSNPRNMENLYDYIPLPRAALCLISGVKRGKAKXEHG 420  
 DB 361 YHGEPLCDNNTQVRVPCSNPRNMENLYDYIPLPRAALCLISGVKRGKAKXEHG 420  
 QY 421 PLAMGNINLFDYDPTLVSGKALNMPVPHGLEDLNPIGVTSNPNKEPCLBELPDMF 480  
 DB 421 PLAMGNINLFDYDPTLVSGKALNMPVPHGLEDLNPIGVTSNPNKEPCLBELPDMF 480  
 QY 481 SSVVKEPDMASYIEEHANMSVSRSEAGFSYSHAGLSNRLARDNELRENDYQOLRAITTRPL 540  
 DB 481 SSVVKEPDMASYIEEHANMSVSRSEAGFSYSHAGLSNRLARDNELRENDYQOLRAITTRPL 540  
 QY 541 SEITEQEKDFLMSHHYCVNTPELIPKLLSVKMSRDEVAVQWGLVDMWPIKPEQAME 600  
 DB 541 SEITEQEKDFLMSHHYCVNTPELIPKLLSVKMSRDEVAVQWGLVDMWPIKPEQAME 600  
 QY 601 LLDGNYPPMVGAFVRCLEKYLTDKLSQVLIQVQVLYKQYQYDNLVRFLLKALTN 660  
 DB 601 LLDGNYPPMVGAFVRCLEKYLTDKLSQVLIQVQVLYKQYQYDNLVRFLLKALTN 660  
 QY 661 QRIGFHFMHLKSEMHNTKVSQRFGLLESYCRACGMYLKHLNROVEAMEKILNTDILK 720  
 DB 661 QRIGFHFMHLKSEMHNTKVSQRFGLLESYCRACGMYLKHLNROVEAMEKILNTDILK 720  
 QY 721 OEKKEOTQVQMKFLVEQMRPDPMDALOGFISPLNPAHQNLNLEECRINSSAKRPLW 780  
 DB 721 OEKKEOTQVQMKFLVEQMRPDPMDALOGFISPLNPAHQNLNLEECRINSSAKRPLW 780  
 QY 781 LNMENPDISELLFQNNELIFKNGDDLRODMLTLQIRIMENIWNQOGDLMLPYGLS 840  
 DB 781 LNMENPDISELLFQNNELIFKNGDDLRODMLTLQIRIMENIWNQOGDLMLPYGLS 840  
 QY 841 IGDGVLGLLEVANSHTIMQIOCKGKGLAQLQNSHTLQWLKDKNGEITYDAIDLFTS 900  
 DB 841 IGDGVLGLLEVANSHTIMQIOCKGKGLAQLQNSHTLQWLKDKNGEITYDAIDLFTS 900  
 QY 901 CAGCYATITLIGIDRHANSINWKDGOFLHIDFGFLDHKKKKPKYKREKRPVLTQDF 960  
 DB 901 CAGCYATITLIGIDRHANSINWKDGOFLHIDFGFLDHKKKKPKYKREKRPVLTQDF 960

DB 901 CAGCYATITLIGIDRHANSINWKDGOFLHIDFGFLDHKKKKPKYKREKRPVLTQDF 960  
 QY 961 LVIISGAOECTTREFEERFOEMCYAYLAIRQHANLFINLPSMMLGSGMPELOSFDIA 1020  
 DB 961 LVIISGAOECTTREFEERFOEMCYAYLAIRQHANLFINLPSMMLGSGMPELOSFDIA 1020  
 QY 1021 YIRKTLALDTEQEALEYFMKQNDAHGGWTTKMDMIFHTIKOHALN 1068  
 DB 1021 YIRKTLALDTEQEALEYFMKQNDAHGGWTTKMDMIFHTIKOHALN 1068

RESULT 2  
 ID 039483 PRELIMINARY; PRT: 1083 AA.  
 AC 039483;  
 DT 01-JAN-1998 (TEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)  
 DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)  
 DE Gag-V-phosphoinositide 3-kinase catalytic subunit fusion protein (fragment).  
 GN Gag-V-p3K.  
 OS Avian sarcoma virus 16.  
 OC Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses.  
 OX NCBI\_Taxid=60629;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9733438; Pubmed=9188528;  
 RA Chang H.W., Aoki M., Fruman D., Auger K.R., Bellacosa A.,  
 RA Tsichlis P.N., Cantley L.C., Roberts T.M., Vogt P.K.;  
 RT "Transformation of chicken cells by the gene encoding the catalytic  
 RT subunit of p13-kinase."  
 RL Science 276:1848-1850(1997).  
 DR EMBL; AF001075; AAB62532.1;  
 DR InterPro; IPR000008; C2.  
 DR InterPro; IPR001263; PI3Ka.  
 DR InterPro; IPR002420; PI3K\_C2.  
 DR InterPro; IPR003113; PI3K\_p85B.  
 DR InterPro; IPR000341; PI3K\_ras\_bind.  
 DR InterPro; IPR000403; PI3\_P14\_kinase.  
 DR Pfam; PF00613; PI3Ka; 1.  
 DR Pfam; PF00792; PI3K\_C2; 1.  
 DR Pfam; PF02192; PI3K\_p85B; 1.  
 DR Pfam; PF00794; PI3K\_rbd; 1.  
 DR Pfam; PF00454; PI3\_P14\_kinase; 1.  
 DR SMART; SM00239; C2; 1.  
 DR SMART; SM00145; PI3Ka; 1.  
 DR SMART; SM00146; PI3K; 1.  
 DR SMART; SM00142; PI3K\_C2; 1.  
 DR SMART; SM00143; PI3K\_p85B; 1.  
 DR SMART; SM00144; PI3K\_rbd; 1.  
 DR PROSITE; PS00915; PI3\_4\_KINASE\_1; 1.  
 DR PROSITE; PS00916; PI3\_4\_KINASE\_2; 1.  
 DR PROSITE; PS50290; PI3\_4\_KINASE\_3; 1.  
 KM Kinase.  
 FT NON TER  
 SQ SEQUENCE 1083 AA: 125869 MW: 371EF7055A78ACB8 CRC64:

Query Match 95.3%; Score 5443; DB 15; Length 1083;  
 Best Local Similarity 95.9%; Pred. No. 0;  
 Matches 1012; Conservative 27; Mismatches 16; Indels 0; Gaps 0;

QY 14 HLMPPRIIVECLLPNGMTVTECLREATLTITIKHELFKARKYPLDQDESSYIFSV 73  
 DB 14 HLMPPRIIVECLLPNGMTVTECLREATLTITIKHELFKARKYPLDQDESSYIFSV 73  
 QY 29 HLMPPRIIVECLLPNGMTVTECLREATLTITIKHELFKARKYPLDQDESSYIFSV 88  
 DB 29 HLMPPRIIVECLLPNGMTVTECLREATLTITIKHELFKARKYPLDQDESSYIFSV 88  
 QY 74 TOEAREEFDETRRLCDLRFQPLKVIIEPVGNREKILNREIGFAIGMPCFEDWYKD 133  
 DB 74 TOEAREEFDETRRLCDLRFQPLKVIIEPVGNREKILNREIGFAIGMPCFEDWYKD 133  
 QY 89 TOEAREEFDETRRLCDLRFQPLKVIIEPVGNREKILNREIGFAIGMPCFEDWYKD 148  
 DB 89 TOEAREEFDETRRLCDLRFQPLKVIIEPVGNREKILNREIGFAIGMPCFEDWYKD 148  
 QY 134 PEVQDFRNILNVCKEAVDLRDLNSPHSRAMVYVYPNVSSPELPKHLYNKLKGOITIV 193  
 DB 134 PEVQDFRNILNVCKEAVDLRDLNSPHSRAMVYVYPNVSSPELPKHLYNKLKGOITIV 193  
 QY 149 PEVQDFRNILNVCKEAVDLRDLNSPHSRAMVYVYPNVSSPELPKHLYNKLKGOITIV 208  
 DB 149 PEVQDFRNILNVCKEAVDLRDLNSPHSRAMVYVYPNVSSPELPKHLYNKLKGOITIV 208

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QY 194 IMVIVSPNDKOKYTLKINHCVPEQVIAEAIIRKTKSMILSSQOLKCVLEFYQKXITLK 253
DB 209 IMVIVSPNDKOKYTLKINHCVPEQVIAEAIIRKTKSMILSSQOLKCVLEFYQKXITLK 268
QY 254 VCGDEYFLEKYPLOSXYKIRSCIMLGMPHLMMAKESLYSOLPMDCEFMPSYRRIST 313
DB 269 VCGDEYFLEKYPLOSXYKIRSCIMLGMPHLMMAKESLYSOLPMDCEFMPSYRRIST 328
QY 314 ATPYNGESTSKSLMVINSALRIKILCATYVNVNIRIDKIYVRTGIYHGGEPLCDNVNT 373
DB 329 ATPYNGEATKAKSLMTINSALRIKILCATYVNVNIRIDKIYVRTGIYHGGEPLCDNVNT 388
QY 374 QRPVCSNPRNEMNYITIPDLPRARLCLSTCSVKGKCAKEEHCPPLANGINLPDYT 433
DB 389 QRPVCSNPRNEMNYITIPDLPRARLCLSTCSVKGKCAKEEHCPPLANGINLPDYT 448
QY 434 DTLVSGMALNLMVPHGLDLNLPICVTSNPNKETPCLELEEDWSSVVKPFDMVIE 493
DB 449 DTLVSGMALNLMVPHGLDLNLPICVTSNPNKETPCLELEEDWSSVVKPFDMVIE 508
QY 494 EHAMSVSRBAGSYSHAGLSNRLARDNELRENDKEQLRAICTRDPLEITEQKDFLMS 553
DB 509 EHAMWTSIRBELGFVSYAGLSNRLARDNELRENDKEQLRAICTRDPLEITEQKDFLMS 566
QY 554 HRHVCVTIPILPKLLSVKNSPDVAOYQVCLVKNPPIKPEQAMELLDGNYDPVARG 613
DB 569 HRHVCVTIPILPKLLSVKNSPDVAOYQVCLVKNPPIKPEQAMELLDGNYDPVARG 628
QY 614 FAVRCLEKYLTDKLSQYLOLVOLKYEOYLDNLVRFILKRLTNORIGHFFHMLKS 673
DB 629 FAVRCLEKYLTDKLSQYLOLVOLKYEOYLDNLVRFILKRLTNORIGHFFHMLKS 688
QY 674 EMHNKTVSQRFGLLESYCRACGYLKLHNRQVAMEKILNLTDLKQEKDEFOYQOMK 733
DB 689 EMHNKTVSQRFGLLESYCRACGYLKLHNRQVAMEKILNLTDLKQEKDEFOYQOMK 748
QY 734 FLYEONRPRPMDALQGLSPDLNPAHOLGNRLBECRINSAGKPLMNMENPDIMSELL 793
DB 749 FLYEONRPRPMDALQGLSPDLNPAHOLGNRLBECRINSAGKPLMNMENPDIMSELL 808
QY 794 FQNNELIFKNGDDLROMLTLQIIRIMENIMONOGDLNMLPYCCLSIGCVGLIEVVRN 853
DB 809 FQNNELIFKNGDDLROMLTLQIIRIMENIMONOGDLNMLPYCCLSIGCVGLIEVVRN 868
QY 854 SHTIMOJQCKGKLGALQFNSHTLHOMLKDNKKEIYDAIIDLPTSCAGCYVATFLGI 913
DB 869 SHTIMOJQCKGKLGALQFNSHTLHOMLKDNKKEIYDAIIDLPTSCAGCYVATFLGI 928
QY 914 GDBHNSNIMYKDDQGLFHDGFHLDHKKKFGYKREBVPFVLTODELIVISKAQOECTK 973
DB 929 GDBHNSNIMYKDDQGLFHDGFHLDHKKKFGYKREBVPFVLTODELIVISKAQOECTK 988
QY 974 TREFERQEMCYAYLAIRQHANIFTLBSMILSGMPELOSPFDIYIRKTLALDKTEQ 1033
DB 989 TREFERQEMCYAYLAIRQHANIFTLBSMILSGMPELOSPFDIYIRKTLALDKTEQ 1048
QY 1034 EALEYFMKONDAHNGMTKMDIIFTIKOHALN 1068
DB 1049 EALEYFMKONDAHNGMTKMDIIFTIKOHALN 1083

```

## RESULT 3

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Q9PTES PRELIMINARY; PRT; 852 AA.
ID 09PTES;
AC 09PTES;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DE Phospholipase 3 kinase catalytic subunit (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.

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OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Distal nephron;
RA Al-Khalili O.K., Tran T., Eaton D.C.;
RT "Molecular cloning of Xenopus laevis phospholipase 3 kinase
  catalytic subunit mRNA."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Distal nephron;
RA Al-Khalili O.K., Eaton D.C.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF04924; AAF15300.1;
DR InterPro: IPR000008; C2.
DR InterPro: IPR001263; P13K.
DR InterPro: IPR002420; P13K_C2.
DR InterPro: IPR003113; P13K_p85B.
DR InterPro: IPR000341; P13K_rae_bind.
DR InterPro: IPR000403; P13_P14_kinase.
DR Pfam: PF00613; P13K.1.
DR Pfam: PF00792; P13K_C2.1.
DR Pfam: PF02192; P13K_p85B.1.
DR Pfam: PF00794; P13K_id.1.
DR Pfam: PF00454; P13_P14_kinase.1.
DR SMART: SM00239; C2.1.
DR SMART: SM00145; P13K.1.
DR SMART: SM00146; P13K.1.
DR SMART: SM00142; P13K_C2.1.
DR SMART: SM00144; P13K_Pbd.1.
DR PROSITE: PS00915; P13_4_KINASE_1; 1.
DR PROSITE: PS00916; P13_4_KINASE_2; 1.
DR PROSITE: PS50290; P13_4_KINASE_3; 1.
KW Kinase.
FT NON_TER 1
FT NON_TER 852
SQ SEQUENCE 852 AA; 98705 MW; 15C1F3CCDDE28884 CRC64;

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Query Match 71.9%; Score 4104; DB 13; Length 852;  
Best Local Similarity 89.6%; Pred. No. 3.6e-311;  
Matches 763; Conservative 43; Mismatches 46; Indels 0; Gaps 0;

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QY 84 DETRRLCDLRLPQPLKVLIEPVNGREKILNREIGFALIGMPVCEPDVMDKPEVODFFRNI 143
DB 1 DETRRLCDLRLPQPLKVLIEPVNGREKILNREIGFALIGMPVCEPDVMDKPEVODFFRNI 60
QY 144 LNVCKEAVDIRDINSFHSRAMVYVPPNVBSSPELPKHINYKLDKGOIIVIVIVSPND 203
DB 61 LNVCKDSVEIRDANGPISRALVYVPPNVBSSPELPKHIESKLDKGOIIVIVIVSPNNE 120
QY 204 KQVYTLKINHDCVPEQVIAEAIIRKTKSMILSSQOLKCVLEFYQKXITLKVCCDEYFLE 263
DB 121 KQVYTLKINHDCVPEQVIAEAIIRKTKSMILSSQOLKCVLEFYQKXITLKVCCDEYFLE 180
QY 264 KYPLSQYKIRSCIMLGMPHLMMAKESLYSOLPMDCEFMPSYRRISTARPYNGETS 323
DB 181 KYPLSQYKIRSCIMLGMPHLMMAKESLYSOLPMDCEFMPSYRRISTARPYNGETS 240
QY 324 TKSILWINSALRIKILCATYVNVNIRIDKIYVRTGIYHGGEPLCDNVNTQRPVCSNPRW 383
DB 241 AKSLWAINSTLRIRIKILMATYVNVNIRIDKIYVRTGIYHGVEPLCDNVNTQRPVCSNPRW 300
QY 384 NEWLNDIYIPDLPRARLCLSTCSVKGKCAKEEHCPPLANGINLPDYTDLVSGKML 443
DB 301 NEWLNDIYIPDLPRARLCLSTCSVKGKCAKEEHCPPLANGINLPDYTDLVSGKML 360
QY 444 NLMPVPHGLDLNLPICVTSNPNKETPCLELEEDWSSVVKPFDMVIEEHAMSVSR 503
DB 361 NLMPVPHGLDLNLPICVTSNPNKETPCLELEEDWSSVVKPFDMVIEEHAMSVSR 420
QY 504 AGFSYSYHAGLSNRLARDNELRENDKEQLRAICTRDPLEITEQKDFLMSHRHYCVTIE 563
DB 421 LGYVSHSGLSNRIYRENVRENDKEQLRAISNRDPLEITEQKDFLMSHRHYCVTIE 480

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QY 564 ILPKLLSVKMSRDEVAQMYCLVKDMPPIKEQAMELLDCNYDPDPMRGPAVFCLEKYL 623
D 481 VLSKLLSVKMSRDEVAQMYCLVKDMPPIKEQAMELLDCNYDPDPMRGPAVFCLEKYL 540
QY 624 TDDKLSQVLLQVLYKQEQYLDNLVRFLLKALTNQRIQHFFPMHLKSPHNKTVSQR 683
D 541 TDDKLSQVLLQVLYKQEQYLDNLVRFLLKALTNQRIQHFFPMHLKSPHNKTVSQR 600
QY 684 FGLLSEYCRACGMYLKLHNRQVEAMEKLINLTDLKQEKDETOYQOMKELVEOMBRPD 743
D 601 FGLLSEYCRACGMYLKLHNRQVEAMEKLINLTDLKQEKDETOYQOMKELVEOMBRPD 660
QY 744 FMDALQGFSLPNAHQIGNLRLBECRISSAKRPLMLNMPDMLSEFLFONNEIIFKN 803
D 661 FMDALQGFSLPNAHQIGNLRLBECRISSAKRPLMLNMPDMLSEFLFONNEIIFKN 720
QY 804 GDDLROMLTLQIIRIMENIWONQGLDRLM.PYGLSITGDCVGLIEVVRNSHTIMOQCK 863
D 721 GDDLROMLTLQIIRIMENIWONQGLDRLM.PYGLSITGDCVGLIEVVRNSHTIMOQCK 780
QY 864 GGLKALQFNSHTLHQLKDKNKGEIYDAIDLFTSCAGYCVATFVLIGDRHNSIMV 923
D 781 GGLKALQFNSHTLHQLKDKNKGEIYDAIDLFTSCAGYCVATFVLIGDRHNSIMV 840
QY 924 KDGOLFHIIDFG 935
D 841 KDGOLFHIIDFG 852

RESULT 4
Q8BT19 PRELIMINARY; PRT: 1064 AA.
ID Q8BT19 AC Q8BT19;
AC Q8BT19;
DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
DE Phosphatidylinositol 3-kinase catalytic subunit.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL: AK090116; BAC41102.1;
SQ SEQUENCE 1064 AA; 121753 MW; 3E96729B25C52D1C CRC64;

Query Match 34.6%; Score 1974; DB 11; Length 1064;
Best Local Similarity 39.4%; Pred. No. 6,8e-145;
Matches 440; Conservative 196; Mismatches 371; Indels 110; Gaps 23;

QY 1 MPPRRSSG-ELMGH---LMPRIIVECLPNGMVTLECLREATLITIKHLPKREARKY 56
D 1 MPPRRSSG-ELMGH---LMPRIIVECLPNGMVTLECLREATLITIKHLPKREARKY 60
QY 57 PLHQLLQDESSYIFVSVTOEAREEFDETRRLCDLRLPQPLKYLIEPVGNREKILNRE 116
D 61 PPHNLLMDLSDSYMFACVNTAVYBELDETRRLCDVRPLVLKCVTRSCDPAEK-LDSK 119
QY 117 IGFALGPVCFEDMVNDQPEVQDFRRNITLVNCKEAVDLRLNBSHSAAMYVPPNVASSSE 176
D 120 IGVRIKGIKHEFDALQDPEVNEFRRRKRFSEAKIQSLVGLSWIDWLKHTYTP--EHEPS 177
QY 177 LKXHTINKLKDGOIIVIVIVIVISPNNDKQYTLKINHDCVPEQVIAEAIKRTKRSMLSS 236
D 178 VLENEDKLYGKLVVAVHP---ENSQVFSQVSPNINPIKINELAIQKR----- 225
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QY 237 EQLKLCVLEYQK-----YILKYGCGDEYFLEKYPYLSQYKIRSCIMLGRPMILM 288
D 226 -----LITRGEDASPCDYLQVSGREYVFGHPLIQOYINCMNRLLPHFILV 278
QY 289 AKESLYSOLPMDCFTPSPYRRISTATPYMNGESTK---SLWVINSALRIKILCATYVN 345
D 279 ECKIKKMEQEMIALAEMINRNSNLP.LP.PPKTRVISHIWDNNNPQITLVKGN--K 336
QY 346 VNIRIDIKYVRFGIYHGGPPLCDNVNTQRPVCSNRR--KHEMNLYDIY.PDLPRARICL 404
D 337 LNTBEYTKVHVRAGLPHGTLLCTKVSSSEISGKNHINMEQLEFIDINICDLFRMARLCP 396
QY 405 SICS-----VGRGKAK-----EEHCPLANGINIFDYTDLVSGKALNTM 446
D 397 AVTAVALDKVTKSTKTINPSKYQTRKAGKAVYPAWNTVMFDRKQGRSDVILHSW 456
QY 447 -PYPHGLLEDLNPIGVTSNP-----NKEITPCELEFDWESSVVKFPDMGV 491
D 457 SSFPDELEMLNMGVQTQVPAENATLHITPEPKKQCPYPPFD-----KI 505
QY 492 IEHAWKSVSRKAGFSTSHAGLSNRLARDNELBNDKEQLALCTDPLSEITEQEKDFL 551
D 506 IERAAEIASGDSA--NVSRRGKKFLA-----VLKEJLDRPLSQCGENEMDLI 552
QY 552 WSHRHVC-VTIPELLPKLLSVKMSRDEVAQMYCLVKDMPPIKEQAMELLDCNYPPDM 610
D 553 WTLRQDCRENPPQSLPKLLSITKNNKLEDAVQALQIITPKLP.PREALELDFENYDQY 612
QY 611 VRGFAVRCLEKYLTDKLSQYLLQVLYKQEQYLDNLVRFLLKALTNQRIQHFFPMH 670
D 613 VREYAVGCL--ROMSDELSQYLLQVLYKQEQYLDNLVRFLLKALTNQRIQHFFPMH 671
QY 671 LKSEMNKTVSQRFGLLSEYCRACGMYLKLHNRQVEAMEKLINLTDLKQEKDETOYQ 730
D 672 LRSEVHTPAVSQGVGVLLEAVCRGSGVMKVLRSQVEALNKLKTLNLSILKLAVALKSRK 731
QY 731 QMKRLVQMRPDPMDALQGFSLPNAHQIGNLRLBECRISSAKRPLMLNMPDMLMS 790
D 732 GKEAMHTCLQSAVREKLSLQSPNPVLSLSELYVKCKYMSKMPFLW-----VYS 785
QY 791 ELFPONNE--IIFKNGDLRQDMLTLQIIRIMENIWONQGLDRLM.PYGLSITGDCVGLI 848
D 786 SRATGEDSVGIFKNGDGLRQDMLTLQIIRIMENIWONQGLDRLM.PYGLSITGDCVGLI 845
QY 849 EVVNSHTIMOQC-KGGLKALQFNSHTLHQLKDKNKGEIYDAIDLFTSCAGYCV 907
D 846 EVVNSTETIADIQUNSSNVATAFAFNKDALMLKEVNSGDDLRALIEFTLSCAGYCV 905
QY 908 TFIIGIGDRHNSIMVWDDQGLPHIDFGHFLDHKKKFGYKREVPVLVQDFLIVISKG 967
D 906 SYVLGIGDRHNSIMVWDDQGLPHIDFGHFLDHKKKFGYKREVPVLVQDFLIVISKG 965
QY 968 AOECKTREFRPOEMCYKAYLAIRQHANLFINLSMNLGSGMDELQSPDDIAYIRKTLA 1027
D 966 --KGNTEKFERPQCCDAVLILRRGNLFTLFAIMLTGLBELTSVKDIOQLXSLA 1023
QY 1028 LDKTQEALEYFMKMDAHHGWTTKMDYLFHTIKQ 1064
D 1024 LKSEEBALQKQKFDALRESWTTKVMMAHTVRK 1060

RESULT 5
Q8CJ28 PRELIMINARY; PRT: 1043 AA.
ID Q8CJ28 AC Q8CJ28;
AC Q8CJ28;
DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, last sequence update)
DE Phosphoinositide 3-kinase PI10delta.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129P2/Olaheis;  
RA MEDLINE=22160404; PubMed=12130661.  
RA Okenhang K., Bilancio A., Farjot G., Priddle H., Sancho S.,  
RA Besker E., Pearce W., Week S.E., Salpekar A., Waterfield M.D.,  
RA Smith A.J., Vanhaesebroeck B.,  
RT "Impaired B and T cell antigen receptor signaling in pl1delta PI 3-  
RT kinase mutant mice";  
RL Science 297:1031-1034(2002).  
RM EMBL; AF532989; AA05615.1; --  
KM Kinase.  
SQ SEQUENCE 1043 AA; 119712 MW; AD8DE07DF8F47795 CRC64;  
  
Query Match 34.4%; Score 1966; DB 11; Length 1043;  
Best Local Similarity 39.8%; Pred. No. 2.8e-144;  
Matches 430; Conservative 188; Mismatches 389; Indels 74; Gaps 19;  
  
QY 16 MP-----RILVECLPNCMIVTLECLREATLITIKHELFEARKYPLHQ 60  
DB 1 MPGVDCMEFMTKEESQSVVVDLPTGVYLNFPVSNANLSTIKOYLHRAQYEPFLH 60  
  
QY 61 LLODESSYIFVSVTOEAREBEPFBETRRLCDLRLFOPLKVIPEVGNREKILNREIGFA 120  
DB 61 MLSDEPARYVFTCVNQTAEQDELEDEORLDCIOFLPLRLVAREGDEVKILNSQISL 120  
  
QY 121 IGMVCEPDMVKDEVDQFRNIIINLVCEAVDLRLDLSPHRAMVYVPPNVESPELPK- 179  
DB 121 IKGKIHFDLSLRDEVDNDFRTKROFCCEAAHROQLGWEMLOYSPFQLEPARGWRA 180  
  
QY 180 ---HIYNKLDKQIIVIVIVSVSPNDKQKTYTLKINHDCVEQYIAEARIKTKTSMILSS 236  
DB 181 GLLVNSR-----ALVVVVKFEGSESESTFOVSTDMPLAMACLRKK-----A 225  
  
QY 237 EQLKCVLEVOGKYLTKVCGDEYFLEKYPISQYKTRISCTMLGRMPLMLAKESLYSQ 296  
DB 226 TVFPQPLVEQPEEYALQVNGRHEYLGNYPCHFOYICSLHSGILPLTWVHSSILAM 285  
  
QY 297 LPMOCFTMPSRSRISTATPYMNGETSKSLMVINSALRIKILCATYVNNIRIDIKIV 356  
DB 286 RDEGSNAPVOYOKPRAPRPPIPAKPPSSVSLMSLEQPFSEILIGRKVNADER--MKLV 343  
  
QY 357 RTGIYHGEPLCDVNTQV-PCSNPRNEMWNLDIYIPDLRAARLCTISV----- 409  
DB 344 QAGLFGHEMLCKTVSSSEVAVVCEPVMKQLEFDISCDLPRAKILCFALYAVVERAKK 403  
  
QY 410 --KGRKAKEHCHPLANGNINLPDYDTLVSGKALMLMP-VPHGLEDLNPIGVTSNP 466  
DB 404 ARSTFKKSKKADCPDIAMNMLFPYKQDKTGERCLVWMPSPVDEKGBLLNPAQTVAGNP 463  
  
QY 467 NKETPCLELEFDWSSVVKPPDMGVIEBHAWMSVREGFYSAGLSNRLARNEIREN 526  
DB 464 NTESAA-----ALVYLPE---VAHPYFALCKILELGNHGRGRIT--EEEL--- 508  
  
QY 527 DKEOLAICTRDPLSEITOEKDFLWMSRHVYCT-IPEILPKLITSVKMSRDEVAOMYC 585  
DB 509 ---QLRBILERRSGGELYEHKXDLVWKMREHVOHFEBALARLVLTKMKNHEVAVMLY 565  
  
QY 586 LVKMDPIKPEQAMLLDCNYPDMVGFVAVRCLKXYLTDKLSQYLLOLVOLKYEQYL 645  
DB 566 LLSGMPFLPYLSALELDFSPDCYVSPAIKSLRK-LTDEDLQYLLQVLQVLYKESYL 624  
  
QY 646 DNLIVRLTKKALTNQIIGFFPHLKSSEANKVVSQRFGLLESYCRACSMYIKHLNRQ 705  
DB 625 DCELTKFLGSAALNRRIGHFLFWHLRSEMHVPSVALRFGIMEAYCRGSHHKKVMKQ 684  
  
QY 706 VEAMEKILNITDLIOEKDETOKVOMKFLVEQ--MRPDMALAQGFSPLNPAHOLGNL 764  
DB 685 GEALSKALKANDPVKYSQ--KTTKPTKEMHNMCMRETYMEALSHSQSPDSTLLEEV 743  
  
QY 765 RLEBCRISSAKRPLMLNWNPNIMSELIFQNNEIFKNGDDLQDMLTLOIIRIMENIW 824

DB 744 CVEOCTFWDSSKMKPLMTMYSSEBAGSA---GNVGIIFKNGDILQDMLTLOIMQIMVLYM 800  
  
QY 825 QNOGLDRLMLPYGSLIGDCVGLLEVVRNRTIWOIQ-CGSLKGAQOFNSHTLHMKD 883  
DB 801 KQEBLDLRMPYVGLPLGDRGTGLLEVHSHSTIANIQLNKSNNMATAAFNDALLMLKS 860  
  
QY 884 KMKGEIYDAIDLTPRSACAGCVATFLLIGIDRRNSINMYDDQLPHIDFGFLDHKK 943  
DB 861 KNPBDAIDRAIEFTLSCAGCVATVYLGIDRRNSIMIRESCQLPHIDFGFLGNKPT 920  
  
QY 944 KEGYKRRRVPVLTQDPLVIVSKAGQECTYREERFOEMCYKALAIROHANLFINLFS 1003  
DB 921 KFGINRRRVFFILTYDFVHVHIOQ--KTNNSKEFERFGYCERAYTILRRHGLFLHLFA 978  
  
QY 1004 MMLGSGMPELOSFPDIYIKRTIALDKTEQALAEYFKOMNDAHGWTMKDIFHTIK 1063  
DB 979 LMRAGLPBESCKDIDQYLDKSLALGKTEEBALKHFRVKTPEALRESWKTQVNLHNVS 1038  
  
QY 1064 Q 1064  
DB 1039 K 1039

RESULT 6  
ID 08CI98 PRELIMINARY; PRT; 1037 AA.  
AC 08CI98;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DE Phosphatidylinositol 3-kinase catalytic delta polypeptide.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Salivary gland;  
RA Straubeberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC035203; AA035203.1; --  
KM Kinase.  
SQ SEQUENCE 1037 AA; 119130 MW; 4446B78B5F37A0E2 CRC64;  
  
Query Match 34.4%; Score 1964.5; DB 11; Length 1037;  
Best Local Similarity 40.1%; Pred. No. 3.6e-144;  
Matches 426; Conservative 189; Mismatches 389; Indels 59; Gaps 18;  
  
QY 20 ILVECLPNCMIVTLECLREATLITIKHELFEARKYPLHQLLQDESSYIFVSVTOEARE 79  
DB 12 VVVDFFLPTGVYLNFPVSNANLSTIKOYLHRAQYEPFLHMSDPEAVYFTCVNQTABQ 71  
  
QY 80 EEFEDETRRLCDLRLFOPLKVIPEVGNREKILNREIGFAIGMPVCEPDMVKDEVDQF 139  
DB 72 QLEDEQRRLCDIQFLPLVRLVAREGDRVKKLNSQISLILKIGHFPSLSDPEVND 111  
  
QY 140 RKNILNVCKEAVDLRLDLSPHRAMVYVPPNVESPELPK-----HIYNKLDKQIIVIV 195  
DB 132 RTKROFCCEAAHROQLGWEMLOYSPFQLEPARGWAGLRLVNSR-----ALL 183  
  
QY 196 VIVSPNNDKQKTYTLKINHDCVPEQVIAEATRKTRSMILSSBDLKVLEVOGKYLKYC 255  
DB 184 VNVKFGSESESTFOVSTDMPLAMACLRKK-----ATVFPQPLVEQPEEYALQVN 236  
  
QY 256 GCOEYFLEKYPISQYKTRISCTMLGRMPLMLAKESLYSOLPMDFTMPSYSRRISTAT 315  
DB 237 GRHEVLYGNVPLCHFOYICSLHSGILPLTWVHSSILAMRDEGSNAPVOYOKPRAPRP 286  
  
QY 316 PYMNGETSKSLMVINSALRIKILCATYVNNIRIDIKIVYRGYIHGGEPLCDVNTQV 375  
DB 297 PIPAKRPSSVSLMSLEQPFSEILIGRKVNADER--MKLVVAGLFGHEMLCKTVSSSE 354

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Qy 376 V-PCSNPRMNMELVNDIYIPDLPRARLCLISCSY-----KGRKAKEHCPILAMGN 426
Db 355 VNVSEBPWKORLEBDSVCLPRARLCPALYAVEAKARSTKSKSADCEPIAMAN 414
Qy 427 INLPDYDTDLVSGKALNLAMP-VPHGLEDLNPIGVTSNPNKETPCLLEBDFWSSVVK 485
Db 415 LMLDYDQDLKGTGRCLYMPVSPDEKCELLNPGATVANGNTSEAA-----ALVIY 466
Qy 486 FPDMSVIEEHANWSVREAGFSYSHAGSNFLARDNEIRENDKEQLRAICTRDLSETTE 545
Db 467 LPE---VAPHPVYFPALKEKILELGHNGRGRITTEEOU-----OLREILRRSGELYE 517
Qy 546 OEXOFELMHRHYCVT-IPEILPKLLSVKMSRDEVAQMYCLVCMPIKPEQAMELDLC 604
Db 518 HEKDLVWKRHEVDQHPPEALARLLVTKMNGHEVAQMLYILCSMPRLPVSALLELD 577
Qy 605 NYPDPWVGFVAVRCLEKYLTDKLSQYLLOLVQVLYKEQYLDNLVRLPKKALTNRIG 664
Db 578 SFPDCYVSFAIKSLRK-LTDELFQYLLQVLYQVLYKESYLDCELTFRILGRALANRIG 636
Qy 665 HFFPMHLKSEMNKTVSQRFGLLESYCRACGMYLKHLNROYEAMEKILNLTDLKQEK 724
Db 637 HFLFMHLSEMHVPSVALRFGIMEAYCRGSTHNMKVLKQGEALSKLALNDFVKVSSQ 696
Qy 725 DETQVQMKFLVEQ-MRRPDEMDALQGFSLPILNPAHQGNL-RLEBGRIMSARPLMLN 782
Db 697-KTKPQTKEMHMCROBTMEALSHLOSPLDPSLTLEBVCSTVQCTFPMOSKMPILIM 755
Qy 783 WENPDMSELLFONNEIFKNGDDLRODMTLQIIRIMENIWONQGLDRLMLPYGCLSIG 842
Db 756 YSSEAGSA---GNVGIIIFKNGDDLRODMTLQIMQLMDVLMKQGLDRLMTPYGCPLTG 812
Qy 843 DCVGLIEVVRNSHTTMOIQ-CGGLKALQFNSHTLHOMLKXKNGEYDAIDLFTSC 901
Db 813 DRTGLIEVVLHSDITANIQLNKSNAATPAFVKDALLMWLKSNGEALDRAIEBFTLSC 872
Qy 902 AGCVATATFLIGDHHNSIMWKDGOLEHIDFGHLOHKKKFGYKBERVVFVLTQFL 961
Db 873 AGCVATVVLGIDHNSDINIMRESGOLPHIDFGHFGFKFGKFGINERVPFILTDFV 932
Qy 962 IYISGAOECTKTREFEFOEMCYAYLAIROHANLFINLFSMELSGMPELOSFDIAY 1021
Db 933 HVIQOG--KTNSEKFERPRGVCERAYTLIRRHGILFHLFALMAAGIPELSCKDIOY 990
Qy 1022 IRTKLALDKTEQALEYFKQNDAHHGSGWTTKMDIHTTIQO 1064
Db 991 LKDSLALGKTEBEALKHFRVKFNEALRESWTKVWMLAHNVSK 1033

RESULT 7
QBSB14 PRELIMINARY; PRT; 1047 AA.
ID QBSB14;
AC QBSB14;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Phosphatidylinositol 3-kinase catalytic delta polypeptide.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Arter and vein;
RX MEDLINE=2354683; PubMed=1246851;
RA The PANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK040867; BAC30725.1;
SQ SEQUENCE 1047 AA; 120186 MW; 73654D27449A30B2 CRC64;

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Query Match 34.4%; Score 1963; DB 11; Length 1047;
Best local Similarity 39.6%; Pred. No. 4,8e-144;
Matches 429; Conservative 189; Mismatches 390; Indels 76; Gaps 19;

Qy 16 MPP-----RLVECLLPNGMTVTLBCLRENTVLTITIKELFKERKRYPLHQ 60
Db 1 MPPGVDCPMEFWTKEESQSVVVDVFLPTGVLYNFPVSRNMLSTIKQVLMHRAQYEFLH 60
Qy 61 LLODESSYIVSVTQAEAREEFDETRRLCDLRFQFELVAVIPVGNREKILNREIFA 120
Db 61 MLSPBEAVFTCVNQTAEQOELEDEORLCDIOFPLVRLVAREGDRVKKLINSQSL 120
Qy 121 IGMVCEFDVWKQPEVODFRRNILLMWCKEAVDLRLNSPBRAMVYVPPNVSSPELIPK- 179
Db 121 IKGKHLFDSLRODEVNDFPTKORQFCEBAARQUGVEMWLOYSFPMQLEPSARGMRA 180
Qy 180 ---HIYKLDKQGITVIVYIVSBNNDKQKTYTLKINHDCYPEQVIAAIFKTRSMILSS 236
Db 181 GLLRVSNR-----ALVNVKFEGBESFTQVSTKMDPLMLMACALRKK-----A 225
Qy 237 EQLKLCVLEYQKYLKAVCGODEYFLEKYPILSOYKYIRSGIMLGRMPLMLMAKESLYSQ 296
Db 226 TVFRQPLVEQPEEYALVNGRHELYLGNYPILCHFQYICSLHSGLTPLHLMVSSSLAM 285
Qy 297 LPMDCFTMPSYSRRISTATPYMNGETSTKSLWYNSALRIKICATYVNVNIRIDIKIYV 356
Db 286 RDEQSNAPQYQKRAKRPPIPAKKPSVSLSLEQFSEILBGRVYNDER--MKLVV 343
Qy 357 RTGIYHGEPLCDNVNTORV-PCSNPRMNMELVNDIYIPDLPRARLCLISCSY----- 409
Db 344 QAGLPHNEMLCIKTVSSSEVAVCSBPWKORLEBDSVCLPRARLCPALYAVEAKAKK 403
Qy 410 --KGRKAKEHCHPLANGNINLPDYDTLVSGKALNLAMP-VPHGLEDLNPIGVTSNP 466
Db 404 ARSTKSKSKADCEPIAMANLFPYKQDLKTEGCLTMMSVSPBEKELLNPACTVGNP 463
Qy 467 NKETPCLLEBDFWSSVVKPPDMSVIEEHANWSVREAGFSYSHAGSNFLARDNEIREN 526
Db 464 NTEBAA-----ALVIYLPB---VAPHPVYFPALKEKILELGHNGRGRITTEEOU--- 509
Qy 527 DKEQRLAICTRDLSETTEQEKDFLMSHRHYCVT-IPEILPKLLSVKMSRDEVA---Q 582
Db 510 ---OLREILRRSGELYEHEKDLVWKRHEVDQHPPEALARLLVTKMNGHEVAQLSQ 566
Qy 583 MYCLVQMPRIKPRQAMELDLCNYPDPWVGFVAVRCLEKYLTDKLSQYLLOLVQVLYKE 642
Db 567 MLYLLCSMPRLPVSALBELDPSFDCYVSFAIKSLRK-LTDELFQYLLQVLYQVLYKE 625
Qy 643 QYLDNLVRFLLKXALTNRIGHFFFMHLKSEMNKTVSQRFGLLESYCRACGMYLKHL 702
Db 626 SYLDCSELTKFLGRALANRKHGFLFMHLREEMHVPSVALRFGIMEAYCRGSTHMKVL 685
Qy 703 NROYEAMEKILNLTDLKQEKKDETQKQKFLVEQ-MRRPDEMDALQGFSLPILNPAHQ 761
Db 686 MKQGEALSKLALNDFVAVSSQ-KTKPQTKEMHMCROBTMEALSHLOSPLDPSLT 744
Qy 762 GNLRLEGRINSSAKRPLMLWENPDIMSELFONNEIFKNGDDLRODMTLQIIRIME 821
Db 745 EBYVCEQCTFMDSKKPLMIWYSSSEAGSA---GNVGIIIFKNGDDLRODMTLQIMQLMD 801
Qy 822 NIMQNGIDLMLPYGCLSIGDCVGLIEVVRNSHTTMOIQ-CGGLKALQFNSHTLHOW 880
Db 802 VLMQEGIDLMTPTGCLPTGDRGLIEVVLHSDITANIQLNKSNAATPAFVKDALLMW 861
Qy 881 LKDKKGEIYDAIDLFRSCAGYCVATFIIGIGDRNSNIMWKDGOLEHIDFGHFLDH 940
Db 862 LKSKNPGALRAIEEFTLSCAGYCVATYVIGIGRHSNDINIMRESGOLFHDGFHFGN 921
Qy 941 KKKKGYRREVPFVLTDQDLIVISKGAOECTKTREFEFOEMCYAYLAIROHANLFIN 1000
Db 922 FTKTKGIRREVPFILTDFVHVIQOG--KTNNSKFERPRGVCERAYTLIRRHGLPLH 979
Qy 1001 LFSMMLSGMPELOFDDIAIYIRKTLALDKTEQALEYFKQNDAHHGSGWTTKMDIHT 1060

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Db      980 LFALMRAAGLPBELSCSKDIQYLKDSLALGKTEEBELKHFVKFNEALRESKTKTVNMLAH 1039
Qy      1061 TIKQ 1064
Db      1040 NVSK 1043

RESULT 8
000334 PRELIMINARY; PRT; 1068 AA.
AC 000334
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Phosphatidylinositol 3-kinase delta catalytic subunit.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mahlum C.E., Becker K.P., Morris A.J.
RT "H. sapiens mRNA for phosphoinositide 3-kinase delta catalytic
RT subunit."
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U57843; AAB53966.1; -.
DR InterPro; IPR001263; PI3Ka.
DR InterPro; IPR002420; PI3K_C2.
DR InterPro; IPR003113; PI3K_p85B.
DR InterPro; IPR000341; PI3K_ras_bind.
DR InterPro; IPR000403; PI3_P14_kinase.
DR Pfam; PF00613; PI3Ka; 1.
DR Pfam; PF00792; PI3K_C2; 1.
DR Pfam; PF02197; PI3K_p85B; 1.
DR Pfam; PF00794; PI3K_rbd; 1.
DR Pfam; PF00454; PI3_P14_kinase; 1.
DR SMART; SM00146; PI3Kc; 1.
DR SMART; SM00142; PI3K_C2; 1.
DR SMART; SM00143; PI3K_p85B; 1.
DR SMART; SM00144; PI3K_rbd; 1.
DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR PROSITE; PS50290; PI3_4_KINASE_3; 1.
KM Kinase.
SQ SEQUENCE 1068 AA; 121879 MW; 2B342FDA445C9A31 CRC64;

Query Match 33.3%; Score 1903.5; DB 4; Length 1068;
Best Local Similarity 38.3%; Pred. No. 2,2e-139;
Matches 434; Conservative 179; Mismatches 367; Indels 153; Gaps 23;

Qy      16 MPF-----RIIVECLLPNGMIVTLECLREALTITTKELFKEAKRYPLHQ 60
Db      1 MPFGVDCPMEFMTKEENORVVVDLLPLPGVYLVPPVSNNALSTIKLMLHRAQYEPFLFH 60

Qy      61 LLODESSYIFVSYQTEAREEFPDETRRLCDLRFQFLKTYIEVNGNREEKILNREIGFA 120
Db      61 MLASPKAYVFTICINOTAEQGLEDEQRRLCDVQFPFLPKRYVAEGSRVKKLINSQISL 120

Qy      121 IGMVFCEFDWYKDEVDQFRNIIIVNCKEAVDLRLDLSNPSHRAMYVPVNVSSPE---- 176
Db      121 IKGKLFHFDLSLDEVDNDFRAKMCQFCGEAARQQLGMEAMLQYSPFLQLEPSAQWTGP 180

Qy      177 -----LPHKINVKLDKQGIIVIVIVYVBNNDKQYTKLKNIDCVPEVOIVAAIRKTRSM 232
Db      181 GTLRLPR-----ALLVNVKFGESSEFTQVSTKVDPLMLMACALRK----- 224

Qy      223 LLSSEQKLCVLEQGYKYLKVCSCDEFEKXVPLSQYKTYRSCIMLGMPNMLMAKES 292
Db      225 ---ATVTRQPLVEGPEDEYTLQVNGRHELYLGSYPLCQFQV----- 261

Qy      293 LYSQLPMDCTFMPYSRRISTATPYMNGETSKGLMWINSALRIKIICATVYVNVNIDID 352

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Db      262 ---QKPR-----AKPPIPAKKSSVSLNSLEOPFRFIELIQSKVNADER--M 304
Qy      353 KIYVRTGIYHGGEPLCDNVNTQRP--CSNPRNEMLVYDIYIPDLPPAARLCTISCSV-- 409
Db      305 KLVVQAGLFHGNEMLCTVSSSEVSVCSEPVWQORLEFDINICDLPMAALCFALYAVIE 364
Qy      410 -----KGRKAKEEHCPLAGNINIFDYTDTLVSGMALNLMP-VPHGLEDLINPIGVT 462
Db      365 KAKKARSTKKKSKKADCPRIAMNIMLFYDKQQLKTGRCLYMPSPVDEKCELLNPIGTV 424
Qy      463 GSNPNKET-----PCLF-----LEFDMSSVYKPPDMSVIEHA 496
Db      425 RSNENTDSAAALLICLEPVAPHPYUYPALBKLPQGMLLASREW-----PELLMMLHA 478
Qy      497 NWSY-SRQAFSYSHAGL-----SNRLARDNEL-----RENDKEQYRAI 534
Db      479 EDSAPSRMIGVAPNGLVLPGLVQAPDACSRLQLLEIGRSHSECYHVTBEOQLREI 538
Qy      535 CTRDPLSEITEOEKDFLMSHRHYCVT-IPRLPLRLLSVKNRSDEVAQWYCLVKDWPPI 593
Db      539 LERRSGELYEHKEDLVWKLRIHEVQEHFPEALARILLVTGMKHEDVADPALPAVSMPEL 598
Qy      594 KPEQAMLLDCNTPDEPMVGRPAVRCLEXYLTDKLSQYLQLVQVLYKYEOYLDNLVRF 653
Db      599 PVLATLRLDFSPDCVSGSFAIKSLRK-LTDELFPQYLLQVQVLYKYESYLLDCELTKFL 657
Qy      654 LKKALTNQRIQHFFFMHLKSEMHNKTVSORFGLLSYSCACGMYLGHNLROYAMEKLI 713
Db      658 LERLALNKRKIGHFLFMHLRSEMHVPSVALRFGILLEYACGSGTHMKVLMKGQALSKLK 717
Qy      714 NLTDILKQEKDETOKVOMKFLVEO--NRPDFDALQGFSLPPLNPAHQLGNRLBECRIM 772
Db      718 ALNDFVLTSSQ-KTPKQQTKEMLHLCWRGEAYLEASHLOSPLDSPTLAAVECEQCTFM 776
Qy      773 SSARPLMLMWNENDINSELLFQNNELIFKNGDDLRQDMLTQIIRIMENINQNGIDLR 832
Db      777 DSKKKPLMIWYSNEASG---GTVGIIFFKNGDRLRQDMLTQIIMQDMLMKQEGIDLR 833
Qy      833 MLPYGLSLSDDCVGLIEVENSHTIQIOC-KGSLKCALQFNSHTLQWLKDNKKGFIYD 891
Db      834 MTPYGLCLPTGDRGLLEVLRSDTIANTIQNKSMAATAAFNCDALNMLSKNPGALD 893
Qy      892 AAIDLFTSCAGCVATFLLIGIDGRHNSNTMVXDQGLFHIIDGPHLDHKKKFGYKRR 951
Db      894 RAIEEFTLSGAGCVAAIYVVGIDGRHSDNIMIESQGLFHIIDGPHLGNTKTFGINRR 953
Qy      952 VPFVLITQDFLIVISKGAQECTKREPERFQEMCYKAVLAIRQHANLFINLPSMWLGSQMP 1011
Db      954 VPFILTYDLVHVLIQGG--KTNNSEKFERFPGYCERAVTILRRHGLFLHLFALMRAAGLP 1011
Qy      1012 ELQSFQDAIYIKRTIALDKTEQALIEFMKQNDAHNGGTTTKMDWTFHRIKQ 1064
Db      1012 ELSCSKDIQYLKDSLALGKTEEBELKHFREKNEALREGKTKTVNMLAHNVSK 1064

RESULT 9
P91634 PRELIMINARY; PRT; 1068 AA.
AC P91634
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Phosphatidylinositol 3-kinase catalytic subunit (EC 2.7.1.137)
DE (PI3K2E protein) (CG4141 protein).
GN PI3K2E OR CG4141.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97133288; PubMed=8978685;

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Db 1013 KHGCLISLPSFMSMTSTGLPELSSEKDLVLTVDYTEKARSHFAKSEALANSWK 1072  
Qy 1053 TRKMDWTFHTIKOH 1065  
Db 1073 TSLMWSHNSFSKN 1085

RESULT 10  
ID Q91XL6 PRELIMINARY; PRT; 291 AA.  
AC Q91XL6;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Phosphatidylinositol 3-kinase alpha catalytic subunit (EC 2.7.1.137)  
DE (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxId=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Mistlar; TISSUE=Brain;  
RA Schaefer M., Plum C., Albrecht N., Reusch P.;  
RT "Expression of phosphatidylinositol 3-kinases in rat vascular smooth  
RT muscle cells.";  
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF395897; AAK83379.1; -  
DR InterPro; IPR000403; P13\_P14\_kinase.  
DR Pfam; PF00454; P13\_P14\_kinase.1.  
DR SMART; SM00146; P13Kc.1.  
DR PROSITE; PS00915; P13\_4\_KINASE\_1; 1.  
DR PROSITE; PS00916; P13\_4\_KINASE\_2; 1.  
DR PROSITE; PS50290; P13\_4\_KINASE\_3; 1.  
KW Kinase; Transferase.  
FT NON\_TER 1  
FT NON\_TER 291  
SQ SEQUENCE 291 AA; 33934 MW; CF0B1EA450F8E78E CRC64;

Query Match 26.7%; Score 1527; DB 11; Length 291;  
Best Local Similarity 99.3%; Pred. No. 8e-111;  
Matches 289; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 705 QVEAMEKILNLTDLKQEKDETOVKQKFLVEQRRRPFMDALQGFSLPMPAHQNL 764  
Db 1 QVEAMEKILNLTDLKQEKDETOVKQKFLVEQRRRPFMDALQGFSLPMPAHQNL 60  
Qy 765 RLEBCRIMSSAKRPLMLNWPDIIMSELIIFONNEIIFKNGDGLFQDMLTLOIRIMENIW 824  
Db 61 RLEBCRIMSSAKRPLMLNWPDIIMSELIIFONNEIIFKNGDGLFQDMLTLOIRIMENIW 120  
Qy 825 QNOGLDRLMLPYGLSTIGDCVGLIEVYVNSHTIMOIOCKGLKALQNSHTLHQLKDK 884  
Db 121 QNOGLDRLMLPYGLSTIGDCVGLIEVYVNSHTIMOIOCKGLKALQNSHTLHQLKDK 180  
Qy 885 NKGSIYDAIDLFTKSCAGYCVATFIIGIDRHSNINWKKDGLFHDIFGFLDHHKKK 944  
Db 181 NKGSIYDAIDLFTKSCAGYCVATFIIGIDRHSNINWKKDGLFHDIFGFLDHHKKK 240  
Qy 945 FGYYRERVPLVLTODFLIVISKAQECTKTRFERFQEMCYKATLAIROHA 995  
Db 241 FGYYRERVPLVLTODFLIVISKAQECTKTRFERFQEMCYKATLAIROHA 291

RESULT 11  
ID Q9BZC8 PRELIMINARY; PRT; 1102 AA.  
AC Q9BZC8;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Phosphoinositide-3-kinase gamma catalytic subunit (EC 2.7.1.137).  
GN P13CG.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95350661; PubMed=7624799;  
RA Stoyanov B., Volinia S., Hancock T., Rubio I., Loudchenkov M.,  
RA Malek D., Stoyanova S., Vanhaesebroeck B., Dhand R., Nurnberg B.,  
RA Gierschik P., Seedorf K., Hansen J.J., Waterfield M.D., Wetzker R.;  
RT "Cloning and characterization of a G protein-activated human  
RT phosphoinositide-3 kinase.";  
RL Science 269:690-693 (1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Michael M., Schaefer M., Stoyanov B., Wetzker R., Nurnberg B.;  
RT "Regulation of a G-protein-activated phosphoinositide-3-kinase.";  
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF327656; AAG6115.1; -  
DR InterPro; IPR001263; P13Ka.  
DR InterPro; IPR002420; P13K\_C2.  
DR InterPro; IPR000341; P13K\_ras\_bind.  
DR InterPro; IPR000403; P13\_P14\_kinase.  
DR Pfam; PF00615; P13Ka.1.  
DR Pfam; PF00792; P13K\_C2.1.  
DR Pfam; PF00794; P13K\_rbd.1.  
DR Pfam; PF00454; P13\_P14\_kinase.1.  
DR SMART; SM00145; P13Ka.1.  
DR SMART; SM00146; P13Kc.1.  
DR SMART; SM00142; P13K\_C2.1.  
DR SMART; SM00144; P13K\_rbd.1.  
DR PROSITE; PS00915; P13\_4\_KINASE\_1; 1.  
DR PROSITE; PS00916; P13\_4\_KINASE\_2; 1.  
DR PROSITE; PS50290; P13\_4\_KINASE\_3; 1.  
KW Kinase; Transferase.  
SQ SEQUENCE 1102 AA; 126481 MW; 402B867EBDD2191A CRC64;

Query Match 25.8%; Score 1472.5; DB 4; Length 1102;  
Best Local Similarity 33.4%; Pred. No. 9.4e-106;  
Matches 385; Conservative 192; Mismatches 402; Indels 173; Gaps 40;

Qy 1 MPPRSSGELMGHILMPRLIVLECLP-----NGMI-----VTLEC 36  
Db 23 MKPSAASLSSMELIP-----IEFVLPISQKCKSPETALLHVAHGNTVQMKQAVLRA 78  
Qy 37 LREATLITIGELFKKARKYPLHQL-----QDESSYIVSVTQEAERESEFPETRL 89  
Db 79 LETSVAADFYHRL-----GPHHFLLLYQKGGWYEIYDYQVYVQTLDCLRWKAATHRSP 132  
Qy 90 CDRLPQPLKVIIEVGNREKILNREIGFAIGPVCEFPMDVDEVDPRRNILNVCKE 149  
Db 133 GQIHLVQ-----RHPSSESOAFQROTLALIGDVTDVSNVHDELFTFRGLVTPRMA 186  
Qy 150 AYDLRLNSBHSRAMYVPPNVSSPELPKHIIYNKLDKQIIVIVIVASPNNDKQKYL 209  
Db 187 EVASRD-----PLVYMHGHWVTSKP-LPEYLMWKILANNICIFVI-----HSTTSQT 233  
Qy 210 KINHDCVPEOVIATAIRK-KTRSMILSSQKLQVLEFGKYLTKVCGDEFLKLYPL 267  
Db 234 KVSPPDDTPGAILDSFFTKAKKSLMDIPES-----QSBQDPLRVLCGDBEVLVGETPI 287  
Qy 268 SOYKIRISCIIMLRMPVLML-----MAKESLYSOLPM--DCEFTMPSYSRISATPYNM 319  
Db 288 KNFQWVRHCLKNGEELIHVLDTPEDPALDVRKAEWPLVDCGTGVGYHQLT-----IH 342  
Qy 320 GE-----TSTKSLWVINSALRIKILCAVYVNVNIRID-----KIYRTGIYHGE 365  
Db 343 GXDHESVFTVSLWDCBRKFRVK-----IRGIDIPVLPHNTDITFVVEANIQHGQ 392  
Qy 366 PLCDNVTVQVPCSNPRMWNWLVYDIYIPLPAAKLCLSGCYK-----GRKAKEHCP 421  
Db 393 VLCQRRTPKRPFTTEVLMVWLEFSIKIKDLPKALLNLQIYCGKAPALSSKASAESPS 452



QY 991 IROHAFINFSMMLSGMPELOSFDIATIRKTLALDKTEQALFEMQANDAHHG 1050  
Db 1020 LRHHHTNLLILFMSMLMTGMQOLTSKEDIEYIRDALTVGKNEDAKKFFLDQIEVCRDKG 1079  
QY 1051 WTTKMDWIFHTI 1062  
Db 1080 WTVQPNWFLHLV 1091

RESULT 13  
Q9EQL1  
ID Q9EQL1 PRELIMINARY; PRT; 1113 AA.  
AC Q9EQL1  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Phosphatidylinositol 3-kinase gamma isoform.  
GN PI3KCG.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RA Chakravarti S., Mccoll S.R.;  
RT "Cloning of a murine ortholog of PI 3-kinase gamma."  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF208345; AAG41122.1;  
DR MGD; MGI:1353576; P13KCG.  
DR InterPro; IPR001263; P13Ka.  
DR InterPro; IPR002420; P13K\_C2.  
DR InterPro; IPR000341; P13K\_ras bind.  
DR InterPro; IPR000403; P13\_P14\_Kinase.  
DR Pfam; PF00613; P13Ka; 1.  
DR Pfam; PF00792; P13K\_C2; 1.  
DR Pfam; PF00794; P13K\_rbd; 1.  
DR Pfam; PF00454; P13\_P14\_Kinase; 1.  
DR SMART; SM00145; P13Ka; 1.  
DR SMART; SM00146; P13K; 1.  
DR SMART; SM00142; P13K; 1.  
DR SMART; SM00144; P13K\_rbd; 1.  
DR PROSITE; PS00915; P13\_4\_KINASE\_1; 1.  
DR PROSITE; PS00916; P13\_4\_KINASE\_2; 1.  
DR PROSITE; PS50290; P13\_4\_KINASE\_3; 1.  
KM Kinase.  
SQ SEQUENCE 1113 AA; 127538 MW; 6729FBE8ASD35691 CRC64;

Query Match 25.7%; Score 1467; DB 11; Length 1113;  
Best Local Similarity 33.1%; Pred. No. 2,6e-105;  
Matches 381; Conservative 199; Mismatches 411; Indels 160; Gaps 38;

QY 1 MPPRSSGELGMLHMPRIIVECLPENGMTV-----LECREATLITIKELKEA 53  
Db 23 MKPSSAAGSLSSMELIP-----IEFVLPTSQRIKTPETALHVAHGNGVEQMKQWLR 78  
QY 54 RKYPL-----HQLQDESSYIFVSVTQEAEREPEFDETRRLCDLRLPQPLK-----V 101  
Db 79 LETSVAAEFHRLRDPDQFLLYKQKQWYELDYKYYQVYQVDTDCIHYMKHMKSGQIHHV 138  
QY 102 IEPVGNNEEKILNEIGFAIGMPVCEPDMVKDEPEVDFRRNIILNCKEAVDLRDLNSPHS 161  
Db 139 QRHVPSSETLAFQKQLSLIGYDVTDISNVHDELEFTRRLVYPRMAEVAGRDAK----- 194  
QY 162 RAMVVPNNVSSSELKRYHYNKLDKQQLIVYVIVISPNNDKRYTLKINHDCVPEQVI 221  
Db 195 --LVAMHPWTSK-LPDYLSKIANNCIFIVI-----HNGTISQTIKVSADDPGTL 245  
QY 222 AEAIRK--KTRSMLSSEQLKLVLEYQKYLKVGCGDEFLKPYLSQYKXIRSCIML 279  
Db 246 QSFPTTKAKKSLNINISES-----QSEQDFVLAVCGRDELYVETPLKFWVRQCLKN 299  
QY 280 GRMPTNML-----MAKESLYSQLPM--DQFTMPSYSRISTATAPVMNGE---TSTRSL 327

Db 300 GDEIHLVLDPPDPALDEVERKEEWPVLDCTGVYGHQULT-----IHGXHESVFTVSL 354  
QY 328 WVINSAIRIKILACTYNNVNIIPDID-----KIVYTGIVHGGEPLCDNNNTQVRP 377  
Db 355 WDCRRKFRVK-----IRGIDIPVLPRNDLIVFEANIQHGQVLQQRRTSPRP 404  
QY 378 CSNPRNENWLNVDIYIPDLPPAARLCUJ--CSYGRKGAKEBHC-----LAWG 425  
Db 405 ABEVLNVMVLEFGKIKIDLPKGAALNLIQIVCKTPSLSKASAPTPGSESGKAQOLLYV 464  
QY 426 NINLFYDTDLVSGKALNIMPVPHLED--LNPICVT-GSNPNKE-TPCLELEPWFPS 481  
Db 465 NLLIIDHRLFLRHGDYVLHWMQISGKAEQGSFNAADLTATNPDKENSISILLNYC 524  
QY 482 SVVFPMSVIEEHNANVSREAGFSYSHAGLSRLARDNELRPNDKEQRAITRDPIS 541  
Db 525 HPIALPKRPTPDDEGRV-----RAEPMQLR--KOLEAIIATDPLN 565  
QY 542 EITEOEKDFLMSHRHYCVTTPILLPKLLSVKNNSREVAQMYCL-----VKDWPPIKPE 596  
Db 566 PLTAEDEKELMHPRYESLKHPRKAVPKLFSSVKMGQGEIVAKTYQLLARREIWDQALDVG 625  
QY 597 QAMELDCNYPDPNVRGFAVRCLEKYITDPKLSQYLIQLVQVLKYEGLDNLVRLFKK 656  
Db 626 LTMQLDLCNFSDEVRAIAVQKLES--LEDDVLIHYLLQLVQAVKFEFPHDSALRPLKR 684  
QY 657 ALTNQRIGHFFPFLKSEM-HNKTVSORFGLLLESYCRAG-MYKHLNNOVEMECILN 714  
Db 685 GLRNKRIGHFLFPLRSEIAQSHYQRFVILAEAYLRGGTAMLDQFTQVHIEMLQK 744  
QY 715 LT-DI--LKQEKDETKV--QMKFLVEQMRPDPMDALQFLSPNPAHOLGNRLREEC 769  
Db 745 VTIDIKLSAEKDVSSQVLSQKQKLESQNSLPS--FRVPYPLGAKGLVLEKC 801  
QY 770 RINSAPRPLMLNWE--NPDISELLEFQNN-----IIFKQDDLRQDMLTLOIRIMENIW 824  
Db 802 KVAASKKKPLMERKCADPTVLS-----NETIGIIFKHDDLRQDMLTLOIRIMESI 855  
QY 825 QNGGLDRLMPLPYGLSLGDCVGLIEVVRNSHTIMQI-QCKGGLKALQFNSHTLHQLKD 883  
Db 856 ETSRLDLCPLPYGISISGDKIGMIEIKVADTTAIOQSTVGATGA--FDEVLNHWLKE 913  
QY 884 KNK-GEIYDAIDLFRTSCAGYCAAFILGIGRHSNINWMDGOLFHIIDFGFHLHKK 942  
Db 914 KCPLEKFOAAVERFYVSCGYCATFVLGIGRHNINIMSETGNLFHIDFGHILGNK 973  
QY 992 ROHANLFINFSMMLSGMPELOSFDIATIRKTLALDKTEQALFEMQANDAHHG 1051  
Db 1032 RHHHTNLLILFMSMLMTGMQOLTSKEDIEYIRDALTVGKSEBDAKKFFLDQIEVCRDKG 1091  
QY 1052 WTTKMDWIFHTI 1062  
Db 1092 WTVQPNWFLHLV 1102

RESULT 14  
Q61182  
ID Q61182 PRELIMINARY; PRT; 1658 AA.  
AC Q61182;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Phosphoinositide 3-kinase.  
GN PIK3CA OR CPK-M.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=baib C; PubMed=8662856;
RX MEDLINE=96278930; Williams L.T.;
RA Molz L., Chen Y.W., Hirono M.,
RT "Cpk is a novel class of Drosophila Ptdins 3-kinase containing a C2
  domain.";
RL J. Biol. Chem. 271:13892-13899(1996).
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; U52193; AAC52604.1; -.
DR HSSP; P21707; IBYN.
DR MGD; MGI:1203729; P1K3C2a.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001263; P1K3a.
DR InterPro; IPR002420; P1K3_C2.
DR InterPro; IPR000341; P1K3_ras_bind.
DR InterPro; IPR000403; P13_P14_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00613; P1K3a; 1.
DR Pfam; PF00792; P1K3_C2; 1.
DR Pfam; PF00794; P1K3_rbd; 1.
DR Pfam; PF00454; P13_P14_kinase; 1.
DR Pfam; PF00787; P13_P14_kinase; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00145; P1K3a; 1.
DR SMART; SM00146; P1K3a; 1.
DR SMART; SM00142; P1K3_C2; 1.
DR SMART; SM00144; P1K3_rbd; 1.
DR SMART; SM00312; P13_P14_kinase; 1.
DR PROSITE; PS00004; C2 DOMAIN 2; 1.
DR PROSITE; PS00915; P13_4_KINASE 1; 1.
DR PROSITE; PS00916; P13_4_KINASE 2; 1.
DR PROSITE; PS0290; P13_4_KINASE_3; 1.
DR PROSITE; PS0195; P13_4_KINASE_3; 1.
DR KINASE.
SQ SEQUENCE 1658 AA; 187439 MW; BBC8E81DE20F20 CRC64;

Query Match 18.4%; Score 1049.5; DB 11; Length 1658;
Best Local Similarity 33.1%; Pred. No. 1.7e-72;
Matches 270; Conservative 141; Mismatches 297; Indels 107; Gaps 24;

QY 296 QLPMDCFMPSY-----SRISTATPYMNGSTSTSLWYNSALRIKIKLCATYVAVN 347
DB 614 QVSMHDLTAIYDLRLANSSRCSTGCP--RGSNITKEMATATQLOFTYVAAGISISN 671
QY 348 -IRIDIKIYVRTGIYHGEPLCDVNTQVPCSNP-----RWENWLVNIDYIPDLPRAR 401
DB 672 WVSNEYKYLLCSLSHNGKDLFKPIQSKKVGTYKNFYLIKWDLILFPIQISQLPLESV 731
QY 402 LCLSLCSV-----KRRKAKEHCHLANGNIN--LPDYDTPLVSGKALNIMP 447
DB 732 LHLTLFGVLNOSGSGSPDSNKRKG-----PEALGKYSLTLPDKRFITCGTKLLYIMT 785
QY 448 VPHGLEDLNPFGVGSNPNK-----ETPCLLEFPWFSSVVFPMVSIVIEHANVSARE 503
DB 786 SSH-----TNSIGALPKKSYMERIYLVDF-----PSPADII----- 820
QY 504 AGFSYSHAGLSNRLARDNELR--END-KEQLRAICTRPDLSEITQEOKFLWSHRHYCVT 560
DB 821 ----YTSQIDRNIIQQDKLETLESIDIKKLDIITHRDSFSLSKEDKVFLEWENYYCCK 876
QY 561 IPEILPKLLISV---KMSRDEVAQMYCLVKDMPPIKEQAMELLDCNYPDPMYRGFAVR 617
DB 877 HNCPLPKILASAPNKMWAN---LATYSLHLHWPPLCPILAELLDARADAGVSLANS 933
QY 618 CLEKLTLDKLSQYLIQVQVLYKQYDNLVRFLLKALTNORIGHFFPHLSEMHN 677
DB 934 WMEA-ISDELDLDPQVQALKYETIYANSSIVRELSALNGIOLASLYLLDALHD 992
QY 678 KTVSQRFGILLSEYCRACGMYLK-HLNROVAMEKILNLTDLIKOEKDETOKVOMKFLV 736
DB 993 THFGSRYEIVLQALLSVGSGKGLREELSKQMKLVOLLGVAEKVQAGSSTRQVVLQK--- 1049

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QY 737 EOMRRPDMALOGFL-----SPINAHQGLRLEECRIMSSAKRPLMNNENPDIMS 790
DB 1050 -----SMERVQGFLLRNKCRPLPKRSYVAXELNIKSCGFSSNAPLVTWMDPLG 1102
QY 791 ELLEFQNNELFKNGDDRLQDMTLQITRIMENIWOGLDLRLPYCGLISGDCVGLIEV 850
DB 1103 EEI-----NMFVKVEDIRQDMALQWIKIMDKITWKEGLDLRWVIFPCLSTGDRGVVEL 1158
QY 851 VRNSHTIMQIQCKGLGALQFNSHTLQWLKQKNKQ-ELYDAIDLFTSCAGYCATF 909
DB 1159 VPASDTLRKIQVEGVYGS--FKDKPLAEWLKRKNPSEEEYKASENFITYSCAGCCVATY 1216
QY 910 ILIGDRHNSNINWQDQGLFHDIFGHFLDHKKKFKGKEERYVPVLTQDFLLIVISKGAQ 969
DB 1217 VLGIQDRHNDINIMRSGHMFHIDFGKFLGHAQMFSGFKDRAPFVLTSMAYVINGEK 1276
QY 970 ECTYREFEERPOEMCYAVLAIROHANLFTNLFSGMIGSGMPELOSFDDIAYIRKTLALD 1029
DB 1277 ---PTIRFQLFVDLCCQAVNLIKQTNLFNLISLIMPGLPELITSIQDKYVYDALQPO 1333
QY 1030 KTEQEALEYFMKQNDAHHGWTTKMDMIFHTIKQ 1064
DB 1334 TTDAEATIFPTR-LIESLSIATKFNPFTHMLAQ 1367

RESULT 15
AD Q61194 PRELIMINARY; PRT: 1509 AA.
ID Q61194
DC 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE P170 phosphatidylinositol 3-kinase.
GN P1K3C2A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10990;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96278746; PubMed=8663140;
RA Vitbasius J.V., Gultherme A., Czech M.P.;
RT "Mouse p170 is a novel phosphatidylinositol 3-kinase containing a C2
  domain.";
RL J. Biol. Chem. 271:13304-13307(1996).
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; U55772; AAB07682.1; -.
DR HSSP; P21707; IBYN.
DR MGD; MGI:1203729; P1K3C2a.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001263; P1K3a.
DR InterPro; IPR002420; P1K3_C2.
DR InterPro; IPR000341; P1K3_ras_bind.
DR InterPro; IPR000403; P13_P14_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00613; P1K3a; 1.
DR Pfam; PF00792; P1K3_C2; 1.
DR Pfam; PF00794; P1K3_rbd; 1.
DR Pfam; PF00454; P13_P14_kinase; 1.
DR Pfam; PF00787; P13_P14_kinase; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00145; P1K3a; 1.
DR SMART; SM00146; P1K3a; 1.
DR SMART; SM00142; P1K3_C2; 1.
DR SMART; SM00144; P1K3_rbd; 1.
DR SMART; SM00312; P13_P14_kinase; 1.
DR PROSITE; PS00004; C2 DOMAIN 2; 1.
DR PROSITE; PS00915; P13_4_KINASE 1; 1.
DR PROSITE; PS00916; P13_4_KINASE 2; 1.
DR PROSITE; PS0290; P13_4_KINASE_3; 1.
DR PROSITE; PS0195; P13_4_KINASE_3; 1.

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 6, 2003, 14:37:15 ; Search time :8 Seconds

(without alignments)  
2792.864 Million cell updates/sec

Title: US-09-325-095-37

Perfect score: 5709  
Sequence: 1 MPRPSSGELWGIHMPRI.....GWTTKMDWIFHTIKOHALNX 1069

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt 41.1\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5709	100.0	1068	P11A_BOVIN	P32871 bos taurus
2	5657	99.1	1068	P11A_HUMAN	P42336 homo sapien
3	5645	98.9	1068	P11A_MOUSE	P42337 mus musculu
4	1976.5	34.6	1044	P11D_HUMAN	O00329 homo sapien
5	1968	34.5	1070	P11B_RAT	O92110 rattus norv
6	1966	34.4	1070	P11B_HUMAN	P42338 homo sapien
7	1958	34.3	1043	P11D_MOUSE	O35904 mus musculu
8	1477.5	25.9	1102	P11G_MOUSE	O91hg7 mus musculu
9	1467	25.7	1101	P11G_HUMAN	P48736 homo sapien
10	1465.5	25.7	1102	P11G_PIG	O02697 sus scrofa
11	1370	24.0	1570	P3K1_DICDI	P54673 dictyostell
12	1262.5	22.1	1858	P3K2_DICDI	P54674 dictyostell
13	1109	19.4	1585	P3K3_DICDI	O94125 caenorhabd
14	1096	19.2	1146	AGEL_CAEEL	O00750 homo sapien
15	1064.5	18.6	1634	PK3B_HUMAN	O70167 mus musculu
16	923	16.2	1506	PK3G_MOUSE	O75747 homo sapien
17	881.5	15.4	1448	PK3G_HUMAN	O70173 rattus norv
18	875	15.3	1505	PK3G_RAT	P50520 schizosacch
19	685	12.0	801	VP34_SCHPO	P54676 dictyostell
20	661.5	11.6	816	P3K4_YEAST	P42343 glycine max
21	648.5	11.4	875	VP34_YEAST	P42339 arabidopsi
22	645	11.3	814	P3K1_SOYBN	P42348 glycine max
23	635	11.1	814	P3K1_ARATH	O92213 candida alb
24	629	11.0	812	P3K2_SOYBN	P42336 homo sapien
25	602	10.5	1020	VP34_CANAL	P37297 saccharomyc
26	442	7.7	854	P14K_HUMAN	P31297 saccharomyc
27	442	7.7	1900	STT4_YEAST	P31297 saccharomyc
28	297	5.2	1066	P1K1_YEAST	P54667 dictyostell
29	268.5	4.7	1093	P14K_DICDI	O10366 schizosacch
30	242.5	4.2	851	YDBG_SCHPO	P38110 saccharomyc
31	205.5	3.6	2787	TELI_YEAST	P42346 rattus norv
32	202.5	3.5	2549	FRAP_RAT	P42345 homo sapien
33	196.5	3.4	2549	FRAP_HUMAN	

34	195.5	3.4	2549	1	FRAP_MOUSE	O91hg9 mus musculu
35	192	3.4	4188	1	PRKD_HUMAN	P78527 homo sapien
36	184	3.2	2470	1	TOR1_YEAST	P31659 saccharomyc
37	180.5	3.2	4128	1	PRKD_MOUSE	P97313 mus musculu
38	173.5	3.0	2335	1	TOR1_SCHPO	O14356 schizosacch
39	172	3.0	2473	1	TOR2_YEAST	P32600 saccharomyc
40	166.5	2.9	2386	1	RAD3_SCHPO	O02099 schizosacch
41	157.5	2.8	2368	1	ESR1_YEAST	P38111 saccharomyc
42	143.5	2.5	3056	1	ATM_HUMAN	O13315 homo sapien
43	141	2.5	3066	1	ATM_MOUSE	O62388 mus musculu
44	140	2.5	2337	1	TOR2_SCHPO	O91hg2 schizosacch
45	138	2.4	4540	1	DYHC_PARTE	O27171 parametrium

## ALIGNMENTS

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RESULT 1
ID P11A_BOVIN STANDARD; PRT; 1068 AA.
AC P32871;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE alpha isoform (EC 2.7.1.153) (P13-kinase p110 subunit alpha) (Ptdins-
DE 3-kinase p110) (P13K).
GN PK3CA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92354059; Pubmed=1322797;
RA Hiles I.D., Otsu M., Volinia S., Fry M.J., Gout I., Dhand R.,
RA Panayotou G., Ruiz-Larrea F., Thompson A., Totty N.F., Hsuan J.J.,
RA Courtneidge S.A., Parker P.D., Waterfield M.D.;
RT "Phosphatidylinositol 3-kinase: structure and expression of the 110
RT kd catalytic subunit.";
RL Cell 70:419-429 (1992).
CC -!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
CC -!- PREFERENCE FOR PTDINS(4,5)P2.
CC -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidy1-1D-myo-inositol 4,5-
CC bisphosphate = ADP + 1-phosphatidy1-1D-myo-inositol 3,4,5-
CC triphosphate.
CC -!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC SUBUNIT.
CC -!- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC EMBL: M93252; AAA0698.1; -
CC PIR: A43322; A43322.
CC InterPro: IPR000008; C2.
CC InterPro: IPR000403; P13_P14_kinase.
CC InterPro: IPR002420; P13K_C2.
CC InterPro: IPR003113; P13K_P85B.
CC InterPro: IPR000341; P13K_P85B_bind.
CC InterPro: IPR001263; P13Ka.
CC Pfam: PF00454; P13_P14_kinase; 1.
CC Pfam: PF00792; P13K_C2; 1.
CC Pfam: PF02192; P13K_P85B; 1.
CC Pfam: PF00794; P13K_P85B; 1.
DR

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DR Pfam; PF00613; PI3Ka; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00142; PI3K_C2; 1.
DR SMART; SM00143; PI3K_P85B; 1.
DR SMART; SM00144; PI3K_hdb; 1.
DR SMART; SM00145; PI3Ka; 1.
DR SMART; SM00146; PI3K; 1.
DR PROSITE; PS5004; C2_DOMAIN_2; FALSE_NEG.
DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR PROSITE; PS50290; PI3_4_KINASE_3; 1.
DR Transferase; Kinase; Multigene_family.
KM TRANSFERASE; Kinase; Multigene_family.
FT DOMAIN 319 428 C2_DOMAIN.
FT DOMAIN 797 1068 PI3K/PI4K.
SQ SEQUENCE 1068 AA; 124327 MW; C753DC2CF39FDDF0 CRC64;

Query Match 100.0%; Score 5708; DB 1; Length 1068;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1068; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPRPSGELMGILMPRIIVECLIPNGMIVTLECLREATLITIKHELFKARKYPLHQ 60
DB 1 MPPRPSGELMGILMPRIIVECLIPNGMIVTLECLREATLITIKHELFKARKYPLHQ 60
QY 61 LLDDESYIFVSVTQEARREFFPDETRRLCDLRLFPPLKATIEYVGNREKILNREIGFA 120
DB 61 LLDDESYIFVSVTQEARREFFPDETRRLCDLRLFPPLKATIEYVGNREKILNREIGFA 120
QY 121 IGMVPCEDMWKDEVDVDFRRNIIIVNCKEAVDLRLDNLNPHSRAMVYVYVNTSESSPELPKH 180
DB 121 IGMVPCEDMWKDEVDVDFRRNIIIVNCKEAVDLRLDNLNPHSRAMVYVYVNTSESSPELPKH 180
QY 181 IYNNKLDKQIIVIVWIVVSPNNDKQYTLKINHDCVPEQVIAEAIKRTKRSMLSSSEQLK 240
DB 181 IYNNKLDKQIIVIVWIVVSPNNDKQYTLKINHDCVPEQVIAEAIKRTKRSMLSSSEQLK 240
QY 241 LCVLEYGQKYLILKVCCEDEYLEKYPILSQYKIRSCIMLGMPNIMLMAKSLVSQLPMD 300
DB 241 LCVLEYGQKYLILKVCCEDEYLEKYPILSQYKIRSCIMLGMPNIMLMAKSLVSQLPMD 300
QY 301 CETMYSRRISTATPYNNGESTSLWVINGSLIKILICATYVWVNRIDIKIYVITGI 360
DB 301 CETMYSRRISTATPYNNGESTSLWVINGSLIKILICATYVWVNRIDIKIYVITGI 360
QY 361 YHGSPELCDNVNTQRPVPCSNPRNEMLVNIDYIPDLPRARLCLISGVKGRKAKKEHC 420
DB 361 YHGSPELCDNVNTQRPVPCSNPRNEMLVNIDYIPDLPRARLCLISGVKGRKAKKEHC 420
QY 421 PLAMGNINLFDYDTLTVSGKALNIMPVPHGLEDLNPIGVGNSPNKETTPLELEFDMF 480
DB 421 PLAMGNINLFDYDTLTVSGKALNIMPVPHGLEDLNPIGVGNSPNKETTPLELEFDMF 480
QY 481 SSVVFPMPMSVTEEHANMSVSREAGFSYSHAGLSNRILADNLEFRENDEKQLALICTRDL 540
DB 481 SSVVFPMPMSVTEEHANMSVSREAGFSYSHAGLSNRILADNLEFRENDEKQLALICTRDL 540
QY 541 SEITEQEKPLFMSHRYCVTIEIPILKLLSVKMSRDEVAQMYCLVCKWPIKEQANE 600
DB 541 SEITEQEKPLFMSHRYCVTIEIPILKLLSVKMSRDEVAQMYCLVCKWPIKEQANE 600
QY 601 LLDENVPMVGVFAVRCLIEKLTDDKLSQYLIQVQVTKRQYLDNLLVRFLLKALTN 660
DB 601 LLDENVPMVGVFAVRCLIEKLTDDKLSQYLIQVQVTKRQYLDNLLVRFLLKALTN 660
QY 661 QSIGHFFHMLKSEHNKTVSQRFGLLESYCRACGMVSKHINROVEAMEKILINTDIK 720
DB 661 QSIGHFFHMLKSEHNKTVSQRFGLLESYCRACGMVSKHINROVEAMEKILINTDIK 720
QY 721 QEKKDETQYOMKFLVEOMRRPDMFALOGFLSPLNPAHQNLRLBECRINSSAKRPLM 780
DB 721 QEKKDETQYOMKFLVEOMRRPDMFALOGFLSPLNPAHQNLRLBECRINSSAKRPLM 780
QY 781 LNMENPDIMSELLFQNNELIFKNGDDLRODMTLTQIIRIMENIMQNGDLRLMYPGCL 840

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DB 781 LNMENPDIMSELLFQNNELIFKNGDDLRODMTLTQIIRIMENIMQNGDLRLMYPGCL 840
QY 841 IGDCCGLIEVYNSHTIMQIOCKGGIKGALQPSHTLHQMWDKNGCELYDAIDIFTS 900
DB 841 IGDCCGLIEVYNSHTIMQIOCKGGIKGALQPSHTLHQMWDKNGCELYDAIDIFTS 900
QY 901 CAGYCAVTFILIGDHNHNSIMWKDGOLEPHIDFGHFLDHKKKPKFYKEERVVFLTQDF 960
DB 901 CAGYCAVTFILIGDHNHNSIMWKDGOLEPHIDFGHFLDHKKKPKFYKEERVVFLTQDF 960
QY 961 LIVISKAQOECTYRFEFRFOEMCYKAYLAIROHANLFINLFSWMLSGMPELQSFDDIA 1020
DB 961 LIVISKAQOECTYRFEFRFOEMCYKAYLAIROHANLFINLFSWMLSGMPELQSFDDIA 1020
QY 1021 YIRKTLALDTEQDALEYFMKQNDAAHGGWTTKMMIFHTIKOHALN 1068
DB 1021 YIRKTLALDTEQDALEYFMKQNDAAHGGWTTKMMIFHTIKOHALN 1068

RESULT 2
ID P11A_HUMAN STANDARD; PRT; 1068 AA.
AC P42336; Q99762;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE alpha isoform (BC 2.7.1.153) (PI3-kinase p110 subunit alpha) (PtdIns-
DE 3-kinase p110) (PI3K).
GN PIK3CA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95229146; PubMed=7713498;
RA Volinia S., Hiles I., Ormondtroyd E., Nizetic D., Antonacci R.,
RA Rocchi M., Waterfield M.;
RT "Molecular cloning, cDNA sequence, and chromosomal localization of
RT the human phosphatidylinositol 3-kinase p110 alpha (PIK3CA) gene.";
RL Genomics 24:472-477(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97196568; PubMed=9043658;
RA Stridlyant S.M., Aherm J., Controy R.R., Barnett S.F., Ledder L.M.,
RA Oliff A., Heimbrook D.C.;
RT "Cloning and mutagenesis of the p110 alpha subunit of human
RT phosphoinositide 3'-hydroxylkinase.";
RL Bioorg. Med. Chem. 5:65-74(1997).
CC -!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A
CC PREFERENCE FOR PTDINS(4,5)P2.
CC -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidy1-ID-myo-inositol 4,5-
CC bisphosphate = ADP + 1-phosphatidy1-ID-myo-inositol 3,4,5-
CC triphosphate.
CC -!- SUBUNIT: HETEROIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC SUBUNIT.
CC -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC -!- SIMILARITY: Contains 1 C2 domain.
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CC -----
CC EMBL; Z29090; CAA82333.1; -
CC EMBL; U79143; AAB39753.1; -
CC PIR; I38110; I38110.
CC Genew; HGNC:8975; PIK3CA.

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MM, 171834; .  
 DR GO; GO:0007048; P:oncogenesis; TAS.  
 DR Interpro; IPR000008; C2.  
 DR Interpro; IPR000403; P13\_P14\_Kinase.  
 DR Interpro; IPR002420; P13\_K\_C2-  
 DR Interpro; IPR003113; P13\_K\_P85B.  
 DR Interpro; IPR003441; P13\_K\_P85B.  
 DR Interpro; IPR001263; P13\_K\_P85B.  
 DR Pfam; PF00092; P13\_K\_P85B; 1.  
 DR Pfam; PF00192; P13\_K\_P85B; 1.  
 DR Pfam; PF00794; P13\_K\_P85B; 1.  
 DR Pfam; PF00613; P13\_K\_P85B; 1.  
 DR SMART; SM00239; C2; 1.  
 DR SMART; SM00142; P13\_K\_C2; 1.  
 DR SMART; SM00143; P13\_K\_P85B; 1.  
 DR SMART; SM00144; P13\_K\_P85B; 1.  
 DR SMART; SM00145; P13\_K\_P85B; 1.  
 DR SMART; SM00146; P13\_K\_P85B; 1.  
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 DR PROSITE; PSS00916; P13\_4\_KINASE\_2; 1.  
 DR PROSITE; PSS0290; P13\_4\_KINASE\_3; 1.  
 DR TRANSFERASE; Kinase; Multigene Family.  
 FT DOMAIN; 319 428  
 FT DOMAIN; 797 1068  
 FT CONFLICT; 43 43  
 FT CONFLICT; 170 187  
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 FT CONFLICT; 286 287  
 FT CONFLICT; 332 332  
 FT CONFLICT; 346 346  
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 FT CONFLICT; 751 751  
 FT CONFLICT; 767 767  
 SO SEQUENCE 1068 AA; 124412 MM; 9E16BA7401A87B57 CRC64;

Query Match 99.1%; Score 5657; DB 1; Length 1068;  
 Best Local Similarity 98.9%; Pred. No. 0;  
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QY 1 MPRPSSGELMGTHLMPRLVLCCLPNCMTVTECLRENTLTITKELFKARKPYLHQ 60  
 DB 1 MPRPSSGELMGTHLMPRLVLCCLPNCMTVTECLRENTLTITKELFKARKPYLHQ 60  
 QY 61 LLDDESSYIFVSVTOEAREEPFDETRRLCDLRFQFLVIEVGRREKILNREIGFA 120  
 DB 61 LLDDESSYIFVSVTOEAREEPFDETRRLCDLRFQFLVIEVGRREKILNREIGFA 120  
 QY 121 IGMVCEFDWVKDPEVODFRRLNLTNCKEAVDLRLDLSPHSRAMYVYPVVESSPELPKH 180  
 DB 121 IGMVCEFDWVKDPEVODFRRLNLTNCKEAVDLRLDLSPHSRAMYVYPVVESSPELPKH 180  
 QY 181 IYKKLDKGOIIVIVWVISPNDKOKYTKLKNHDCVEQVIAEIRKTRSMLLSSQLK 240  
 DB 181 IYKKLDKGOIIVIVWVISPNDKOKYTKLKNHDCVEQVIAEIRKTRSMLLSSQLK 240  
 QY 241 LCVLEVOGKYLIVCGDEYFLEKYPISQYKTRSCIMLGRMPLMLMAESISYQPLMD 300  
 DB 241 LCVLEVOGKYLIVCGDEYFLEKYPISQYKTRSCIMLGRMPLMLMAESISYQPLMD 300  
 QY 301 CFTMPYSRRISTATPYMNGESTSKSLMTVNSALRIKILCATYVNVNIRIDIKIYVGTI 360  
 DB 301 CFTMPYSRRISTATPYMNGESTSKSLMTVNSALRIKILCATYVNVNIRIDIKIYVGTI 360  
 QY 361 YHGGEPLCDNVNTQRPVCSNPRNEMWLYDIYIPDLPRARLCLISGVGRGAKKEHC 420  
 DB 361 YHGGEPLCDNVNTQRPVCSNPRNEMWLYDIYIPDLPRARLCLISGVGRGAKKEHC 420  
 QY 421 PLAMGNINLEFDYDTLVSGKMLNLMVPRHGLDLNPIGVTSNPKETPCLELEDFW 480  
 DB 421 PLAMGNINLEFDYDTLVSGKMLNLMVPRHGLDLNPIGVTSNPKETPCLELEDFW 480

QY 481 SSVYKPEPMKSVIEEHANVSREAGFSYHAGLSNRLARDNELRENDKEQLRAICTRDP 540  
 DB 481 SSVYKPEPMKSVIEEHANVSREAGFSYHAGLSNRLARDNELRENDKEQLRAICTRDP 540  
 QY 541 SETTEOEKDFLMSHRHCVTIPILPLKLLSVKNSDEVAQWYCLVKDMPPIKPEAME 600  
 DB 541 SETTEOEKDFLMSHRHCVTIPILPLKLLSVKNSDEVAQWYCLVKDMPPIKPEAME 600  
 QY 601 LLDENVDPVWVGAFAVRCLEKYLTDKLSOYLQLOVQLYEDYLDLRLFRLLKRLTN 660  
 DB 601 LLDENVDPVWVGAFAVRCLEKYLTDKLSOYLQLOVQLYEDYLDLRLFRLLKRLTN 660  
 QY 661 ORIGHFFFMHLKSEMNKTYSQRFGLLESYCAACGYLKLNRQYAEKLLINTDILK 720  
 DB 661 ORIGHFFFMHLKSEMNKTYSQRFGLLESYCAACGYLKLNRQYAEKLLINTDILK 720  
 QY 721 QEKDEYQK 780  
 DB 721 QEKDEYQK 780  
 QY 781 LNMENPDINSLEFONNEIFKNQDDLRQDMLTLOIIRIMENTIMONOGDLRLMPYGLS 840  
 DB 781 LNMENPDINSLEFONNEIFKNQDDLRQDMLTLOIIRIMENTIMONOGDLRLMPYGLS 840  
 QY 841 IGDVGLIEVVRNSHTIMOIQCKGKGLQFNSHTLQWLKDKNGEYDAADLFTRS 900  
 DB 841 IGDVGLIEVVRNSHTIMOIQCKGKGLQFNSHTLQWLKDKNGEYDAADLFTRS 900  
 QY 901 CAGYCATPFLIGDRHNSNIMYKDDQQLPHIDFGLHKKKFGYKREVPVLTQDF 960  
 DB 901 CAGYCATPFLIGDRHNSNIMYKDDQQLPHIDFGLHKKKFGYKREVPVLTQDF 960  
 QY 961 LVIYSGAOECTREPERFOEMCYKAYLAIRQANLFTNLSFMMGSGSPELQSPDDIA 1020  
 DB 961 LVIYSGAOECTREPERFOEMCYKAYLAIRQANLFTNLSFMMGSGSPELQSPDDIA 1020

RESULT 3  
 ID P11A MOUSE STANDARD; PRT; 1068 AA.  
 AC PA2337;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit,  
 DE alpha isoform (EC 2.7.1.153) (P13-kinase p110 subunit alpha) (Ptdins-  
 DE 3-kinase p110) (P13K).  
 GN PI3KCA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RA MEDLINE=94187738; PubMed=8139567;  
 RX Kippel A., Escobedo J.A., Hirano M., Williams L.T.;  
 RT "The interaction of small domains between the subunits of  
 RT phosphatidylinositol 4,5-bisphosphate 3-kinase determines enzyme activity".  
 RL Mol. Cell. Biol. 14:2675-2685 (1994).  
 CC - FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 WITH A  
 CC PREFERENCE FOR PTDINS(4,5)P2.  
 CC - CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-  
 CC bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-  
 CC trisphosphate.  
 CC - SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)  
 CC SUBUNIT.  
 CC - SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.  
 CC - SIMILARITY: Contains 1 C2 domain.

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CC -----
DR EMBL; U03279; AAA18334.1; -.
DR MG1; MGI:1206581; P13Ka.
DR InterPro; IPR000008; C2.
DR InterPro; IPR000403; P13_P14_kinase.
DR InterPro; IPR002420; P13K_C2.
DR InterPro; IPR003113; P13K_C85B.
DR InterPro; IPR003411; P13K_ras_bind.
DR InterPro; IPR01263; P13Ka.
DR Pfam; PF00454; P13_P14_kinase; 1.
DR Pfam; PF00792; P13K_C2; 1.
DR Pfam; PF02192; P13K_C85B; 1.
DR Pfam; PF00794; P13K_Pdb; 1.
DR Pfam; PF00613; P13Ka; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00142; P13K_C2; 1.
DR SMART; SM00143; P13K_P85B; 1.
DR SMART; SM00144; P13K_Pdb; 1.
DR SMART; SM00145; P13Ka; 1.
DR SMART; SM00146; P13K; 1.
DR PROSITE; PS00004; C2 DOMAIN 2; FALSE_NEG.
DR PROSITE; PS00915; P13_4_KINASE_1; 1.
DR PROSITE; PS00916; P13_4_KINASE_2; 1.
DR PROSITE; PS50290; P13_4_KINASE_3; 1.
DR TRANSFERASE; Kinase; Multigene family.
KW DOMAIN 319 428 C2 DOMAIN.
FT DOMAIN 797 1068 P13K/P14K.
SQ SEQUENCE 1068 AA; 124453 MW; 67F54FCF8747FE1C CRC64;

Query Match 98.9%; Score 5645; DB 1; Length 1068;
Beet Local Similarity 98.8%; Pred. No. 0;
Matches 1055; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

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DB 1 MPPRSSGELMGILHMPRIILVECLIPNGMITVECLREALTITIKHELFKARKYPLHQ 60
QY 61 LLODESSYIFVSVTQEAEREERFDETRRLCDLRLFQPLKYIEPVGNEEKILNREIGFA 120
DB 61 LLODESSYIFVSVTQEAEREERFDETRRLCDLRLFQPLKYIEPVGNEEKILNREIGFA 120
QY 121 IGMPCVEDMKYKDEPVQDFRRNIILNVCEAVDLRLNPHSRAMVVPVNVSSPELPEKH 180
DB 121 IGMPCVEDMKYKDEPVQDFRRNIILNVCEAVDLRLNPHSRAMVVPVNVSSPELPEKH 180
QY 181 IYNNKLDKQOIIIVIVIVISPNNDKQYTLKINHDCVCPQVIAEAIRKKTGRLSSSEDLK 240
DB 181 IYNNKLDKQOIIIVIVIVISPNNDKQYTLKINHDCVCPQVIAEAIRKKTGRLSSSEDLK 240
QY 241 LCVLEYQKQYILKYVCGDEYFLKXPYLSQYKXIRSCIMLGRMPNIMLMAKESLYQLPMD 300
DB 241 LCVLEYQKQYILKYVCGDEYFLKXPYLSQYKXIRSCIMLGRMPNIMLMAKESLYQLPMD 300
QY 301 CPTMSYSRRISTATAPYNGSTSLWVINSALRIKILCAVYVNVNIRDIDKIYVRGI 360
DB 301 CPTMSYSRRISTATAPYNGSTSLWVINSALRIKILCAVYVNVNIRDIDKIYVRGI 360
QY 361 YHGGPPLCDNVVTPVPCSNPRMNMWLVYDIYIPDLPRARLCLTICSGYGRGAKKEBHC 420
DB 361 YHGGPPLCDNVVTPVPCSNPRMNMWLVYDIYIPDLPRARLCLTICSGYGRGAKKEBHC 420
QY 421 PLAMGNINILFDYDTDTLVSGKALNIMPVPHGLEDDLNPIGVTSNPNKTEPCLLEPDMF 480
DB 421 PLAMGNINILFDYDTDTLVSGKALNIMPVPHGLEDDLNPIGVTSNPNKTEPCLLEPDMF 480

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QY 481 SSVYKEPDMSVIREHANWSYREAGFSYSHAGLSNRLARNDLRENDKQALACTRDP 540
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QY 541 SEITEORCKDFLMSHRHYCTTPEILPKLLISVKNRSDEVAQMYCLVKMPPIKPEQAME 600
DB 541 SEITEORCKDFLMSHRHYCTTPEILPKLLISVKNRSDEVAQMYCLVKMPPIKPEQAME 600
QY 601 LLDONYPDPMPVNRGPAARCLEKYLTDKPLSQYLLQVQLVLYKEQYLDNLVRFLLKALTN 660
DB 601 LLDONYPDPMPVNRGPAARCLEKYLTDKPLSQYLLQVQLVLYKEQYLDNLVRFLLKALTN 660
QY 661 QRIHGFPEFMHLSKSEMNKTYSORFGLLBSYCACGNYLKHINROYAMEKILNLTDLK 720
DB 661 QRIHGFPEFMHLSKSEMNKTYSORFGLLBSYCACGNYLKHINROYAMEKILNLTDLK 720
QY 721 QEKKDETQYQMKFLYEQMRPDPMDALQGLFSLPAPAGLGNLRLPECKINSSAKRPLW 780
DB 721 QEKKDETQYQMKFLYEQMRPDPMDALQGLFSLPAPAGLGNLRLPECKINSSAKRPLW 780
QY 781 LMNENPDIMSELLFONNEIIFKNGDDLRODMLTLQIIRIMENIMONOGDLRLMPLGCLS 840
DB 781 LMNENPDIMSELLFONNEIIFKNGDDLRODMLTLQIIRIMENIMONOGDLRLMPLGCLS 840
QY 841 IGDVGLIEVVRNSHTIMQIQCKGGLKALQFNSHTLHQLKDKNKGEIYDAAIDLETRS 900
DB 841 IGDVGLIEVVRNSHTIMQIQCKGGLKALQFNSHTLHQLKDKNKGEIYDAAIDLETRS 900
QY 901 CAGYCVATFLIGIDRRNSINMYKDGQLFHIQGHLDHKKKFGYKRRVFPVLTQDF 960
DB 901 CAGYCVATFLIGIDRRNSINMYKDGQLFHIQGHLDHKKKFGYKRRVFPVLTQDF 960
QY 961 LIVISKAQOECTREPERFOEMCYKAYLAIROHANFLINLFSMMLSGSMBELQSPDIA 1020
DB 961 LIVISKAQOECTREPERFOEMCYKAYLAIROHANFLINLFSMMLSGSMBELQSPDIA 1020
QY 1021 YIRKTLALDXTQDEALEYFMKQNDAAHGGWTKMDMIFHTIKOHALN 1068
DB 1021 YIRKTLALDXTQDEALEYFMKQNDAAHGGWTKMDMIFHTIKOHALN 1068

RESULT 4
P1ID HUMAN STANDARD; PRT; 1044 AA.
AC 000329; O15445;
ID 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,
DE delta isoform (BC 2.7.1.153) (P13-kinase p110 subunit delta) (PtdIns-
DE 3-kinase p110) (P13K) (p110delta).
GN P13CD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N. A.
RP MEDLINE=9727223; PubMed=9113989;
RA Vanhasebeoeck B.A.M., Welham M.J., Kotani K., Stein R., Warne P.H.,
RA Zvelebil M.J., Higashi K., Voljani S., Dowward J., Waterfield M.D.,
RT "p110delta, a novel phosphoinositide 3-kinase in leukocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4330-4335(1997).
RN [2]
RP SEQUENCE FROM N. A.
RP MEDLINE=97382246; PubMed=9235916;
RA Chantry D., Vojtek A., Kashishian A., Holtzman D.A., Wood C.,
RA Gray P.W., Cooper J.A., Hoekstra M.F.;
RT "p110delta, a novel phosphatidylinositol 3-kinase catalytic subunit
RT that associates with p85 and is expressed predominantly in
RT leukocytes.";
RL J. Biol. Chem. 272:19236-19241(1997).
CC -1- CATALYTIC ACTIVITY: ATP + 1-phosphatidy1-ID-myo-inositol 4,5-

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bisphosphate = ADP + 1-phosphatidy1-D-myo-inositol 3,4,5-trisphosphate.  
CC -1- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.  
CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY) SUBUNIT.  
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LEUKOCYTES.  
CC -1- SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.  
CC -----  
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CC -----  
DR EMBL: Y10055; CAJ71149.1; -;  
DR EMBL: U64553; AAC25677.1; -;  
DR Genew; HGNC:8977; PI3KCD.  
DR MIM; 602839; -;  
DR GO; GO:0005942; C:1-phosphatidylinositol 3-kinase complex; NAS.  
DR GO; GO:0016303; F:phosphatidylinositol 3-kinase activity; NAS.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.  
DR GO; GO:0007165; P:signal transduction; NAS.  
DR InterPro; IPR000403; PI3\_P14\_kinase.  
DR InterPro; IPR002420; PI3K\_C2.  
DR InterPro; IPR003113; PI3K\_P85B.  
DR InterPro; IPR000341; PI3K\_rae\_bind.  
DR InterPro; IPR001263; PI3K.  
DR Pfam; PF00454; PI3\_P14\_kinase; 1.  
DR Pfam; PF00792; PI3K\_C2; 1.  
DR Pfam; PF02192; PI3K\_P85B; 1.  
DR Pfam; PF00794; PI3K\_rbd; 1.  
DR Pfam; PF00613; PI3K\_a; 1.  
DR SMART; SM00142; PI3K\_C2; 1.  
DR SMART; SM00143; PI3K\_P85B; 1.  
DR SMART; SM00144; PI3K\_rbd; 1.  
DR SMART; SM00146; PI3K\_a; 1.  
DR PROSITE; PS00915; PI3\_4\_KINASE\_1; 1.  
DR PROSITE; PS00916; PI3\_4\_KINASE\_2; 1.  
DR PROSITE; PS00290; PI3\_4\_KINASE\_3; 1.  
DR TRANSFERASE; Kinase; Multigene family.  
KW DOMAIN 776 1029 PI3K/PI4K.  
FT DOMAIN 253 253 S -> N (IN REF. 2).  
FT CONFLICT 675 675 R -> S (IN REF. 2).  
SQ SEQUENCE 1044 AA; 119548 MW; B68B6F06A5A97A CRC64;

Query Match 34.6%; Score 1976.5; DB 1; Length 1044;  
Best Local Similarity 39.9%; Pred. No. 4,2e-127;  
Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

QY 16 MRP-----RTLVETLPNGMIVTLEICREATLTITKHELEKREARKYLIHQ 60  
DB 1 MRPGVDCMEFWTKENQSVVDFLLPTGVLENPVSRNANLSTIKQLMHRRAQYEFLFH 60

QY 61 LLODESSYIFVSYQEAEREEFDETRRLCDLRLFOPLKVIIEVGNREKILNRIGFA 120  
DB 61 MUGSPFAVYVTCINQTELEQGELEDEQRRLCDVQEPFLVLLVAREGRVKKLINSQSL 120

QY 121 IGMFVCEFDNVKQDEVDFFRNILNVCKEAVLDRLNLSPHSRAMYVPNVESSEPE---- 176  
DB 121 IKGKLEHFDLCPDEVNDFRKMKCOQCEFAARQQLGWEAMLCQSPFLQLEPSAQWGP 180

QY 177 -----LPHKIVNKKDKGQIIVIVWYVSPNNDKQYTIKINHDCVPEVIAEARKKTRSM 232  
DB 181 GTRLPLRR-----ALLVNVKPEGSESESFYQSTKDVPLALMACARKK----- 224

QY 233 LLSSEQLKLVLEQGYKYLKVGCCDEYFLEKYPVLSQYKIRSCIMLRPNMLMAKES 292  
DB 225 ---ATVFRQPLVQRPEDYTLQVNGRHEYLKGSYPLCOFYICGLSHGSLPHLTMHSSS 281

QY 293 LYSQLPMDCTMPSYSRRISTATPRYNGESTKSLWVINSALRIKILCATYVNVNIRDD 352

DB 282 ILANRDEQSNPAQVQRPRAKPPPIPAKKPPSSVLSMSLEQPFRIELIQSKRVNADER--M 339

QY 353 KIYRTGIYIGGEPLCDNVNTORVP--CSNPRNMENILYDIPDLPAARLCISGCV-- 409  
DB 340 KLVVQAGLPHGNEMLCCTVSSSEVSSSEVWQKORLEFDINICDLPMAALCPALYVIE 399

QY 410 -----KGRKGAEEHCPLAMGNINLPDYTDITVSGKRALNLP-VPHGLEDLNPIGYT 462  
DB 400 KAKKARSTKKSKKADCPIAMAMLMFDYDQKGTGERGLYMPSPVDEKELLNPGTV 459

QY 463 GSNPNKTP-----CLELEFDWFSVVKFPDMSVIEBHANWSVREAGFSYSHAGLSNRL 517  
DB 460 RSNPNNDSSAALLICLP---EVAPHPYVALEKILE-----L 494

QY 518 ARDNE---LRENDKEQRAICTRDPVSEIRQEKDFLMSHRHYCVT-IPEILPKLLSVK 573  
DB 495 GRHSECVHTVEEOLOUREILERRGSELTVEHEDVLWKLRHVEHFPAALARKLLVTK 554

QY 574 MNSRDEVAQWYCIWKWPPRIKPEQAMELDCNYPDPWVRGFAVRCLEKYLTDKLSQYL 633  
DB 555 MNKHEDVAQWLYLILGSPBELPVLSALELDFSPFDCHVGSFAIKSLRK-LTDELPGYL 613

QY 634 QLVQVLKYEOYLNLVRFLLKALTNQRIGHFFPWHLKSEMNKTVSQRFGLLBSYCR 693  
DB 614 QLVQVLKYESYLDCELTCKFLDLRALNRKIGHFLFWHLRSEMHVPSVALRFGILVAYCR 673

QY 694 ACGWYVLCNLRQVYAEWKILNLTDLIKOEKKDEFQKQWKFVBO--MRRPDPMALQGF 752  
DB 674 GRTHMKVLMKQGBALSKLALNDPVKLSQ-KTPKQYKELMHLCKRQAVYLEALSHLQ 722

QY 753 SPLNPAHQNLRLREGRINSSAKRPLMLNMENPDINSELFPONNELIPKNGDRLQDML 812  
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DB 790 TLQMIQIMDLVLMKQGBALDLMETPEYGLPTGDRGLIEVLRSDTIANIQKNSMATAA 849

QY 872 FNSHTLHOMLKDNKKGIVDAIDLFRSGAGCVATFLLIGDRHNSNMVMDQGLFH 931  
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DB 968 RRRGLFLHLFALMRAAGPELSCSKDIOYLKDSLALGKTEEBALKHFRVFNDALEESW 1027

QY 1052 TTKMDMIFHTIKQ 1064  
DB 1028 KTKVNMVLHANVSK 1040

RESULT 5  
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ID PI1B\_RAT STANDARD; PRT; 1070 AA.  
AC Q921D0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit, beta isoform (EC 2.7.1.153) (PI3-kinase p110 subunit beta) (Ptdins-3-kinase p110) (PI3K) (PI3Kbeta).  
GN PI3KB.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;

QY	354	IYRTGTGHHGEEPLCDVNTQRPVCSNPR -WNEMLVNDIYIPDLPRARLCLTICS----	408
Db	351	VHVRAGLPHCTELLCTKVVSSELSGKNDHIMNQLBERDINIICDLPARARLCPAIVAYLADK	410
QY	409	VKCRKGAK-----EBHCPLANGINLPDYDTLVSGKALNLW -PVRPGL	453
Db	411	VKTIKKSTKRTINPSKQYOTIRKAGKVHVPAAVNMVDFPKQLSGVDIILSWSSFPDELE	470
QY	454	DLNLPICGVTSNP-----NKEPTCLBLEFDMFSSVVRKPDMSVLEEHANWS	499
Db	471	EMLNPMETVOINPRAENATLALHFKPENKKQOPYYPEFD-----KILEKAEIA	519
QY	500	VSRBAGSYVHAGLSNRNLADNELRENDKEQLPAICTRDLSEITEOKDFLWSHRHYC-	558
Db	520	SGBSA--NVSSRGKFLA-----VKEIIDRDLPSQCEWEMDLIWLTRQDCR	566
QY	559	VTIPEILPKLLSVKXNSRDEVAQMWCLVDPWPRIPEQAMELIDCNYPRPMVRGFAVRC	618
Db	567	ENFPQSLPKLLISTIKWKLDEVAQLOALLOIWPCLPREALELDFNFYPRQYAREVAVGC	626
QY	619	LEKLTLDKLSQYLILQVLVQVLYKTEQYIDLNLVFLKALTNQRIHGFPMHLKSEHNK	678
Db	627	L-RMSDEEELSQYLLQVLVQVLYKTEPEFLDCLSRFLERALDNRRIQGLFWHLRSEVTP	685
QY	679	TYSORFELLLESYCRACGMYLKHNLROVEMEKILNLTDLKQEKDQETQVKQKFLVEQ	738
Db	686	AVSLQGFVILLEYAYCRSGVGHMKVLSKQVEYLNKLKTINSILKLNAMKLNPAKKGEMHTC	745
QY	739	MRREDFDALQGLFSLPNPAHOLGNLLEBCRIMSASAKRPLMWENPMISELLPQNE	798
Db	746	LKQSAVREALSLDQSLPNCVILISELYVEKCRVWDSQMKPLMWYSNRAGGEDAV---G	801
QY	799	IIFPNQDGLRQDMKTLTOIRIMENIQONOGLDRLMPLPYGLSLSDGCGLIEVRANSTIM	858
Db	802	VIFKNGDGLRQDMKTLQMLRLMDLMLKEMAGLIDRLMPLPYGLSLSDGCGLEVAVSTETIA	861
QY	859	QIQC-KGGLGALQFNSHTLQWMLKDKNGKEIYDAATDLFTRSCAGCVATPFIIGDRH	917
Db	862	DIQNSSNVATAAFANFNKDALINMLKEKNSGDDLRALIEETLSGAGCVASVYIGIDRH	921
QY	918	NSNINWDDQGLPHIDPGHFLDHKKKFGYKREKRVFVLTODFLIVISKAQOECTKREF	977
Db	922	SDNIMVKKTGQLPHIDFGHLIGNKSKFGAKREKRVFVLTYDFVHVIQGG--KTGNTEKF	979
QY	978	ERPOEMCYKAYLAIQGANLFINLFSMGLSGMPFELSPFDIATIKRTALADKTEQDALE	1037
Db	980	GRFQCCEDBAYLLIRRRGNLFITFLFALMTAGLPELTSVXDIOYLDKSLALGKSEBALK	1039
QY	1038	YFMKQNDANHHGWTQMDMIFHIKO	1064
Db	1040	QFKQKFEALRESWTTKYVNMMAHTVRK	1066

RESULT 6

P11B_HUMAN	STANDARD;	PRT;	1070 AA.
AC	P42338;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit, beta isoform (BC 2.7.1.153) (P13-kinase p110 subunit beta) (PtdIns-3-Kinase p110) (PI3K)		
DE	(P13K) (P13Kbeta).		
GN	PIK3CB.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteheria; Primates; Carnivora; Hominoidea; Homo.		
OX	NCBI_Taxid:9606;		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=94067128; PubMed=8246984;		
RA	Hu P., Mondino A., Skolnik E.Y., Schlessinger J.:		
RT	"Cloning of a novel, ubiquitously expressed human		



DB 974 GNTKGFRCCECDAYLILRRHGNLFTLFTALMTAGLPELTSVXDIOYLKDSLALGKS 1033  
 QY 1032 EORALEYFMKQNDAAHHGWTMTDMIFPHIKQ 1064  
 DB 1034 EEBALQKQKQFDEALRESWTYVNMVAHTVRK 1066

RESULT 7  
 P11D\_MOUSE STANDARD; PRT: 1043 AA.  
 ID P11D\_MOUSE  
 AC 035904;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,  
 delta isoform (EC 2.7.1.153) (P13-kinase p110 subunit delta) (PtdIns-  
 3-kinase p110) (P13K) (p110delta).  
 GN PI3KCD.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=97382246; PubMed=9235916;  
 RA Chanzy D., Vojtek A., Kaeshian A., Holtzman D.A., Wood C.,  
 Gray P.W., Cooper J.A., Hoekstra M.F.;  
 RT "p110delta, a novel phosphatidylinositol 3-kinase catalytic subunit  
 that associates with p85 and is expressed predominantly in  
 leukocytes.";  
 RT J. Biol. Chem. 272:19236-19241 (1997).  
 RL J. Biol. Chem. 272:19236-19241 (1997).  
 CC -1- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-D-myo-inositol 4,5-  
 CC bisphosphate = ADP + 1-phosphatidyl-ID-myo-inositol 3,4,5-  
 CC triphosphate.  
 CC -1- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.  
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)  
 CC SUBUNIT.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LEUKOCYTES.  
 CC -1- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL, U8587; AAC25676.1; -  
 CC DR PIR, T43502; T43502.  
 CC MGD, MGI:1098211; P13cd.  
 DR InterPro: IPR000403; P13\_P14\_kinase.  
 DR InterPro: IPR002420; P13K\_C2.  
 DR InterPro: IPR003113; P13K\_P85B.  
 DR InterPro: IPR000341; P13K\_tas\_bind.  
 DR InterPro: IPR001263; P13Ka.  
 DR Pfam: PF00454; P13\_P14\_kinase; 1.  
 DR Pfam: PF00792; P13K\_C2; 1.  
 DR Pfam: PF02192; P13K\_P85B; 1.  
 DR Pfam: PF00794; P13K\_P85; 1.  
 DR Pfam: PF00613; P13Ka; 1.  
 DR SMART, SM00142; P13K\_C2; 1.  
 DR SMART, SM00143; P13K\_P85B; 1.  
 DR SMART, SM00144; P13K\_P85; 1.  
 DR SMART, SM00145; P13Ka; 1.  
 DR SMART, SM00146; P13K; 1.  
 DR PROSITE, PS00915; P13\_4\_KINASE\_1; 1.  
 DR PROSITE, PS00916; P13\_4\_KINASE\_2; 1.  
 DR PROSITE, PS0290; P13\_4\_KINASE\_3; 1.  
 DR Transferase; Kinase; Multigene family.  
 KW TRANSFERASE; KINASE; MULTIGENE FAMILY.  
 FT DOMAIN 775 1028 P13K/P14K.

SO SEQUENCE 1043 AA; 119647 MW; A998F9E092CA361D CRC64;  
 Query Match 34.3%; Score 1958; DB 1; Length 1043;  
 Best Local Similarity 39.7%; Pred. No. 7, 6e-126;  
 Matches 429; Conservative 187; Mismatches 391; Indels 74; Gaps 19;  
 QY 16 MPP-----RIIVCECLPENGIVTLCELEATLITIKHELFEKARKYPLHQ 60  
 DB 1 MPPGVDCPMEFWTKESOSVVDPLFLPTGVINLFPVSRNANLSTIKOVLMMHRAQVEPLPH 60  
 QY 61 LLODESSYIFVSTQDAEREBFFDETRRLCDLRFQPLKVIPEVGNREKELNBEIGA 120  
 DB 61 MLSDPEAYVFTCNQAOEQLEDEQRRLCDIOPLFLVRLVARBGRVYKILNIGSLIL 120  
 QY 121 IGMPEVEFPMVKDPEVQDFRRRIINLVCKEAVDLRLNDSHSAAMYYPNVESPELPK- 179  
 DB 121 IAKGHEFSLRDPVENDFRTKRFCEBAAHROQLGWEVWLQYSFPLQLEPSANGMFA 180  
 QY 180 ---HIYNKLDKQGLIVIVIVISPNNDKOKYTLKINHDCVPEQVIAEAIRKTRMLSS 236  
 DB 181 GLIRVSNR-----ALVNVKFESESSEFTFOVSTKMPALAMCALRK-----A 225  
 QY 237 EQLKLCVLEYOGKYLKVCODEYFLEKYPLSQKYIRSCIMGRPNIMLMAKESLYSQ 296  
 DB 226 TVFRQPLVEQPEEYALQVNGRHELYGNYPPLCHFQYICLSHSGLTPHILTMHSSILM 285  
 QY 297 LPMDCFTMPSYRRITATPYPMNGESTSKSLWINALIKILCATYVNVNIRIDIKIYV 356  
 DB 286 RDEQSNPAPQVQPRKAPPEIPAKKSSVSLWLEQPFSELEGRKVNDE--MKLYV 343  
 QY 357 RTGIYHGEPLCGNVNTQRY-PCSNPRMFWLNYDYIIPDLPRARLCLISCSV----- 409  
 DB 344 QAGLPHENELCKTVSSSENVCSSEPMKORLEFDSVCDLPRMARLCPALYAVEKAKK 403  
 QY 410 --KGRKAKEHNPPLAWGNLFDYDTLVSGMALNLP-VPHGLDLNPLPGVTGSPN 466  
 DB 404 ARGTRKSKKADCPAIANMLPFDYKQDLKTGRCLYMPSPVDEKCELLPAGTVRGNP 463  
 QY 467 NKETPCELEFDMFSSVYKFPDMSVIEEHANMSVSEAGSYHAGISNRLANDNELEN 526  
 DB 464 NTESSA-----ALVTVPE--VAPHPVYPALEKILELRHGRGRIT-EEEL--- 508  
 QY 527 DKQBLRAICTRDLPLSETTEQKDFPLMGRHYCT-IPLEIPKLLSVKMSRDEVAQMYC 585  
 DB 509 ---QLRILEBRSGGEYEHKEKLVKMGRIHVEGHEPEALARLLVTKMKHDEVAQMYL 565  
 QY 586 LVKQMPRIKQEOAMELIDCVYDPMVNGFAVRCLKYLITDLSQYLQVLYVLYKCYL 645  
 DB 566 LIGCMPPELPVLSALBELDSSFPDCYVGSFAIKSLRK-LTDDELFOYLQVLYVLYKESYL 624  
 QY 646 DNILVRLKALTNQKIGHFFFWHLKSEMNKTVSQRFGLLESYGRACGMVYKHLNRQ 705  
 DB 625 DCELTKFLGLRALNRIKGFHFWHLSEMNVPVALRFGILMAYCRGSGTHHKVLMKQ 684  
 QY 706 VEAMEKILNLDILKOEKKDCTQVOMKFLVEQ--MRBPDEFDALQGFPLNPAPHQNL 764  
 DB 665 GEALSKLALNDPVKVSQ-KTKPKQTKEMMHMKQGETYMEALSHQSPLDSPTLLEEV 743  
 QY 765 RLEBCRIWSAKRPLMWNPNIDMSBELFPONNIEIFKNGDRLQDMTLQIIMENIW 824  
 DB 744 CVEQCTFSDSKMKPLMIYSSSEBAGS---GNVGIIIFKNGDRLQDMTLQIIMIDVLM 800  
 QY 825 QNQGILDLMLPYGCLSTGDCVGLIEVRANSHTIQIQC-KSGLGAALOFSHTLQHWLKD 883  
 DB 801 KOEGLDLMTFYGCLPTGDRTGLIEVLAHSPTIANIQINKSNMATAAFNDALINMLKS 860  
 QY 884 KKKGEITAAIDLFRSCAGYCVATFPIIGIDRHSNINWVDQOLFPIIDGFLDHKKK 943  
 DB 861 KNPGBALRALBEFTLSAGYCVATFVIGIDRHSNINWVDQOLFPIIDGFLDHKKK 920  
 QY 944 KFGYREVRVPLTODFLIVISKGAOECTKREFRPOEMCYKAYLAIRQANLFINLFS 1003  
 DB 921 KFGIRKREVPFILTYDFVHVIQGS--KTNNSKFERFRGVCERAVYTLIRRGGLFLHIFA 978



QY 1004 MMLGSGMPELQSPDDIAYIRKTLALDTEQEALEYFNKQNNDAHGGWTKMDIPIFTIK 1063  
 Db 979 IMBAAGHPELSCSKDIDYLDKSLALGKTEBEALKHFFVKNFNEALRESWTKVWMLAINVS 1038  
 QY 1064 Q 1064  
 Db 1039 K 1039

RESULT 8  
 P13G\_MOUSE STANDARD; PRT: 1102 AA.

ID P13G\_MOUSE STANDARD; PRT: 1102 AA.  
 AC 09UG7;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,  
 DE gamma isoform (EC 2.7.1.153) (P13-kinase p110 subunit gamma) (Ptdins-  
 DE gamma p110) (P13K) (P13Kgamma).  
 GN P13KCG OR P13KGI.  
 OS Mus musculus (mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hirsch E.;  
 RT "Murine P13Kgamma: cDNA cloning and gene structure description";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Wymann M.P., Hirsch E.;  
 RT "Murine G protein-coupled phosphoinositide 3-kinase gamma cDNA and  
 RT genomic organisation";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE  
 CC PTDINS-4,5-BISPHOSPHATE (PTDINS(4,5)P2) (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + 1-phosphatidy1-1D-myo-inositol 4,5-  
 CC bisphosphate = ADP + 1-phosphatidy1-1D-myo-inositol 3,4,5-  
 CC triphosphate.  
 CC -1- ENZYME REGULATION: ACTIVATED BY BOTH THE ALPHA AND THE BETA-GAMMA  
 CC G PROTEINS (BY SIMILARITY). MORMANNIN SENSITIVE IN NM RANGE.  
 CC -1- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.  
 CC -1- SUBUNIT: HETERODIMER OF A 101 kDa SUBUNIT AND A 120 kDa CATALYTIC  
 CC SUBUNIT (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.  
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 CC  
 DR EMBL; AJ249413; CAB89851.1; -;  
 DR EMBL; AJ249414; CAB89851.1; JOINED.  
 DR EMBL; AJ249415; CAB89851.1; JOINED.  
 DR EMBL; AJ249416; CAB89851.1; JOINED.  
 DR EMBL; AJ249417; CAB89851.1; JOINED.  
 DR EMBL; AJ249418; CAB89851.1; JOINED.  
 DR EMBL; AJ249419; CAB89851.1; JOINED.  
 DR EMBL; AJ249420; CAB89851.1; JOINED.  
 DR EMBL; AJ249420; CAB89851.1; JOINED.  
 DR MGD; MGI:135376; P13KCG.  
 DR InterPro; IPR000403; P13\_P14\_kinase.  
 DR InterPro; IPR002420; P13K\_C2.  
 DR InterPro; IPR000341; P13K\_raf\_bind.  
 DR InterPro; IPR001263; P13Ka.  
 DR Pfam; PF00454; P13\_P14\_kinase; 1.  
 DR Pfam; PF00792; P13K\_C2; 1.  
 DR Pfam; PF00794; P13K\_tbd; 1.

DR Pfam; PF00613; P13Ka; 1.  
 DR SMART; SM00142; P13K\_C2; 1.  
 DR SMART; SM00144; P13K\_tbd; 1.  
 DR SMART; SM00145; P13Ka; 1.  
 DR SMART; SM00146; P13KCG; 1.  
 DR PROSITE; PS00915; P13\_4\_KINASE\_1; 1.  
 DR PROSITE; PS00916; P13\_4\_KINASE\_2; 1.  
 DR PROSITE; PS50290; P13\_4\_KINASE\_3; 1.  
 KM Transferase; Kinase; Multigene family.  
 FT DOMAIN 18 1073 POLY-ARG.  
 FT 828 1073 P13K/P14K.  
 SQ SEQUENCE 1102 AA; 126361 MW; 89E94CFDD0C31D57 CRC64;

Query Match 25.9%; Score 1477.5; DB 1; Length 1102;  
 Best Local Similarity 33.3%; Pred. No. 5.5e-93;  
 Matches 380; Conservative 199; Mismatches 412; Indels 149; Gaps 37;

QY 1 MPBPSSGELIWMHLPRLVCELLPNGNIVT-----LECLREATLITTHHELFKEA 53  
 Db 23 MKPRSAAGSLSSWELIP---IEFVLPTSQRISKPTETALHVAHGQNVQMKQAQWLRA 78  
 QY 54 RKYPPL-----HOLLQDESSYIFVSVYQEAAREFPETRLCDRLPQPLK-----V 101  
 Db 79 LETSVAAEFYHRLGPPQFLLYLQKQWEIYDRYVQVOTLDLHYWKLMHKSPGOIHVV 138  
 QY 102 IEPVGRREKILNREIGFAIGMPVCEFDWYKQDEVDPRNLIIVCKEAVDLRLDNPSS 161  
 Db 139 QRHVPSBEETLAPKQULTSLGIVDTISVHDELEFTRRLVTPRMAEVAGDAK---- 194  
 QY 162 RANVYVPVNVSSPELPHKIIYNKLDKQIIVVIVVSPNNOKYTLKINHCVBEQVI 221  
 Db 195 --LYAHMPWTSKP--LPDYLSKKIANNCFIVT-----HRCGTSQTIKVASADDTGTL 245  
 QY 222 AEAIRK--KTRSLSSSEQKLCVLEQGYILKYCGCBYFLKXYPLOGYKIRSCIML 279  
 Db 246 QSFETTKAKKSLMNPES-----QSEDPVLVRCGRBEYLVGETPLKQFQWVROCLKN 299  
 QY 280 GRMPLML-----MAKESLYSQLPM--DCFTMPSRRISTAPYMNCE---TSTKSL 327  
 Db 300 GDEIHLVLTDPRLADVEKBEWPLVDCTGVGTGHEQTL-----IHGDHSSVTVSL 354  
 QY 328 WINSALRIKILCATYVNVNIRDID-----KIYVRTGIYHGGEPLCDNVNTPRV 377  
 Db 355 WDCDRFRVK-----IRGIDIPVLPRNTDLVFPANIQHQOVLQCRRTSPKPF 404  
 QY 378 CSNPRNENLVNDIYIPDLPRARLCLST--CSVKRKAKEHCP-----LAWG 425  
 Db 405 AEEVLNVWLEFGIKIKIDLPKCALINLQIYCCPTSLSSKASAEPTGSESKGKAOULLYV 464  
 QY 426 NINLPYDTTLVSGKALMLMPVPHLED--LLNPICVT--GSNPNKE--TPCELEFDWPS 481  
 Db 465 NLLILHRELRHGDVYLHMQVSGKAEQGSFNADKLTSATPDKENSISITLDNYC 524  
 QY 482 SVKFPDMSVIEBHANSVSRKAGFSYSHAGLSNRLARDNELRENDKEQRLAICTRDPSS 541  
 Db 525 HPALCPKHPPTPPEEDRV-----RAEMPNQRL-----KQLEALIAIDPLN 565  
 QY 542 EITEQEKDVLMSHRHYCVTIPILLPLLLSVKNSDEVAQMYCL-----VQDWPIKPE 596  
 Db 566 PLTAEDKELHMFRRYSLELGHPRAYPPLFSSVYKGOQEIYAKTYOLAREEIMQSAIDVG 625  
 QY 597 QAMELLDCNVPBMVNGFAVRCLEKTLTDKLSOYLIOIVQVLYKQYLDNLLVRLKK 656  
 Db 626 LTMQLDNCPSDBNVAVIAVQKLES--LEDDDVLYHLLQVAVKFPYHDSALARFLLR 684  
 QY 657 ALTNORIGHFFFMHLKSEM--HNKTVSQRFGLLESYCRAGC--MYLGLHRLROYEAMEKLN 714  
 Db 685 GLRNKRKIGHFLMFLRSEIQAQRHYQQRFAVILAEALRCCGAMIQDPFOGHVIEMLK 744  
 QY 715 LT-DI--LKQEKDEYQY--QMKFLVEQMRKRPDFDALOGFLSPINPAPHQGNRLBEC 769  
 Db 745 VVIDIKSLAEKYDVSSQVISOIKQKLESLQNSNLPES---FRVPYDPLKAGTLVIEKC 801

QY 770 RIMSAKRPLMLNME--NPDIIMSELLFQNN-----11FKNGDDIRQDMLTIQIIRIMENTW 824  
DB 802 KWASAKKKPLMEFKADPVLVS-----NETIGIIFKHGDDIRQDMLTIQIIRIMESIW 855  
QY 825 QNQGDLRLMPLPGCLSGDCVGLIEVRNSHTTMOI-QCKGGLKGLQENSHLHOMLKD 883  
DB 856 ETESLDLCPLPYGCLISGDKIGMIEYKQDFTTIAQIQOSTVGNTGA--FQDEVLNHMLKE 913  
QY 884 KNR-GEYDAIDLFTRSCAGCVATPILGIDRHSNINWKKDQGLFHIDFGHLDHKK 942  
DB 914 KCPTEEFQAAVERFVYSCAGVATPVLGIDRHNINIMISGNLPHIDFGHILGNK 973  
QY 943 KKEGYKERVVFLVTDPLVIVISKGAQECTKREEFERFQEMCKAYIATQHANLFTNL 1002  
DB 974 SFLGINNERVFLVTPDFLFWGSSGKTSR--HFQKFOVCVAVYALRHHTLLILFL 1031  
QY 1003 SMMLGSMPELQSDIDAIYIRKTLALDKTQDALEFEMKQNDHNGMTTKDMWIFHTI 1062  
DB 1032 SMMIMTGMPLQTSKEDIETIRDALTVKSEDAKKYFLDQIEVCGRDKGWTVQFNMFLHLV 1091

RESULT 9  
ID P11G HUMAN STANDARD; PRT; 1101 AA.  
AC P48736;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,  
DE gamma isoform (EC 2.7.1.153) (P13-kinase p110 subunit gamma) (Ptdins-  
DE 3-kinase p110) (PI3K) (PI3Kgamma).  
GN PIK3CG.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95350661; PubMed=7624799;  
RA Stoyanov B., Volinia S., Hanck T., Rubio I., Loubchenkov M.,  
RA Malek D., Stoyanova S., Vanhaesebroeck B., Dhond R., Nuenberg B.,  
RA Gierschik P., Seedorf K., Hsuan J.-J., Waterfield M.D., Wetzker R.;  
RT "Cloning and characterization of a G protein-activated human  
RT phosphoinositide-3 kinase";  
RT Science 269:690-693(1995).  
RN [2]  
RP REVISIONS.  
RA Waterfield M.D.;  
RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE  
CC PTDINS-4,5-BIPHOSPHATE (PTDINS(4,5)P2).  
CC -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidy1-D-myo-inositol 4,5'-  
CC bisphosphate = ADP + 1-phosphatidy1-D-myo-inositol 3,4,5'-  
CC triphosphate.  
CC -!- ENZYME REGULATION: ACTIVATED BY BOTH THE ALPHA AND THE BETA-GAMMA  
CC G PROTEINS.  
CC -!- PATHWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.  
CC -!- SUBUNIT: HETERODIMER OF A 101 kDa SUBUNIT AND A 120 kDa CATALYTIC  
CC SUBUNIT (BY SIMILARITY).  
CC -!- TISSUE SPECIFICITY: PANCREAS, SKELETAL MUSCLE, LIVER, AND HEART.  
CC -!- SIMILARITY: BELONGS TO THE P13/P14-KINASES FAMILY.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL; X83368; CAA58284.1; -.  
DR PDB; 1BBY; 17-NOV-00.  
DR PDB; 1EBZ; 17-NOV-00.

DR Genew: HGNC:8978; PIK3CG.  
DR MIM; 601232; -.  
DR GO; GO:0004429; F.1-phosphatidy1inositol 3-kinase; TAS.  
DR GO; GO:0007186; P-G-protein coupled receptor protein signalin...; TAS.  
DR InterPro; IPR000403; P13\_P14\_kinase.  
DR InterPro; IPR002420; PI3K\_C2.  
DR InterPro; IPR000341; PI3K\_ras\_bind.  
DR InterPro; IPR001263; PI3Ka.  
DR Pfam; PF00454; P13\_P14\_kinase; 1.  
DR Pfam; PF00792; PI3K\_C2; 1.  
DR Pfam; PF00794; PI3K\_tbd; 1.  
DR Pfam; PF00613; PI3Ka; 1.  
DR SMART; SM00142; PI3K\_C2; 1.  
DR SMART; SM00144; PI3K\_tbd; 1.  
DR SMART; SM00145; PI3Ka; 1.  
DR SMART; SM00146; PI3K; 1.  
DR PROSITE; PS00915; P13\_4\_KINASE\_1; 1.  
DR PROSITE; PS00916; P13\_4\_KINASE\_2; 1.  
DR PROSITE; PS50290; P13\_4\_KINASE\_3; 1.  
DR Transferrase; Kinase; Multigene family; 3D-structure.  
FT DOMAIN 18 22 POLY-ARG.  
FT DOMAIN 827 1072 PI3K/PI4K.  
SQ SEQUENCE 1101 AA; 126410 MW; 266BA6495C8A39E CRC64;  
Query Match 25.7%; Score 1467; DB 1; Length 1101;  
Best Local Similarity 35.3%; Pred. No. 2,9e-92;  
Matches 358; Conservative 179; Mismatches 352; Indels 126; Gaps 33;  
QY 107 NREBKILNREIGRGAIGMPVCEFDVYDPEVODFRNINLVNCKEAVLDRLNSPHSRAMY 166  
DB 143 SEESQARQQLTALIGVDVDSNVHDELEFRRGGLVPRMAEVSARD-----PKLYA 196  
QY 167 YPPNVSESPFLPKHIVYKDKQGIIVYIVVSPNNDKQKVTYTKINDCVPEQVIABAIR 226  
DB 197 MHPWVTSKRP-LPEYLMKRIANNCFIYI-----HNSITQSITKVSDDTFFGALLOSFT 249  
QY 227 K--KTRGMLSSSEQLCVLEYGQKYLKVCQDEVEFLKPYLSQYKYRISCIIMGMPN 284  
DB 250 KMAKKSLMDIPES-----QSEDDFVLRVCGRDEVLVGETPIKPFQWVHCLKNGEIH 303  
QY 285 LML-----MAKESLYSQLPM--DCFTMPSYRRISTATPYNGE-----TSTSLVWINS 332  
DB 304 VLDTPPDPALDEVRKEBWLVDCTGVYHEQLT-----IHGKHESVFTSLMCCDR 358  
QY 333 ALRKILICATVYVNNIDID-----KIYRTGIYHGEPLCDNNVQTVPCSNPR 382  
DB 359 KFRVYK-----IRGIDIPVLPRNTDLTVFEVANIIGHQOVLCOQRISPKPTEEV 408  
QY 383 MNEWLNVDIYIPDLPRARLCLTICSVK---GRGKAKEHCHPLAMGNINLFDYDTLV- 437  
DB 409 WNWMLERSIKIKDLPKGLNLNLQYCKAPALSKASAEPSSESCKGVRLVYVNNLLI 468  
QY 438 -----SGKMLNLMPVPHGLEL-LINPIGVY-GSNPNKE-TPCLELEFDMSSVYKF 486  
DB 469 DHRFLRLRGVEYVLMHWQISGGEODGSEFNADKLTSATPDKENSMSSISILDNCHPLAL 528  
QY 487 PDMSTIEHANWWSYRBAEGFSYSHAGLSNRLARQNEIRENKDQLRAICTRDPISIEIQ 546  
DB 529 PKHQPTPPEBGRV-----RAEMPQQLR-----KOLEIAIADPLNPLTAE 569  
QY 547 EKDFLMSHRHYCVTIPILPKLLSVKNSSDEVAQWYCL-----VKDMPRIKEQAMEL 601  
DB 570 DEELMHRRYSLKHPKAYPKLFSSVYKKGQOEIYAKTQGLARREVMQSLADVGLTNO 629  
QY 602 LDCNYPDMVNGFAVRCLEKYLTDKLSQYLIQLVQVLKYEQYLDNLVLEFLKKALTNQ 661  
DB 630 LDCNSDENVARIAVQKLES-LEDDVLAHYLLQLQAVKFPYHDSALARFLKRGLENK 688  
QY 662 RIGHPFPWHLKSEM-HAKTVSGRFGLLLESYCRACGMVLKH-LNQVAMEKLIVLT-DI 718  
DB 689 RIGHFLFWFLRSEIAQSHYQGRFAVILAEYLRGGTLMLEDFTVQOVVTEMLQCVTTLDI 748  
QY 719 --LKEKKDEIQKV--QKKFLVGEQRRRPPDMALGFLSLPLNPAHQNLRLBECRIMSS 774

Db 749 KSLSAEVYVSSQVLSQKLELQNSQLES---FRVYDGLKAGALAEKCKVMAS 805  
 QY 775 AKRPLMLNME--NPDIWSELLFQNN---IIFKNGDDLRODMTLQIRIMENIMQNGL 829  
 Db 806 KKKPLMLEFRCAPPLALS-----NRTIGIIFKGGDLRODMTLQIRIMESWESL 859  
 QY 830 DLMLPYGLSISDCVGLIIVENSHTIMQI--QCKGKLKALQFNSHTLHOMLKDN-KG 887  
 Db 860 DLCLLPYGCISTGDKIGMEIVDATTIAKIQOSTVANTGA--FKDEVLNHMLKEKSPTE 917  
 QY 888 EYDADALIDFTRSCAGCVATFLIGDRHNSNMWDCQLPHIDGHFLDKKKKFGY 947  
 Db 918 EKFQAVERVVYSCAGCVATFVLGIGDRHNDIMITEGTLPHIDGHFLGKYSKFLGI 977  
 QY 948 KREVEFVLTDPLIVISKAQECTREPERFOEMCYKAYLAIRQANLFINLFSMMLG 1007  
 Db 978 MKRVEFVLTPDLFPLWGTSGKKTSP--HFQKQDLCVKAYLRLHHTLILLFSLMLM 1035  
 QY 1008 SGMPQLQSPDDIAYIRKTLALDXTQDALRYFKOMNDHAGGWTTCMDI PFTI 1062  
 Db 1036 TGMPLQTSKEDIYIRDALTVGKNEBDKXKYLQLEVCRCDKGWTQVFNWFLHLV 1090

RESULT 10  
 ID P11G\_PIG STANDARD; PRT; 1102 AA.  
 AC 002697;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit,  
 DE gamma isoform (EC 2.7.1.153) (PI3-kinase p110 subunit gamma) (Ptdins-  
 DE 3-kinase p110) (PI3K) (P120-PI3K).  
 GN PI3KCG.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.  
 OC NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Neutrophils;  
 RX MEDLINE=97248491; PubMed=9094719;  
 RA Stephens L.R., Eguinoa A., Erdjument-Bromage H., Lui M., Cooke F.,  
 RA Coadwell J.J., Strack A.S., Thelen M., Cadwallader K., Tempst P.,  
 RA Hawkins P.T.;  
 RT "The G beta gamma sensitivity of a PI3K is dependent upon a tightly  
 RT associated adaptor, p101.";  
 RT Cell 89:105-114 (1997).  
 RL [2]  
 RP REVISIONS.  
 RA Stephens L.R.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 CC - FUNCTION: 3-PHOSPHORYLATES THE CELLULAR PHOSPHOINOSITIDE  
 CC PTDINS-4,5-BIPHOSPHATE (PTDINS(4,5)P2).  
 CC - CATALYTIC ACTIVITY: ATP + 1-phosphatidy1-1D-myo-inositol 4,5-  
 CC bisphosphate = ADP + 1-phosphatidy1-1D-myo-inositol 3,4,5-  
 CC triphosphate.  
 CC - ENZYME REGULATION: WHEN BOUND TO P101 THE PI3K ACTIVITY OF P120  
 CC COULD BE ACTIVATED GREATER THAN 100-FOLD BY THE BETA-GAMMA G  
 CC PROTEINS.  
 CC - PATWAY: SIGNALING PATHWAYS REGULATING CELL GROWTH.  
 CC - SUBUNIT: HETERODIMER OF A 101 kDa SUBUNIT AND A 120 kDa CATALYTIC  
 CC SUBUNIT.  
 CC - SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.  
 CC -----  
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 CC or send an email to license@isb-sib.ch).

CC -----  
 DR EMBL: Y10743; CAA71731.1; -  
 DR PDB: 1E7U; 01-DEC-00.  
 DR PDB: 1E8X; 01-OCT-02.  
 DR InterPro: IPR000403; PI3\_P14\_kinase.  
 DR InterPro: IPR002420; PI3K\_C2.  
 DR InterPro: IPR000341; PI3K\_ras\_bind.  
 DR InterPro: IPR001263; PI3K.  
 DR Pfam: PF00454; PI3\_P14\_kinase; 1.  
 DR Pfam: PF00792; PI3K\_C2; 1.  
 DR Pfam: PF00794; PI3K\_Ibd; 1.  
 DR Pfam: PF00613; PI3K; 1.  
 DR SMART: SM00142; PI3K\_C2; 1.  
 DR SMART: SM00144; PI3K\_Ibd; 1.  
 DR SMART: SM00145; PI3K; 1.  
 DR SMART: SM00146; PI3K; 1.  
 DR PROSITE: PS00915; PI3\_4\_KINASE\_1; 1.  
 DR PROSITE: PS00916; PI3\_4\_KINASE\_2; 1.  
 DR PROSITE: PS50290; PI3\_4\_KINASE\_3; 1.  
 DR Transferrase; Kinase; Multigene family; 3D-structure.  
 FT DOMAIN 17 22 POLY-ARG.  
 FT 828 1073 PI3K/PI4K.  
 SO SEQUENCE 1102 AA; 126657 MW; 9E7D4211FD626DFC CRC64;

Query Match 25.7%; Score 1465.5; DB 1; Length 1102;  
 Best Local Similarity 33.5%; Pred. No. 3,7e-92;  
 Matches 382; Conservative 204; Mismatches 405; Indels 149; Gaps 39;

QY 1 MPRPSSGGLWGIHLMPPRIIVLVECLLPNGMIYT-----LSCLRBATLITIKHELFKEA 53  
 Db 23 MKRSTASLSSMELIP-----IEFVLPTSQRMKTPETALLNVAHGCHNEOMKAWQLRA 78  
 QY 54 RKYPL-----HOLDQESSYIFVSVTQAEAREBFPETRLDLRFQFP-----LKYI 102  
 Db 79 LRTSVADRYHRIQPHFLLLYQKGGQWYIYDKYQVQVLTDLCKRYKWLHRSFGQIHV 138  
 QY 103 EPVGNKEEKI-LNREIGFAGMPVCEFDWVKDPEVDFFRNILNVKCAVLDRLNPSHS 161  
 Db 139 QNRARSEETLQROQLNALIGVDYDVSVNHDELEFTRRLVTPRMAVAARD----- 192  
 QY 162 RANVTYPRVSVESPELPHKTIYKLDKQIIVIVIVIVSVFNNDKYTKIKINHCVPEQVI 221  
 Db 193 PKLYAHNPWTSKP-LPEYLKKTNNCVFIYI-----HRTTSQTIKVSADDTGTLI 245  
 QY 222 AEALIK--KTRBMLSSSQDLKCVLEYGSKYIKLVGCGDEYFLKRPQYKIRSCIML 279  
 Db 246 QSFPTMAKKSLMDIPES-----QNERDPVLRVCGRDEYLVGETPIKNFQWVRQCLKN 299  
 QY 280 GRMPLML-----MAKSLYGLQPLM--DCTMPSYSRRISTATPYMNGE---TSTKSL 327  
 Db 300 GEEIHVLDTPPDPALDEVRKEEMPLVDDCTGVTGHEQLT-----IHGDHESVPTVSL 354  
 QY 328 WINSALRIKILCATYVNVNIRID-----KIYVGTGIYHGGELPLCNVNTQRPV 377  
 Db 355 WQCDKRFVVK-----INGIDIPVLPRTADLVFVEANIOYGQVLCORRTSPKRF 404  
 QY 378 CSNPRNENLNDIYIPDLPRARCLSL-C-----SVKRRKA-----KEHCLANG 425  
 Db 405 TEEVLNWNVLEFSIKIDLPKALLNLQYCSKAPRLSCTSAEMSPSPSKKAQALLVYV 464  
 QY 426 NINLPDYDTLVSGKALNLMFVPHGLD--LNPPIGVG--SNPNKE--TPCLELEFDWPS 481  
 Db 465 NLLILDRHLRHLNGEVLVHMQLSKGEGOSFNADKLTSTRNPDKENMSISILLDNYC 524  
 QY 482 SVKRPDMSVIEEHNWVSREAGFSYSHAGLSNRLARDNELRENDKEQLAICTRDLPS 541  
 Db 525 HPIALPKRPTDPDPEGDRV-----DAEMPNQAR-----KQLKALITDPLN 565  
 QY 542 ETTQEKDPLVHNRHVCVPIPIELKLLSVKNSRSDVAQWYCL-----VWDWPIRKE 596  
 Db 566 PLTADKELVLFHFRYSLNDPRAVPLPSVVGQDEIVAKTYOLLAKREVDQSDALDVG 625  
 QY 597 QAMELLDCNYPDPNVRGFAVRCLERYLTDDKLSQYLQLVQVLKYEQYLDNLVFLFLKK 656

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Db      626 LTNQGLDNCFSDBENBAIAVOCKLES-LEDDVLAHYLLQJLVQAVKFEFYHSALARFLTKR 684
Qy      657 ALTNOIIGHFFPHALISEM-HNKTVSORFGLLESYCRACGMVLYK-HNROVAMEKLIN 714
Db      685 GIANKRIQHFLFWLFLSEIAQSRHYOQRFVILBAYLRGCGTAMHDFTOQVOVIDMLQK 744
Qy      715 LT-DI-LKQKKDETDQKV--QMKFLVEQMRBDFMDALQGLSPINPAHQNLRLLEC 769
Db      745 VTIIDISLSAEKIDVSSQVLSQKQKLENQN--LNLPSFRVPYDGLKAGALVIEKC 801
Qy      770 RIMSASRPLMLWNE--NPIMSELLFQNN--IFKRGDDLRQMLTQIIRIMNTW 824
Db      802 KMAASKKPKPLMEFKCADPTALS-----NETIGIIFKHGDDLRQDMLIIQIIRIMESIW 855
Qy      825 QNGGLDRLM.PYGLSLIGDCVGLIEVVRNSHTIMQI--QCKGSLGALQFNSHTLHQLKD 883
Db      856 ETESLDLCLPYGCISTDGKIGMTEIVKDATTAIKIQOSTVGTGA--FKDEVLSHMLKE 913
Qy      884 KMK-GEIYDAIDLFTRSCAGCVATFLLIGDRHNSINWKKDQGFHIDFGHLDHKK 942
Db      914 KCPLEEFQOAAVEFVVSACGYCATFVLGIDHNNIMISEGNLFHIDFGHILGNVYK 973
Qy      943 KKEPYKEERYVFLTQDFLIVISKGAOECTKREFPERFOEMCYATYLAIRQHANLFINLP 1002
Db      974 SFLGINKERYVFLTPDFLFWMGTSQKK--TSLHFQKQDQVCAVYALALRHHTLLITLF 1031
Qy      1003 SMMGSGMPELQSDDIATIRKTLALDKTBOALEYEMKKNNDHGGMTKMDMIFHTI 1062
Db      1032 SMMLMGTMPOLTSKEDIERYIDALTVGSKSEDAKPFLLDQLEVCGRDKMTVQFNMFLHV 1091

RESULT 11
P3K1_DICD1
ID      P3K1_DICD1      STANDARD;      PRT;      1570 AA.
AC      P54673;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      Phosphatidylinositol 3-kinase 1 (EC 2.7.1.137) (P13-kinase)
DE      (Pcdins-3-kinase) (P13K).
GN      PI3K OR PIK1.
OS      Dictyostelium discoideum (slime mold).
OC      Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX      NCBI_TaxID=44689;
RN      (1)
RP      SEQUENCE FROM N.A.
RX      STRAIN=AX3;
RX      MEDLINE=96009592; PubMed=7565716;
RA      Zhou K., Takegawa K., Emr S.D., Firtel R.A.;
RT      "A phosphatidylinositol (PI) kinase gene family in Dictyostelium
RT      discoideum: biological roles of putative mammalian p110 and yeast
RT      Vps34p PI 3-kinase homologs during growth and development.";
RL      Mol. Cell. Biol. 15:5645-5656(1995).
CC      -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidy-1D-myo-inositol = ADP +
CC      1-phosphatidy-1D-myo-inositol 3-phosphate.
CC      -!- SIMILARITY: BELONGS TO THE PI3/P13-kinases FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: U23476; AAA85721.1; --
CC      PIR: T18272; T18272.
CC      DICTYDB: DD01099; p13A.
CC      InterPro: IPR000403; P13_P14_kinase.
CC      InterPro: IPR002420; P13K_C2.
CC      InterPro: IPR000341; P13K_xas_bind.
CC      InterPro: IPR001263; P13Ka.

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DR      InterPro: IPR000626; Ubiquitin.
DR      Pfam: PF00454; P13_P14_kinase; 1.
DR      Pfam: PF00792; P13K_C2; 1.
DR      Pfam: PF00794; P13K_Fbd; 1.
DR      Pfam: PF00613; P13Ka; 1.
DR      Pfam: PF00240; ubiquitin; 1.
DR      SMART: SM00142; P13K_C2; 1.
DR      SMART: SM00144; P13K_Fbd; 1.
DR      SMART: SM00145; P13Ka; 1.
DR      SMART: SM00146; P13K; 1.
DR      PROSITE: PS00915; P13_4_KINASE_1; 1.
DR      PROSITE: PS00916; P13_4_KINASE_2; 1.
DR      PROSITE: PS0290; P13_4_KINASE_3; 1.
KW      Transferase; kinase; Multigene family.
FT      DOMAIN 41
FT      DOMAIN 48
FT      DOMAIN 59
FT      DOMAIN 161
FT      DOMAIN 161
FT      DOMAIN 294
FT      DOMAIN 308
FT      DOMAIN 413
FT      DOMAIN 503
FT      DOMAIN 570
FT      DOMAIN 821
FT      DOMAIN 831
FT      DOMAIN 1309
SQ      SEQUENCE 1570 AA; 178374 MW; 55B67B72B34D783 CRC64;

Query Match      24.0%; Score 1370; DB 1; Length 1570;
Best Local Similarity 33.2%; Pred. No. 2e-85;
Matches 371; Conservative 199; Mismatches 363; Indels 184; Gaps 40;

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Qy      33 TLECIKATLITIKHELFKARKYPLHQLDSSSYFVSQGE-AKEEFEPDTRRLCD 91
Db      555 TIENTLKER---LISDYLFNNNSNNNNCKYGGADSYILLPNNPKMRSLVLSKDYILD 611
Qy      92 LRL--PQPLKVIIEPVNGREKILNREIGFALQMPVCF-----DWKDPVQDFRR 141
Db      612 KRAQGLPKLVIE-----KSTLIDSPDELSPSEVEIRKLIPIGTWRGEEVEYFRR 666
Qy      142 NILNCKEAVDLRLDPSHPBAMVYPPNVESELPKHYINKDKQOIIIVIMVISP 201
Db      667 -----VTSRLRY-----EALP-----LIKSIQSTLVLRLSP- 693
Qy      202 NDKQYTLKINHDCVPEQVIAEALR-----KKTREMLL--SSEQL--KLCVLEY- 246
Db      694 -----LPIVGNKTLISIFLPIYQVYTLTLDLELNETADQFTNRLFTKNS 739
Qy      247 -----QGYILNVCDCDEYFLEKYPLOYKYIRSCIMGRMNLMM--AKESLYSQ 297
Db      740 KHLNPNVSNHILKLVGSSDPIHGHPIRTFESIRNHIIQGTQPOLTIQRKPELDPO 799
Qy      298 PMDCFTMS--YRRISTATPVNAGETSTK-----SLWYNALRLRXI 338
Db      800 FKPRDYPPELIIHDSCSNAINCNNNTNSNNNNINFDNMDOIITHISIREIKKPFYKV 859
Qy      339 LCATVANN-IRDD--KIYRTGIGHGGEPLCNVNTQRPV-----CSNPRMNEML 387
Db      860 MGRSTRIPISCKIDISSVIVISILYHGI ECFSAFTQPIPPPAPLAETLSVDWCML 919
Qy      368 NY-DIYIDLPPAARLCLICS-----VKGKCAKEHCEPLANGINLFDYDTL 436
Db      920 VFTNIDYGNLVDARLSISVSANETVDVEIKNLDAATKKTFLIGINIMITDFKYOL 979
Qy      437 VSGKALNIMVYPHGLEDLNLPIGVTSNP-NKETPCLLEFPDMSSVYKPPDMKVIIEH 495
Db      980 RQGWELSLMP-----SDFSNPLGTCNNPSSSQSVGLTFEEFEEPLVLP- 1026
Qy      496 ANWSVREAGPSYSTAGLSN--RLARDNELENDXEOUAICTRPPLSEITOEKDFLMS 553
Db      1027 -----RKTKFSTSVSVIEQPTNTINSNEMR-PFEQITALL--DPLSDLKQEKNOJMT 1076
Qy      554 HRHYCVTIPEILPKLLLSVKMNSRDEVQAWYCLVQDWEPPIKPEQAMELLDCNYPMPVVG 613

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Db 1077 LRHYSILFPQVLPRLMLSVPTQTAIVDAEASLIDRPPKLPYSESLDLAKANKRYRE 1136
Qy 614 FAVRCLEKYLITDCKLSQYLQLVQVLYKEOYLDMVLVRFELKKALINQRIQHPFFWHLKS 673
Db 1137 FAVTCLIED-LSEDELDILQLVQVLYKEPPEHDKLSRFLRLKXILNRNIGHSPFWLKS 1195
Qy 674 EMNKVYSORFGLLESYCAACGYLGHNLKRYVAMKLNLDILKQEK--KDETQKVQ 731
Db 1196 DLHDSNLSERFGLLESYLAACGHRLELKQ--MEVINNLTEVAKIKIPKQODRR-- 1250
Qy 732 MKFLVEQMRBRPFMDALQGFPLSPNPAHOLGNLRECRINSSAKRPLUMNENPDLMSE 791
Db 1251 -EEMIKER---ESLSEWKEKRLHLINPPEBSNGLINKSKMDSKLPRLRSFTNTDMAD 1306
Qy 792 LLEFONNEIIFKNGDDLRQDMLTQIIRIMENIWONQGLDRLMLPYGCLSIGDCVGLIEV 851
Db 1307 PI---EVIFKAGBDDLQDMLTQIMIRLMKLMQKEGLDKLSYSGISITGDMIGMIEV 1362
Qy 852 RNSHTIMQIQ-CGGLKGLALQFNSHTLHOMLKDKNKKEI-YDAALDLFTRSCAGYCATF 909
Db 1363 LNSEETAKLOKSSRG--GAFRFQVSGPOLILOHNSKDMEOKAVDTFIIISGAGYCATY 1420
Qy 910 ILIGIDRHSNINWKKDQGLPHIDFGHFLDKKKKPGYKKEKRVFVLTQDFLYISKGAQ 969
Db 1421 VLGIQDRHNDNLMTYKGRFLPHIDFGHFLGNYKKKFGFKERAFVFPDPCYVM--GK 1478
Qy 970 ECTREPERFEROEWCYKAYLAIRQHANLFINLFSMGLSGMPELQSPFDIAYIRKTLAD 1029
Db 1479 ESKF---FSQFVNYCCGYNIVKRNKALFNNLFAWVSTQIPQLQSMEDLNLYLKESFIS 1535
Qy 1030 KTEQBALEYMKQMDAHGQMTTKMDWTHHTTKQHA 1066
Db 1536 LSDAKAREKFEVALIHES-LATKTTQLNNPFHL-AHA 1570

RESULT 12
P3K2_DICDI STANDARD; PRT; 1858 AA.
ID P3K2_DICDI STANDARD; PRT; 1858 AA.
AC P54674;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Phosphatidylinositol 3-kinase 2 (EC 2.7.1.137) (PI3-kinase)
DE (pdcins-3-kinase) (PI3K).
GN PI3K OR PIK2.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_taxid=44689;
RN SEQUENCE FROM N.A.
RP STRAIN=AX3;
RC MEDLINE=96009592; Pubmed=7565716;
RA Zhou K., Tekegawa K., Emr S.D., Firtrel R.A.;
RT "A phosphatidylinositol (PI) kinase gene family in Dictyostelium
RT discoideum: biological roles of putative mammalian p110 and yeast
RT Vps3p PI 3-kinase homologs during growth and development.";
RL Mol. Cell. Biol. 15:5645-5656 (1995).
CC -1- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol = ADP +
CC 1-phosphatidyl-1D-myo-inositol 3-phosphate.
CC -1- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC -----
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CC -----
CC EMBL: U23477; AAA5722.1; -
CC PIR: T18273; T18273.
CC DictyDb: DDO1100; PI3K.
CC InterPro: IPR000403; PI3_P14_kinase.

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DR InterPro: IPR002420; PI3K_C2.
DR InterPro: IPR000341; PI3K_ras_bind.
DR InterPro: IPR001263; PI3Ka.
DR Pfam: PF00454; PI3_P14_kinase; 1.
DR Pfam: PF00794; PI3K_C2; 1.
DR Pfam: PF00794; PI3K_rbd; 1.
DR Pfam: PF00613; PI3Ka; 1.
DR SMART: SM00142; PI3K_C2; 1.
DR SMART: SM00144; PI3K_rbd; 1.
DR SMART: SM00145; PI3Ka; 1.
DR SMART: SM00146; PI3K_C1.
DR PROSITE: PS00915; PI3_4_KINASE_1; 1.
DR PROSITE: PS00916; PI3_4_KINASE_2; 1.
DR PROSITE: PS50290; PI3_4_KINASE_3; 1.
DR Transferrase; Kinase; Multigene family.
FT DOMAIN 34 POLY-GLY.
FT DOMAIN 166 172 POLY-SER.
FT DOMAIN 185 226 POLY-ASN.
FT DOMAIN 227 235 POLY-THR.
FT DOMAIN 246 253 POLY-SER.
FT DOMAIN 259 268 POLY-ASN.
FT DOMAIN 294 303 POLY-THR.
FT DOMAIN 361 364 POLY-SER.
FT DOMAIN 369 384 POLY-SER.
FT DOMAIN 425 429 POLY-GLN.
FT DOMAIN 439 444 POLY-THR.
FT DOMAIN 445 454 POLY-SER.
FT DOMAIN 562 570 POLY-GLY.
FT DOMAIN 715 727 POLY-THR.
FT DOMAIN 982 990 POLY-GLN.
FT DOMAIN 1015 1049 POLY-ASN.
FT DOMAIN 1598 1858 PI3K_P14K.
SQ SEQUENCE 1858 AA; 203945 MW; A6C0333D4CDDEA03 CRC64;

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Query Match 22.1%; Score 1262.5; DB 1; Length 1858;  
 Best Local Similarity 28.7%; Pred. No. 5,6e-78;  
 Matches 366; Conservative 197; Mismatches 397; Indels 317; Gaps 42;

```

Qy 15 LMPRLIVEGLDNGMI--VTLCEAREATLITIKHLFEARKYR-LHQLODESSYIF- 70
Db 657 LIBEYELKVLVSNSTISNETLP-LRRQTLM--OACNISRLFKHLILKSESTTILD 711
Qy 71 -VSVOEAREEPEFDEFRLCDRL-----POFRLVPIPVGN 107
Db 712 GASTTTTTTTTTTTTANQSSNITTSNSLDTLNNSEIIDVKHQAELFEFLIGT 771
Qy 108 REEKILNREIGAIGMPVCEFDWKPVEQDFERN-----ILNVCKEAVDLRLNSPHSR 162
Db 772 SFTRLVD-----OQOEVSFRDRDPAQFLSNFTSTRNDL-----SQ 807
Qy 163 AMVYVPPNVSSPELPKHIYNKLDKQIIVVIMVIVSPNNDKQKYLKINHOCVPEQVLA 222
Db 808 MIVV-----SSPPLPLTIPNK-----ITIMVLL-PDQK-----IKRVDCPPSSVVG 849
Qy 223 EAIRKTRMLLSSEQKLCLVLEYQK--YLIKVCQDEYFL-----EKYP 266
Db 850 DVKGELEFKKPFAMIDR-----VHTQKRTQDDVFLKVTGREGYILCIHELGNLTSRQRFIP 903
Qy 267 -LSQYKIRSCITMLGMPNLM----- 288
Db 904 TSGGCDPFLMDYDIYIQCVGKNQTVLSTNNISLSLNQVSEKVPIDKILETSPDDYD 963
Qy 289 -----AKSLYSQLPMDCFM----- 304
Db 964 EDLDSINSNSFDLQKSIQOQOQOQOQIQTVINIKETNKENKDSNKENKSSNNNNNNNN 1023
Qy 305 -----PSYRRISTATPYNNGETS-----TKSLMWI- 330
Db 1024 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1083
Qy 331 -----NSALRIKILCATY-VNV-NIRDDI-----KIYRTGTIY 361
Db 1084 VQNFSLPNSKLPINIVKRLFVNINIGLRNLNPNNNEDARKNFADGKNNQPNVFWVAELIY 1143

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QY 344 UNVN---IRDID---KIYVRGCIYHGEBPLCDNNTQVRPCSNPNWNLNDIYIPD 395
D 790 IFASKASEIIGTDSPIQIPIEAAYVFGGELLATQSSKLVSFDQYVWNEVNIPLAVSN 849
QY 396 LPBAARLCISCVKGGKGAKEHCPLAMGNINLFDITDIL-VSGKALMLMPPHLED 454
D 850 IPNGARRCCLGJ---NARYRGDIENIGWGHRIKFSKGLINFPAPSLKIMP-----G 898
QY 455 LINDPIGVTSNPNKETPCLLELEFDMFSSVYKFPDMSYIEEHANVSREAGFSYSHAGLS 514
D 899 KINPIGICVNLBSKDDAIIIAIFPKDYV--PETHYEDDLIEIISKD----- 945
QY 515 NRIARDNEL--RENDKQJRAICTRDLSEITEQEKDFLMSHRNYCVTIPKLLLS 571
D 946 ---ENGNELEPVYIEMEDRVEQIILQDPLYSINKEEHLIWKSHFYCHTRKQALSKLLQS 1002
QY 572 VKNNSREVAQWQCLVNDWMPRIKEQAMELLDCYPRPM-VRGVAVACLEKYLTDLSQ 630
D 1003 VENTNRYQVEARQQLKIMPTLSAVDALELIDPKFACVCEIRETYVCLDQ-MSDYELI 1061
QY 631 YLQLQVQLKYEQYLDLNLVFLFKKALTN-ORIGHFFPHLKSSEMINKTVSQRFGLLLE 689
D 1062 YLLQVQAIKHDPHNSVLSFLIGRWQWQVILGHFFPHLRADIDNOEYCEKFRVLSS 1121
QY 690 SYCR-ACGMYLKHLNRQVEAMEKILNLDLIDKQKDETOKVQMKFLVEQMRPDPMDAL 748
D 1122 GFLRYAPATQMESPKREITTLRIENLAKRKEVPEYKQYVENNLREQSPTTEL--- 1178
QY 749 QGFLSLPNAPHQGNLRECRIMSSAKRPLMLWENPDIIMSEILFONNEIIFKNGDDLR 808
D 1179 ---FVPEPDSIRILNIIPKCKSMDSAKVPPLWTFKNADPAPPI---QMIAKTGDDL 1231
QY 809 QDMULTQIIMINIMONOGDLRMLPYGCLSIGDCVGLLEVANSHTIMQIOG-KGGTK 867
D 1232 QDLITLQLLKMDHMKSQDLIDMTTYRCIATGMCGLLEVPNSTAAKIQAGAGVS 1291
QY 868 GALQFNSHTLQWLKDKNKSE-IYDAIDLFTSCAGCYCATFLIGIDRHNSNIWKKD 926
D 1292 GA-FKQTPFANMLKNNJOTENSQKAVSKFTLSGACVATYVIGIDHNNINIWDIH 1349
QY 927 GQLPHIDFGHFLDHKKKKKFGYKREVPVLTODFLIYSIGADECYKTREREPOEMCYK 986
D 1350 GHLEPHIDFGHFLDNFKTFAGFOREKAPFVLTPDFVYI--GGK--SPNFAFEVDICCK 1404
QY 987 AYLAIRQAHMLPTNLPEMMLGSGMPEUQSPDIAIYKTLALDCTEOALEYFKQNNDA 1046
D 1405 AFNIIINSNAHVFINMFELMLSTGIPERISNDIVYLKDFRLDITDAEASEYFKLIHES 1464
QY 1047 HHGQMTTKMDMIFHTIKQHALN 1068
D 1465 -IGTLTTTINFAIH-IMAHKN 1484

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RESULT 14
AGE1 CAEBL
AC 094135: 017482;          PRT; 1146 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Phosphatidylinositol 3-kinase age-1 (EC 2.7.1.137) (PI3-kinase)
DE (Ptdins-3-kinase) (PI3K) (Ageing alteration protein 1).
GN AGE-1 OR B0334.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2.
RX MORLINE=96320556; PubMed=8700226;
RA Morris J.Z., Tissenbaum H.A., Ruvkun G.;

```

```

RT "A phosphatidylinositol-3-OH kinase family member regulating
RT longevity and diapause in Caenorhabditis elegans."
RT Nature 382:536-539(1996).
RN [2]
RP REVISIONS.
RA Morris J.Z., Tissenbaum H.A., Ruvkun G.;
RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2.
RA Swindburn J., Williams L.;
RU Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP REVISIONS.
RA Durbin R.;
RU Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PHOSPHATIDYLIINOSITOL 3-KINASE HOMOLOG THAT REGULATES
CC LONGEVITY AND DIAPAUSE. COULD FUNCTION IN THE DEVELOPMENT OR
CC NEUROENDOCRINE SIGNALING OF THE DAUER PATHWAY.
CC -!- CATALYTIC ACTIVITY: ATP + 1-phosphatidy1-1D-myo-inositol = ADP +
CC 1-phosphatidy1-1D-myo-inositol 3-phosphate.
CC -!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
CC -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
CC -----
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CC -----
DR EMBL; U56101; AAC94759.1; ALT_INIT.
DR EMBL; Z66519; CA91377.2; JOINED.
DR EMBL; AL110499; CA91377.2; JOINED.
DR EMBL; AL110499; CAB57914.1; -.
DR EMBL; Z66519; CAB57914.1; JOINED.
DR PIR; S71792; S71792.
DR WormPep; B0334.8; CE23506.
DR GO; GO:0005942; C:1-phosphatidylinositol 3-kinase complex; NAS.
DR GO; GO:0007568; P:aging; IMP.
DR GO; GO:0040024; P:dauer larval development (sensu Nematoda); IMP.
DR InterPro; IPR000008; C2.
DR InterPro; IPR000403; PI3 PI4 kinase.
DR InterPro; IPR002420; PI3K C2.
DR InterPro; IPR003113; PI3K_p85B.
DR InterPro; IPR003341; PI3K_ras_bind.
DR InterPro; IPR001263; PI3KA.
DR Pfam; PF00454; PI3 PI4 kinase; 1.
DR Pfam; PF02192; PI3K C2; 1.
DR Pfam; PF02192; PI3K_p85B; 1.
DR Pfam; PF00794; PI3K_rbd; 1.
DR Pfam; PF00613; PI3KA; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00142; PI3K C2; 1.
DR SMART; SM00143; PI3K_p85B; 1.
DR SMART; SM00144; PI3K_rbd; 1.
DR SMART; SM00145; PI3KA; 1.
DR PROSITE; PS00915; PI3_4_KINASE_1; 1.
DR PROSITE; PS00916; PI3_4_KINASE_2; 1.
DR PROSITE; PS50290; PI3_4_KINASE_3; 1.
KW Transferase; Kinase.
FT DOMAIN 851..1127 PI3K/PI4K.
FT VARIANT 826..826 S -> N (IN AGE1 (MG109)).
FT CONFICT 1010..1010 F -> V (IN REF. 1).
SQ SEQUENCE 1146 AA; 132961 MW; 0D362E419407253A CRC64;

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Query Match 19.2%; Score 1096; DB 1; Length 1146;
Best Local Similarity 27.3%; Pred. No. 6.8e-67;
Matches 312; Conservative 219; Mismatches 430; Indels 182; Gaps 39;

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39 EATLTIKIELFK-DARKYPLHQLQDESSYIFVSVTOEAEREFEFDETRLCDLRLFQ 96

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Db      | 70 EIKSDRKHQFELIAPKMGTSVXKPOD--YVFRQUNFGEIIVIFNDQPLSKELHG 127
Qy      | 97 --PFLKXIEPVNGNEEKILNREIGFPAIGMPCVCEPDMKDPVOPFRRIINLVCEANDLR 154
Db      | 128 TFPWLFUYOPDGIRDKELMSDISHCLGYSLDKLEESLDEBELRQFASLWARTKCTLTR 187
Qy      | 155 DLNPHBRAMVVPN--VESSPELPHIYNKLKGQI-IYIWIWVSPNNDKQYTLKI 211
Db      | 188 GL---EGTSHYAFEBEOYLVCGESCPKDESKVKAALISYQMF-----RKRAEI 235
Qy      | 212 NHDCVPROVIAEAIR---KKTSMILSS---EOLKCYLEYQK---YILKVCCEBYF 261
Db      | 236 NGVC--EKMKIQIEFPNPNPKSLHFTLEVEMKRLDOYDTPDDADEGWFQLAGRTEFV 293
Qy      | 262 LE-KYPLSQYKYYINSCLMGRMPLMLMAK-----ESLYS-----QLPMD 301
Db      | 294 TNPDKLTSYDGVSELESYRCPGFVVRQSLVLKDYCRPKRPHYVRAHERKLADV 353
Qy      | 302 FTM-----PSYSRIISTATPYMNGETSRK--SLWVINSALIKILCATYVNVNIRID-- 352
Db      | 354 LSVSIDSTPKQSKSDMYMTDPRPTASLKQVSLMDLDNLMIR-----PVNISGDFP 406
Qy      | 353 ---KIYVRT--GIYHGEPLCDNVNTOFVPCSNBRMN--EWLNVDIYIPDEPRARLCISI 406
Db      | 407 ADVDMYRIEFSVYVGTITLASK--STTKVNAQPAKMKNEWTFPDLVKMDMPSA--VLSI 463
Qy      | 407 CSYGRKGAKEHCPLANGINLPDYDTLVSGKALNM--PVPHGEDLINPIGV--TGS 464
Db      | 464 RVLGKVLKSEEFEGVGNVMSLTDWDELQOGFPLHMLPEPFAANSRIGENGARIGT 523
Qy      | 465 NPNKETPLLEFPMFSSVVKFPDMS-----VIEHANSVREAGFSYSHAGLSRLARD 520
Db      | 524 N-----AAVTIEISSYGRVMPGOGYTYLVKRSTWTER-----LNIWDD 566
Qy      | 521 NELRENDKEQRAICTRDLSE-----ITEOKDFLMSHRHYCVTIPILP 566
Db      | 567 YE-----SCIRDPYKIKLOMYLKHSISGIVLEEDORHMMRRY---IQKEP 612
Qy      | 567 KLL-----LSVKNMSRDEVAQMYCLVKDMPRIKEQAMELLIDCNPDMVGFPAVRCLEK 621
Db      | 613 DLLIVLSLAEVMTDRENFSELYVWLEKMKPPSVAAALTLGKCTDVIKRFVAKELNE 672
Qy      | 622 YLTDDKLSQVLIQVQVLYKEQYLDNLLVRELKALNNORIGHFEFHLSSEMH----- 676
Db      | 673 QLSPTFHLFLPLIQAUKYEPRAOSEVGMMLTRTALCDYRIGHFLRLAEIRLRLDC 732
Qy      | 677 --NKTVSQRFGLLESYCRACGMVYKHLNROVEAMEKLINLTDIKQEKD--ETQKV--Q 731
Db      | 733 DLKSEYKRISLIMAYLRGNEBHKITTRQVDMVDELTRISTLVKGMKPOVATMKLDE 792
Qy      | 732 MKFLVEONRRDPMDALOGFLSPLNPAHQNLRLBECRINSSAARPLMLNWDNDINSE 791
Db      | 793 LRSISHKKNEND-----SPLDPVYKLGEMIDKAIVLGSARPLMLHKONPKRSD 843
Qy      | 792 LIPONNELIPKRGDLDRODMLTQIRIMENIMQOGDLMLPRGCSISDGVCLIVV 851
Db      | 844 LHLPECAIIFKNGDRLQDMLVLOVLEWMDNIMKANDICCLNPAVALPMEGMGIIEV 903
Qy      | 852 RNSHTIMQICKGKAGAL--QFNSTLHOML-----KDKNKEI----- 889
Db      | 904 PNCKTIFETIQTGTMNTAARSIDSFPAWKIRKCGEIDEEKSKKOSTKPIKIKDN 963
Qy      | 890 -----YDAIDLFTRSAGYCVATFPLIGIDRHNSNIMVXDQGLFHIIDFGLDHRKK 943
Db      | 964 TOAMKKYFESYDRFLYSCVGSVALIYINGIKDRHSDNMLTDEGXFHIDFGHIGHKT 1023
Qy      | 944 KFGYKREVPFLTDFLIVISKGQCEKTRERFQEMCKATLARIQANLFINFS 1003
Db      | 1024 KLGIORDOPFLTLEHFTVIRSGSVGNSHLOKFKTLCEAEVVMNNNDLVSFLT 1083
Qy      | 1004 MWLGSMBELGSDFDIAVIRKTLALD-KTEQALFYPMQNMDDAHGGGTTGMDVIFTI 1062

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Db      | 1084 LMDGMLPELSTRADLDLKLTLFCNGESKEARKEFPAGIYEAFNGSWSTKNMLPHAV 1143
Qy      | 1063 KOH 1065
Db      | 1144 KHY 1146

RESULT 15
PK3B_HUMAN
ID PK3B_HUMAN STANDARD; PRT; 1634 AA.
AC 000750; O95666;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing beta
DE polypeptide (EC 2.7.1.154) (phosphoinositide 3-kinase-C2-beta)
DE (Ptdins-3-kinase C2 beta) (PI3K-C2beta) (C2-PI3K).
GN PI3KC2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Breast;
RC MEDLINE=97269668; Pubmed=9144573;
RA Brown R.A., Ho L.K.F., Weber-Hall S.J., Shipley J.M., Fry M.J.;
RT "Identification and cDNA cloning of a novel mammalian C2 domain-
RT containing phosphoinositide 3-kinase, Hsc2-PI3K."
RL Biochem. Biophys. Res. Commun. 233:537-544(1997).
RN [2]
RP SEQUENCE OF 26-1634 FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Monocytes;
RC MEDLINE=99047700; Pubmed=9830063;
RA Arcaio A., Volinia S., Zvelebil M.J., Stein R., Waton S.J.,
RA Layton M.J., Gout I., Ahmed K., Downward J., Waterfield M.D.;
RT "Human phosphoinositide 3-kinase C2beta, the role of calcium and the
RT C2 domain in enzyme activity."
RL J. Biol. Chem. 273:33082-33090(1998).
CC - FUNCTION: PHOSPHORYLATES PTDINS AND PTDINS4P WITH A PREFERENCE FOR
CC PTDINS. DOES NOT PHOSPHORYLATE PTDINS(4,5)P2.
CC - CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4-
CC phosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4-bisphosphate.
CC - SUBCELLULAR LOCATION: FOUND MOSTLY IN THE MICRO SOME, BUT ALSO IN
CC THE PLASMA MEMBRANE AND CYTOSOL.
CC - TISSUE SPECIFICITY: WIDELY EXPRESSED, BUT LEVELS ARE HIGHEST IN
CC THYMUS AND PLACENTA AND LOWEST IN PERIPHERAL BLOOD, SKELETAL
CC MUSCLE AND KIDNEY.
CC - SIMILARITY: BELONGS TO THE PI3/P14-KINASES FAMILY.
CC - SIMILARITY: Contains 1 C2 domain.
CC - SIMILARITY: Contains 1 plox homology (PX) domain.
CC - CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-26 IS THE INITIATOR.
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CC
DR EMBL, Y11312; CAAT72168.1; -
DR EMBL, Y113892; CAAT74194.1; -
DR PIR, JC5500; JC5500.
DR HSSP, P21707; IRSY.
DR Genew, HGNC:8972; PI3KC2B.
DR MIM, 602838; -
DR GO, GO:0005792; C:microsome; NAS.
DR GO, GO:0005886; C:plasma membrane; NAS.
DR GO, GO:0016305; F:phosphatidylinositol 3-kinase, class II act. .; NAS.
DR InterPro, IPR000008; C2.
DR InterPro, IPR000403; PI3_P14_kinase.
DR InterPro, IPR002420; PI3K_C2.

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DR InterPro: IPR000341; P13K\_ras\_bind.  
 DR InterPro: IPR001263; P13Ka.  
 DR InterPro: IPR001683; PX.  
 DR Pfam: PF00168; C2; 1.  
 DR Pfam: PF00454; P13\_P14\_kinase; 1.  
 DR Pfam: PF00793; P13K\_C2; 1.  
 DR Pfam: PF00794; P13K\_rbd; 1.  
 DR Pfam: PF00613; P13Ka; 1.  
 DR Pfam: PF00787; PX; 1.  
 DR SMART: SM00239; C2; 1.  
 DR SMART: SM00142; P13K\_C2; 1.  
 DR SMART: SM00145; P13Ka; 1.  
 DR SMART: SM00146; P13K; 1.  
 DR SMART: SM00312; PX; 1.  
 DR PROSITE: PS00499; C2 DOMAIN 1; FALSE\_NEG.  
 DR PROSITE: PS50004; C2 DOMAIN 2; 1.  
 DR PROSITE: PS00915; P13\_4\_KINASE\_1; 1.  
 DR PROSITE: PS00916; P13\_4\_KINASE\_2; 1.  
 DR PROSITE: PS50290; P13\_4\_KINASE\_3; 1.  
 DR PROSITE: PS50195; PX; 1.  
 KM Transferrase: Kinase; Multigene family.  
 FT DOMAIN 1365 1481  
 FT DOMAIN 156 162  
 FT DOMAIN 169 174  
 FT DOMAIN 1079 1343  
 FT DOMAIN 1517 1608  
 FT CONFLICT 63 63  
 FT CONFLICT 75 75  
 FT CONFLICT 99 99  
 FT CONFLICT 246 246  
 FT CONFLICT 278 278  
 FT CONFLICT 567 567  
 FT CONFLICT 664 665  
 SQ SEQUENCE 1634 AA: 184856 MW: C0B5DF63C668B824 CRC64;

Query Match 18.6%; Score 1064.5; DB 1; Length 1634;  
 Best Local Similarity 27.3%; Pred. No. 1.6e-64;  
 Matches 304; Conservative 181; Mismatches 392; Indels 237; Gaps 34;

QY 104 PVGGRREKILNRELGAIGMVCDFDMDKPEVDPPFRNIIIVKCEAVDLRLNSPSRA 163  
 DB 311 PVGSRPHTVAN-----GHELFVSEERDEEVAAF-CHMLDIRSGSDIOD---YFLT 358  
 QY 164 MYVYPPVAVSESSPELPEKHIVNKLKGQIIIVIVIVISNNNDQKXTLKLINHDCEVQYIAE 223  
 DB 359 GYVMSATVPS---PEHLGDEVNLKTVLC-----DLQNALITFTCC-----YFLT 397  
 QY 224 AIRKKTSMILSSQQLKLVLEYO-----GKYLKVGCGDEYFLKPYLSQYKYIRSCI 277  
 DB 398 ---SSTVDLLIYO---TLCTHDDLRLNVVDGDFVLKPCGLEFLQNGHALSGHEYIQYCR 451  
 QY 278 MLGMPVLMMAKESLYSQ----- 297  
 DB 452 KFDIDIRLQMLEQKVRSDIARLVNDOSPTLNYLVHLQRPVKQTISRQALSILFDY 511  
 QY 298 ---PMDCFM-----PSYSRRI-----STATPYNG----- 320  
 DB 512 HNEVDALFLADGDFPLADRVQSVKALCNALAAVETPEITSALNQLPCPSRMQPKIQK 571  
 QY 321 -----ETSTKSLWVINSAL--RIKLCAVYVNVIR----- 349  
 DB 572 DPSVLAVRENRKVEALTAALDLVELYCNTE--NADPQTAVPGRKHDLVQEAHFARS 630  
 QY 350 -----DIDKIYRTGIYHGGEPLCDNVNTQRYVCSNPR-----WNEWL 387  
 DB 631 LAFTVYATHRIPIMATSYEDFYLSCLSHGKDMCSPLQTRRAHFSKYLFHLIYVDOOI 690  
 QY 388 NYDIYIDLPRAARLCTISCSV-----KGRKAKEHCP--LAWGNINLFDYDTLVSG 439  
 DB 691 CFPIQVVRRLRETYLLCITLALPIPPGSSSEANKQRRVPEALGVTTPLPFRQVLTCG 750  
 QY 440 KMALINMPVPHGLEDDLNLPIGVTSNPNKETP---CLELEPDMFSSVVKFPDMSVIEEHA 496

DB 751 RKLGLMPATQOE-----NP-SARWSADPNFHQPPQSVIIQIDIFPISAFDIKFTS----PGCD 800  
 QY 497 NMSVSRAGFSYSHAGLSNRLARNDELRENDKEQLRAICTRDPLSETTEDEKQFLWHRH 556  
 DB 801 KFSPPRYEFG-----SLEEDQRLKQIMQKESLYWLTDDKGRKLMERY 844  
 QY 557 YCVTIPEILPKLLSV---KWSRDEVAQWYCLVQDMPPIKPEQAMELDCNYPDPVWRG 613  
 DB 845 YCHEVSSSLPLVLASASWEMACLPDI---YVLKQVTHNKHQDALCLLHATFFDQEVRR 901  
 QY 614 FAVRCLEKYLTDKLSQYLQIVQVLYKYEQYLDNLVRFLLKALTNORIGHFFFWHLKS 673  
 DB 902 MAVQWIGS-LSDAELLDYLPQVQALKYECYLDSPVRFILKRAVSDRLVTHYFFMLKD 960  
 QY 674 EMNKVYQSQFGLLBEYCACGMYLK-HLNQVQEMEKLINLIDLKQEKDETKQVQM 732  
 DB 961 GLKDSQFSIRYQYLLAALLCCCGKGLNEEFNRQC---WLVNALAKLAQVREAPASARQ 1016  
 QY 733 KFLVEQRRPDPMDALQGFLS-PLNPAHQNLRLBECRIKMSAKRPLMLNWEKPDIMSE 791  
 DB 1017 GILRTGLEEVKQFPALNGSCLPLSPSLVKGIVPRDCSFFNSAVVPLKLSFQVNDPLGE 1076  
 QY 792 LLEPNNELIFKNGDDLRQDMTLTQIRIMENIWOQGLDRLMPPYGLSLIGDCVGLIEV 851  
 DB 1077 ---NIRVIFKCGDDLQDMTLTQIRIMIRISKIWOQGLDMRWVIFRCFSTGRGRGWYEMI 1132  
 QY 852 RNSHTIQIQCKGKGLKALQFNSHTLHQLKDKKKE--IYDAIDLEPTRSCAGCVATFI 910  
 DB 1133 PNAETLKKIQVEHGVTS--FKORPLADWLQKNPNPGEYEKAVENFIYSCAGCCVATYV 1190  
 QY 911 LGIGDRHNSNIMVYDDGQLPHIDPGHFLDHHKKKFGYKREVPFVLTPQDFLIVISGAOE 970  
 DB 1191 LGICDRHNDIMLKTGHMHIDPGRFLGAQFNGIKRBRAPVFVPSDAVYINGDKP 1250  
 QY 971 CTKTREPERQEMCYKAYIALIQAHLNFIPLFSMILSGSNPELQSFDDIAYIRKTLALDK 1030  
 DB 1251 SSR---FHDVPVLDCCQAYNLIIRKHTHLFLNLGLMISCGIPELSDJEDLKYVVDALRPOD 1307  
 QY 1031 TEOBALEYPMKQNDADHGGWTKMDIPIHTIQ 1064  
 DB 1308 TEANATTYFTR-LIESLSGVATKLNFFIHNLAQ 1340

Search completed: November 6, 2003, 14:43:14  
 Job time : 23 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 6, 2003, 14:40:55 ; Search time 27 Seconds  
(without alignments)  
3807.567 Million cell updates/sec

Title: US-09-325-095-37

Perfect score: 5709  
Sequence: 1 MPRPSSGELWGTHLMPRI.....GWTTKMDWIFHTIKQHALNX 1069

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5708	100.0	1068	1 A43322	1-phosphatidylinos
2	5657	99.1	1068	1 T38110	1-phosphatidylinos
3	1966	34.4	1070	1 A54600	1-phosphatidylinos
4	1958	34.3	1043	2 T43502	1-phosphatidylinos
5	1677.5	29.4	1088	2 T13950	1-phosphatidylinos
6	1428	25.0	1050	1 A57134	1-phosphatidylinos
7	1370	24.0	1570	2 T18272	1-phosphatidylinos
8	1262.5	22.1	1585	2 T18273	1-phosphatidylinos
9	1109	19.4	1585	2 T18274	1-phosphatidylinos
10	1085	19.0	1164	2 S71792	1-phosphatidylinos
11	1064.5	18.6	1634	1 JCS500	phosphoinositide 3
12	1049.5	18.4	1658	2 T42642	phosphoinositide 3
13	919	16.1	1506	2 JCS985	phosphoinositide 3
14	859	15.0	1876	2 T13801	phosphoinositide 3
15	751	13.2	1607	2 T21982	hypothetical prote
16	684	12.0	801	1 T52538	1-phosphatidylinos
17	684	12.0	887	1 S57219	1-phosphatidylinos
18	677.5	11.9	664	2 PC4002	phosphatidylinosit
19	661.5	11.6	816	1 A59003	phosphatidylinosit
20	648.5	11.4	875	1 A36369	1-phosphatidylinos
21	645	11.3	814	2 T07761	phosphatidylinosit
22	635	11.1	814	2 B96630	phosphatidylinosit
23	633.5	11.1	873	2 T25442	hypothetical prote
24	629	11.0	812	2 T07745	phosphatidylinosit
25	625.5	11.0	897	2 T43620	phosphatidylinosit
26	602	10.5	1020	2 T18260	1-phosphatidylinos
27	491.5	8.6	732	2 T08420	1-phosphatidylinos
28	474	8.3	2051	2 P96529	probable Phosphat
29	473	8.3	2028	2 T52022	1-phosphatidylinos

30	442	7.7	854	2 A55404	1-phosphatidylinos
31	442	7.7	1466	2 S65741	1-phosphatidylinos
32	442	7.7	1900	2 S45530	probable 1-phospha
33	434.5	7.6	133	2 PC4348	phosphoinositide 3
34	423	7.4	1877	2 T40550	probable phosphati
35	411.5	7.2	2121	2 T27406	hypothetical prote
36	392.5	6.9	525	2 P96547	probable phosphat
37	362.5	6.3	131	2 PC4346	phosphoinositide 3
38	343.5	6.0	131	2 PC4345	phosphoinositide 3
39	331.5	5.8	131	2 PC4347	phosphoinositide 3
40	310	5.4	379	2 T07607	probable 1-phospha
41	303	5.3	828	2 JCS706	1-phosphatidylinos
42	297	5.2	1066	2 A49335	1-phosphatidylinos
43	291.5	5.1	1121	2 T52631	1-phosphatidylinos
44	268.5	4.7	1093	2 T18275	1-phosphatidylinos
45	265	4.6	604	2 P89453	protein F35H12.4 (

ALIGNMENTS

RESULT 1

A43322  
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 110K chain - bovine  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 10-Sep-1999 #sequence\_rev10-Sep-1999 #ext\_change 10-Sep-1999  
C/Accession: A43322  
R/Hiles, I.D.; Otsu, M.; Volinia, S.; Fry, M.J.; Gout, I.; Dhand, R.; Panayotou, G.; Rui,  
Cell 70, 419-429, 1992  
A/Title: Phosphatidylinositol 3-kinase: structure and expression of the 110 kd catalytic  
A/Reference number: A43322; M0ID:92354059; PMID:1322797  
A/Accession: A43322  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA; protein  
A/Residues: 11068 <Hit>  
A/Cross-references: GB:M93252; NID:g163519; PIDN:AAA30698.1; PID:g163520  
A/Experimental source: brain  
A/Note: sequence extracted from NCBI backbone (NCBIP:110292)  
C/Superfamily: phosphatidylinositol 3-kinase  
C/Keywords: phosphotransferase

Query Match	100.0%	Score 5708	DB 1	Length 1068
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1068	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MPRPSSGELWGTHLMPRI	1	MPRPSSGELWGTHLMPRI
DB	1	MPRPSSGELWGTHLMPRI	1	MPRPSSGELWGTHLMPRI
QY	61	LDDESSYIFVSVTQAEEREFDETRRLCDLRLFPFLKVLIEPVGNREBKINREIGFA	120	LDDESSYIFVSVTQAEEREFDETRRLCDLRLFPFLKVLIEPVGNREBKINREIGFA
DB	61	LDDESSYIFVSVTQAEEREFDETRRLCDLRLFPFLKVLIEPVGNREBKINREIGFA	120	LDDESSYIFVSVTQAEEREFDETRRLCDLRLFPFLKVLIEPVGNREBKINREIGFA
QY	121	IGMPVCEPDMKQPEVQDFRRRLINLVCKEAVDIRDINSFHSRAMYVPPVSSPELPX	180	IGMPVCEPDMKQPEVQDFRRRLINLVCKEAVDIRDINSFHSRAMYVPPVSSPELPX
DB	121	IGMPVCEPDMKQPEVQDFRRRLINLVCKEAVDIRDINSFHSRAMYVPPVSSPELPX	180	IGMPVCEPDMKQPEVQDFRRRLINLVCKEAVDIRDINSFHSRAMYVPPVSSPELPX
QY	181	INVKLKGQITIVIVIVISPNNDKQRTYKINDCVPEQVIAEIKKTRSMLSSEOLK	240	INVKLKGQITIVIVIVISPNNDKQRTYKINDCVPEQVIAEIKKTRSMLSSEOLK
DB	181	INVKLKGQITIVIVIVISPNNDKQRTYKINDCVPEQVIAEIKKTRSMLSSEOLK	240	INVKLKGQITIVIVIVISPNNDKQRTYKINDCVPEQVIAEIKKTRSMLSSEOLK
QY	241	LCVLEVGKTYLKVCCGDEFELEKYPLSOYKYIRSCIMLGRMNLMLMAKESLYSOLPMD	300	LCVLEVGKTYLKVCCGDEFELEKYPLSOYKYIRSCIMLGRMNLMLMAKESLYSOLPMD
DB	241	LCVLEVGKTYLKVCCGDEFELEKYPLSOYKYIRSCIMLGRMNLMLMAKESLYSOLPMD	300	LCVLEVGKTYLKVCCGDEFELEKYPLSOYKYIRSCIMLGRMNLMLMAKESLYSOLPMD
QY	301	CFMPSPYSRRISTATPYNNGESTKSLWVINSALRIKILCATYVNVNINDIDIKYVRTGI	360	CFMPSPYSRRISTATPYNNGESTKSLWVINSALRIKILCATYVNVNINDIDIKYVRTGI
DB	301	CFMPSPYSRRISTATPYNNGESTKSLWVINSALRIKILCATYVNVNINDIDIKYVRTGI	360	CFMPSPYSRRISTATPYNNGESTKSLWVINSALRIKILCATYVNVNINDIDIKYVRTGI
QY	361	YHGGEPICNVVNVQRPVCSNPRNENLVNDIYIPDLPRARICLSTCSVKGKRGAKKEHC	420	YHGGEPICNVVNVQRPVCSNPRNENLVNDIYIPDLPRARICLSTCSVKGKRGAKKEHC
DB	361	YHGGEPICNVVNVQRPVCSNPRNENLVNDIYIPDLPRARICLSTCSVKGKRGAKKEHC	420	YHGGEPICNVVNVQRPVCSNPRNENLVNDIYIPDLPRARICLSTCSVKGKRGAKKEHC

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QY 421 PLAMGNINLFYDITDVLVSGMALNMPVPHGLEDLNPIGVTSNPKEPTELBEFDMF 480
Db 421 PLAMGNINLFYDITDVLVSGMALNMPVPHGLEDLNPIGVTSNPKEPTELBEFDMF 480
QY 481 SSVKKPDMSVIEEHANMSVREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPL 540
Db 481 SSVKKPDMSVIEEHANMSVREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPL 540
QY 541 SEITEQEKDVLMSHRHVCVTIPETLPKLLSVKNSDEVAQWCLVKDMPPIKPEQAME 600
Db 541 SEITEQEKDVLMSHRHVCVTIPETLPKLLSVKNSDEVAQWCLVKDMPPIKPEQAME 600
QY 601 LLDONYPDPWVRGFAVNCLEKYLTDDBLSOYLQLOVQVLYKEOYLDMLVFLKKAALTN 660
Db 601 LLDONYPDPWVRGFAVNCLEKYLTDDBLSOYLQLOVQVLYKEOYLDMLVFLKKAALTN 660
QY 661 QRIGHFFFMHLKSEMHKKTVSQRFGLLLESYCRAQWYLKHLNROVEAMEKILNLTDLK 720
Db 661 QRIGHFFFMHLKSEMHKKTVSQRFGLLLESYCRAQWYLKHLNROVEAMEKILNLTDLK 720
QY 721 QEKXDETQVQMKFLVEQMRPDMALQGFSLPNAHQGNRLBECRIMSSAKRPLW 780
Db 721 QEKXDETQVQMKFLVEQMRPDMALQGFSLPNAHQGNRLBECRIMSSAKRPLW 780
QY 781 LMWNPDMISBLFONNEIIFKNGDDLRODWLTQIIRIMENIMONQGLDRLMPLPGCLS 840
Db 781 LMWNPDMISBLFONNEIIFKNGDDLRODWLTQIIRIMENIMONQGLDRLMPLPGCLS 840
QY 841 IGDGVLGIEVVRNHSHTIMQIOCKGKLGALQFNSHTLHQLKDNKGEIYDAIDLFTRS 900
Db 841 IGDGVLGIEVVRNHSHTIMQIOCKGKLGALQFNSHTLHQLKDNKGEIYDAIDLFTRS 900
QY 901 CAGYCVATFIIGIDRHSNSIMVKDQGLPHIDGHLFDHKKKFGYKREVPVLTODF 960
Db 901 CAGYCVATFIIGIDRHSNSIMVKDQGLPHIDGHLFDHKKKFGYKREVPVLTODF 960
QY 961 LIVISKAQECTKREPERPOEMCKAYLAIRQHANLFINLSMMLSGMPELOSFPDIA 1020
Db 961 LIVISKAQECTKREPERPOEMCKAYLAIRQHANLFINLSMMLSGMPELOSFPDIA 1020
QY 1021 YIRKTLADKTEQALAEYFMKQMDAHHGWTTKMDWIFHTIKQHALN 1068
Db 1021 YIRKTLADKTEQALAEYFMKQMDAHHGWTTKMDWIFHTIKQHALN 1068

RESULT 2
138110
1-phosphatidylinositol 3-kinase (BC 2.7.1.137) alpha isoform - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: I38110; S44127
R:Voljina, S.; Hiles, I.; Ormondroyd, E.; Nizetic, D.; Antonacci, R.; Rocchi, M.; Waterf
Genomics 24, 472-477, 1994
A:Title: Molecular cloning, cDNA sequence, and chromosomal localization of the human pho
A:Reference number: A55636; MUID:95229146; PMID:7713498
A:Accession: I38110
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-1068 <RES>
A:Cross-references: EMBL:Z29090; NID:g472990; PIDN:CAA8233.1; PID:g472991
C:Genetic8:
A:Gene: GDB: PIK3CA
A:Cross-references: GDB:370915; OMIM:171834
A:Map position: 3q26.3-3q26.3
C:Superfamily: phosphatidylinositol 3-kinase
C:Keywords: phosphotransferase

Query Match 99.1%; Score 5657; DB 1; Length 1068;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1056; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPPRSSGELMGILHMPRIILVECLLPNGMIVTLECLRAATLITIKHELFEKARKYPLHQ 60
|||||
```

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Db 1 MPPRSSGELMGILHMPRIILVECLLPNGMIVTLECLRAATLITIKHELFEKARKYPLHQ 60
QY 61 LLDDESSYIFVSVTOAEAREEFPDETRRLCDLRFQPLKVEIPVGNREKILNREIGFA 120
Db 61 LLDDESSYIFVSVTOAEAREEFPDETRRLCDLRFQPLKVEIPVGNREKILNREIGFA 120
QY 121 IGMVCEFDWVKDPEVQDFPRNILLNVCKEAVDLRLDINSPHSRAMVYVPPNVSSPELPKH 180
Db 121 IGMVCEFDWVKDPEVQDFPRNILLNVCKEAVDLRLDINSPHSRAMVYVPPNVSSPELPKH 180
QY 181 IYKLDKQGIIVVIWIVTSVNNDKOKYTLKINHDCVPEQVIAAIRKTRSMLLSSEQK 240
Db 181 IYKLDKQGIIVVIWIVTSVNNDKOKYTLKINHDCVPEQVIAAIRKTRSMLLSSEQK 240
QY 241 LCYLEYQKGIILVYCGDEYFLEKYPISOYKYIRSCIMLGPMNLMMAKESIYSQLPMD 300
Db 241 LCYLEYQKGIILVYCGDEYFLEKYPISOYKYIRSCIMLGPMNLMMAKESIYSQLPMD 300
QY 301 CFMPYSRRIISTATPYMNGESTKSLWVINSALRIKILCATYVNVNIRDIDKIYVRTGI 360
Db 301 CFMPYSRRIISTATPYMNGESTKSLWVINSALRIKILCATYVNVNIRDIDKIYVRTGI 360
QY 361 YHGEPLCDNVNTQVPCSNPRNEMLNVDIYIPDLPRARLCLSTCSVKGRAKEEHC 420
Db 361 YHGEPLCDNVNTQVPCSNPRNEMLNVDIYIPDLPRARLCLSTCSVKGRAKEEHC 420
QY 421 PLAMGNINLFYDITDVLVSGMALNMPVPHGLEDLNPIGVTSNPKEPTELBEFDMF 480
Db 421 PLAMGNINLFYDITDVLVSGMALNMPVPHGLEDLNPIGVTSNPKEPTELBEFDMF 480
QY 481 SSVKKPDMSVIEEHANMSVREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPL 540
Db 481 SSVKKPDMSVIEEHANMSVREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPL 540
QY 541 SEITEQEKDVLMSHRHVCVTIPETLPKLLSVKNSDEVAQWCLVKDMPPIKPEQAME 600
Db 541 SEITEQEKDVLMSHRHVCVTIPETLPKLLSVKNSDEVAQWCLVKDMPPIKPEQAME 600
QY 601 LLDONYPDPWVRGFAVNCLEKYLTDDBLSOYLQLOVQVLYKEOYLDMLVFLKKAALTN 660
Db 601 LLDONYPDPWVRGFAVNCLEKYLTDDBLSOYLQLOVQVLYKEOYLDMLVFLKKAALTN 660
QY 661 QRIGHFFFMHLKSEMHKKTVSQRFGLLLESYCRAQWYLKHLNROVEAMEKILNLTDLK 720
Db 661 QRIGHFFFMHLKSEMHKKTVSQRFGLLLESYCRAQWYLKHLNROVEAMEKILNLTDLK 720
QY 721 QEKXDETQVQMKFLVEQMRPDMALQGFSLPNAHQGNRLBECRIMSSAKRPLW 780
Db 721 QEKXDETQVQMKFLVEQMRPDMALQGFSLPNAHQGNRLBECRIMSSAKRPLW 780
QY 781 LMWNPDMISBLFONNEIIFKNGDDLRODWLTQIIRIMENIMONQGLDRLMPLPGCLS 840
Db 781 LMWNPDMISBLFONNEIIFKNGDDLRODWLTQIIRIMENIMONQGLDRLMPLPGCLS 840
QY 841 IGDGVLGIEVVRNHSHTIMQIOCKGKLGALQFNSHTLHQLKDNKGEIYDAIDLFTRS 900
Db 841 IGDGVLGIEVVRNHSHTIMQIOCKGKLGALQFNSHTLHQLKDNKGEIYDAIDLFTRS 900
QY 901 CAGYCVATFIIGIDRHSNSIMVKDQGLPHIDGHLFDHKKKFGYKREVPVLTODF 960
Db 901 CAGYCVATFIIGIDRHSNSIMVKDQGLPHIDGHLFDHKKKFGYKREVPVLTODF 960
QY 961 LIVISKAQECTKREPERPOEMCKAYLAIRQHANLFINLSMMLSGMPELOSFPDIA 1020
Db 961 LIVISKAQECTKREPERPOEMCKAYLAIRQHANLFINLSMMLSGMPELOSFPDIA 1020
QY 1021 YIRKTLADKTEQALAEYFMKQMDAHHGWTTKMDWIFHTIKQHALN 1068
Db 1021 YIRKTLADKTEQALAEYFMKQMDAHHGWTTKMDWIFHTIKQHALN 1068

RESULT 3
A54600
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1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 110K chain beta isoform - human  
 C/Species: Homo sapiens (man)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C/Accession: A54600  
 R/Hu, P./Mondino, A.; Skolnik, E.Y.; Schlessinger, J.  
 Mol. Cell. Biol. 13, 7677-7688, 1993  
 A/Title: Cloning of a novel, ubiquitously expressed human phosphatidylinositol 3-kinase  
 A/Reference number: A54600; MUID:94067128; PMID:8246984  
 A/Accession: A54600  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-1070 <HU>  
 A/Cross-references: GB:567334; NID:g455759; PIDN:AAB29081.1; PID:g455760  
 A/Note: Sequence extracted from NCBI backbone (NCBIN:140879, NCBIPI:140880)  
 C/Genetics:  
 A/Gene: GDB:PIK3CB; PIK3C1  
 A/Cross-references: GDB:136233  
 C/Superfamily: phosphatidylinositol 3-kinase  
 C/Keywords: phosphotransferase

Query Match 34.4%; Score 1966; DB 1; Length 1070;  
 Best Local Similarity 40.1%; Pred. No. 3e-126;  
 Matches 446; Conservative 194; Mismatches 371; Indels 102; Gaps 25;

QY 1 MPPRPS-GEIKGIH--LMPRIIVECLLPNGMIVTLECLREAVITITIKHELFKEARKY 56  
 Db 7 MPPAMADIDIDWAVDSQIASDGSIPVDFLLPTGTIYIQLEVPREXTISYIKQMLMKQVHNY 66  
 QY 57 PLHQQLDESSYIFVSTQAEEREFEDTRRLCDLRFQPLKVIIEPVGNREKILNRE 116  
 Db 67 PMNMLMDIDSYMFACVNOQAVYEELEDETRRLCDVAFPLVPLKLVTRSCDPEEK-LDSK 125  
 QY 117 IGFALMPVCEPMVQDEVDFFRNILNYCEAV-DLRDNLPSHSRMYVVPVYESSP 175  
 Db 126 IGVLIKQGHFPLSDQDEVEFRKRRKSEKILSLVGL-SMDMLKQTIYP--EHEP 182  
 QY 176 ELRKHLYNKDKQIIVIVIVISPNNDKQYTLKINHCVQVIAEAIIRKTRSMILS 235  
 Db 183 SIPEINDEKLYGGKLIIVAVHF--ENCQVFSFQVSPNNNPPIKVNELAIQKR----- 231  
 QY 236 SEQLKLCVLEQYQK-----YILKVCQGEDEFLEKYPISQYKIRSCIMLGMPYML 287  
 Db 232 -----LTIHKEDEVSYPDYVLQVSGVEVEFGDHPIQOYLRNCVMNRALPFIIL 283  
 QY 288 MAKESLYSQLPMDCTMPYSRISTATPYMGETSTK--SLWVINSALRIKILCATYV 344  
 Db 284 VECCIKKRYVEQGMIAEAINNSNLPRLPRPKTRIISHWENNPPQIVLVGN-- 341  
 QY 345 NVNIRIDIKIYVGTIYHGEPLCDVNTQRPVCSNPR-NWEMLVNDIYIPDLPRARLC 403  
 Db 342 KNTERTVAVHVRAGLFHGTLLCTIVSSEVSGKNDHINPELDFDINICDLPRMARLC 401  
 QY 404 LSLCS-----VKGKQAK-----EEHCLAMGNINLFDYDTTLVSGKALNL 445  
 Db 402 FAYVALDVKYKKSKTKTINPSKYQIRKAGKHYVAVWNTVDFPKGLRTGDIILHS 461  
 QY 446 W-FVPHGLEDLNPICVGTSGNPKETPCLELEFDWSSVYKFPDM-----SVLE 493  
 Db 462 MSSFPLEBEMLMVGTQVNTPTENAT-----ALHAKPEPKKQPPYVPEPKILIE 513  
 QY 494 EHAMSVSREAGSYSHAGLSNRLARDNLENDKQQLRAICTRDLPLSETTEOEKFLMS 553  
 Db 514 KAAEIASDSANVS-SRGG-----KKFLPVLKEILDRDLPLSQCEHMDMLIWT 560  
 QY 554 HHNYCTTI-PEILPKLLSYKKNRSDEVAQMTCLVQDWPIKPEQAMLELIDCNYPRPMVR 612  
 Db 561 LKQDCSEIFPQSLPKLLLSIKMKKEDVQQLQALQIWPGLPPEALTELLDFNYPRQYYA 620  
 QY 613 GFAYRCLAEKYLTDKLSYLIQVLYLKEQVYLDNLVLPFLKKAALTNRIGIFFPMHLK 672  
 Db 621 EYAVGLT-RQMSBEISQYLLQVLYLQVLPKPEFLDCLSRFLERALGNRRIGQFLFWHLR 679  
 QY 673 SEMANKTVSQRFGLLESYCRAQGMYLKHLNRQVEAMEKILNLTILIKQEKKDETQVOM 732

Db 680 SEVHIPAVSVQFVILLEYACRGSGVGMKVLKQVEALNKLKLTNSLTKLNAVKLNRKAKG 739  
 QY 733 KFLVEQRRPDPMDALQGFSLPNPAHQGNLLEECRIWSSAKRPLMLWMPDIMSIL 792  
 Db 740 EAMHTICKQAVREASLDLQSPNVCYIISLVEKCKYKDSQKPLMYLVNN-KVGE- 797  
 QY 793 LPONNIEIFKNGDGLRQDMTLTIQIRIMENIMQNGDLMLPYGCLSIDCVGLLEVR 852  
 Db 798 -DSVGVIKNGGDGLRQDMTLTIQIRIMENIMQNGDLMLPYGCLSIDCVGLLEVR 855  
 QY 853 NSHTIWOIQC-KGGLKGALOFNSHTLHOWLKDNKKEIYDAIDLFTRSCAGYCVATEIL 911  
 Db 856 TSETIADIQLNSGNVAFAAFNNKDALNMLKEVNSGDDLDRAIEEFTLSCAGYCVASYVL 915  
 QY 912 GIDRRNSNIMVMDQDLPHIDRGHLDHKKKFKYKREVPVVLVODFLIVISKGAQEC 971  
 Db 916 GIDRRHSDNIMVKKTQDLPHIDRGHILGNFKSKFKIKREVPVLTLYDFIHYIQG--KT 973  
 QY 972 TKTRFEERFQEMCYKAVLAIRQHANLFINFSMWLQSGMPELQSPFDIAYIRKTLALDKT 1031  
 Db 974 GNTKGRGRQCCEDAYILIRKGNLFTILFALMLTAGLPBELTSVNDIYILKDSIALGKS 1033  
 QY 1032 EOEALYIFMKQNDAAHGGWTTKDWIFPTIKQ 1064  
 Db 1034 EBEALQKQKPFDEALRESWTTKVMWMAHTVRK 1066

## RESULT 4

T43502  
 1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 110K chain - mouse  
 N/Alternate names: p110delta protein  
 C/Species: Mus musculus (house mouse)  
 C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000  
 C/Accession: T43502  
 R/Chanrky, D.; Vojtek, A.; Kaeshian, A.; Holtzman, D.A.; Wood, C.; Gray, P.W.; Cooper, J. Biol. Chem. 272, 19236-19241, 1997  
 A/Title: p110delta, a novel phosphatidylinositol 3-kinase catalytic subunit that associates with p85 and p50  
 A/Reference number: Z22519; MUID:97382246; PMID:9235516  
 A/Accession: T43502  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-1043 <CHA>  
 A/Cross-references: EMBL:U86587; NID:g2331237; PID:g2331238; PIDN:AAC5676.1  
 A/Experimental source: spleen  
 A/Note: highly expressed in lymphocytes and lymphoid tissues  
 C/Superfamily: phosphatidylinositol 3-kinase  
 C/Keywords: phosphotransferase

Query Match 34.3%; Score 1958; DB 2; Length 1043;  
 Best Local Similarity 39.7%; Pred. No. 1e-125;  
 Matches 429; Conservative 187; Mismatches 391; Indels 74; Gaps 19;

QY 16 MPP-----RILVECLLPNGMIVTLECLREAVITITIKHELFKEARKYPLHQ 60  
 Db 1 MPPGVDCPMHEFMTKESQSVVVDLPLPTGVYINLPYSRANLSTIKOYLHRAQYEPRLH 60  
 QY 61 LLDQESSYIFVSTQAEEREFEDTRRLCDLRLFPPLKVIIEPVGNREKILNREIGA 120  
 Db 61 MLSDEPAAVFTCVNQAEOELEDEQRRLCDIOPFLPVLRLVAREGDRVKKLINSQISLL 120  
 QY 121 IGMVCEPDMVQDEVDFFRNILNVCQAVDLRLDLSHNSAMYYPPNVSSPELPR- 179  
 Db 121 IAKGLHFPSLDPEVNDRTYKROFCERAAHRLQGLVEMLYQSFPLQLSPSARGMWA 180  
 QY 180 ---HYNKLDKQIIVIVIVISPNNDKQYTLKINHCVQVIAEAIIRKTRSMILSS 236  
 Db 181 GLLRVSNR-----ALLVWVKFEGSSSESTFFQYKDMPLALMAALARKK-----A 225  
 QY 237 EQLKLCVLEQYQKYLKVCQDEYFLEKYPISQYKIRSCIMLGMPYMLMAKSLYSQ 296  
 Db 226 TVFRQPLVEQPEVALQVNGRHEVLYGNVPLCHFOYICSLHSGLSPHLTWVHSSILAM 285

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QY 297 LPMDCFTMPSYSRRISTATPYMNGETSTKSLMWINSALRIKILICATYVNVNTRDIDKIYV 356
DB 286 RDEQSNPAVOVQFPAKPPPIPAKKSSSVSLWLEQPFSEILEIGRAKVADER--MKLYV 343
QY 357 RRGIVYNGEPLCDNVVQVY-PCSNRMWMLNYDIYIDLPAARLCISIGV-----409
DB 344 QAGLFNGHMLCTYSSSEVNVCSPEVMKQRFEDISVCDLPMAWLCFALYAVVERKAK 403
QY 410 --KGRGAKEEHCPGLMGNINLPDYDTLVSGKQALNLP-VHGEEDLNPIGVTSNP 466
DB 404 AASTKSKKACDPIANALMLFDYDQKGTGERCLYMPSVDEKELLNPAIGVTRGNP 463
QY 467 NKEETPLEDEDFMSSVVKFPMDSVIEEHANMSVSRPAGESYSHAGISNRLANDNLRN 526
DB 464 NMSAA-----ALVILYLP--VAPHPVPFPALEKILGRHGRIRIT-EELI---508
QY 527 DKEQLAICTRDLSEITEOEKDFLMSHRHYCT-IPELIPKLLSKKMSRBEVQWYMC 585
DB 509 ---QLEKILERRSGELIYEHKDLVWKMRHEVQEHFEALARLLLVTKMKHEDVAKMLY 565
QY 586 LVKDWPRIPKQAMELLDCNVPDPMVYGFVAVRCLEKYLTDKLSQYLQLVQVLYKYEQYL 645
DB 566 LDCSWBELPVLSDLDELSSFPDCCYGSFAIKSLRK-LTDELPQYLQLVQVLYKYESYL 624
QY 646 DNLVLFLLKALTNORIGHFFWHLKSEMHNTKVSQRFGLLESYGRACMYLKEHLNRQ 705
DB 625 DCLUTFLGRALANRKHGFLEFPHLSBMHVSVALRFGILMEAYCRSGSTHMKVLMKQ 684
QY 706 VEMAEKILNITDLKQEKDETOKVOMKFLVEQ-MRRPDMALQSLPLNPAHQNL 764
DB 685 GEALSKKALNDPQVSSQ-KTKRPQTKEMHMCROETMEALSHLOSLPDSSTLSEV 743
QY 765 RLBCRIMSASAKPPLMNMENPDIMSELFPONNEIIFKNGDDLRODMLTQIRIMENIW 824
DB 744 CVECTTMDSKMKPLMIMYSSEBNGSA---GNVGIIFKNGDDLRODMLTQIMQMDVLW 800
QY 825 QNQGDLRLMPLVGCSTIGDCVGLIEVVNRNSHTTMOIC-KGGLKALQFNSHTLHQKLD 883
DB 801 KQSLDLRMTPTGCLPTGDRGTGLEVLHSDTIANIQKSNMAATAFNADALMLMKS 860
QY 884 KKKKEIYDAIDLFTSCAGCYCATFTLIGIDRHNSINIMYKDDQLPHIDGHLDKKK 943
DB 861 KNPEALDRAIEEFTLSCAGCYCATYVLGIDRHSNDIMRESGOLPHIDGHLNPKT 920
QY 944 KFGKRRVRPVLVODFLIVISKAOCCTKTREPERPOEMCYKAYLAIRQANLFINLFS 1003
DB 921 KFGINRRVFPILYDFVHVIQGS-KTNSEKFERPRGVCERAVTILRRGGLFLHFA 978
QY 1004 MMLSGMPELQSFDDIAYIRKTLALDKTEQALEYFMKQNDANHHGWTYMDNIFHTIK 1063
DB 979 LMRAGAPELSCSDIOYLKQSLALGKTEBALKHFRVFNALRESWTKVNLAHVVS 1038
QY 1064 Q 1064
DB 1039 K 1039

RESULT 5
T13950
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13950
R:Leevers, S.U.; Weinove, D.; Macdougall, L.K.; Hafen, E.; Waterfield, M.D.
EMBO J. 15, 6584-6594, 1996
A:Title: The Drosophila phosphoinositide 3-kinase Dp110 promotes cell growth.
A:Reference number: 217828; PMID:9713328; PMID:897685
A:Accession: T13950
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Releases: 1-1088 <LEE>
A:Cross-references: EMBL.V09070; NID:g1707447; PIDN:CAA70291.1; PID:g1707448
C:Genetics:

```

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A:Cross-references: FlyBase:FBgn0015279
A:Map position: 3
C:Superfamily: phosphatidylinositol 3-kinase
C:Keywords: phosphotransferase

Query Match          29.4%; Score 1677.5; DB 2; Length 1088;
Best Local Similarity 35.1%; Pred. No. 1.7e-106;
Matches 384; Conservative 217; Mismatches 385; Indels 107; Gaps 28;

QY 24 CLPNGMTVTECLREATLITTKHELFEAKRYPLHOLLQDSSYTFPSVTOEAREBEF 83
DB 49 CLPNGFLEELRVNPANTIQIVIKEMVNAQKQMPGLGVYKEACEQVYGIS-TFNIERYT 107
QY 84 DETRLCDLRKOPFLKIVPEVGNREE-----KILREIGFAIGVCEFDWYK 132
DB 108 DETRLSEV---QPFGLIS-LGERDITTSFSSDYELTKVNGMIG-----TTFDHR 156
QY 133 ---DPEVQFRNINLVCKEAVDLRLDLSPHSRAMVYVPNVSSSEFLPKIYNKLDKQ 189
DB 157 THQSPFIDDFRLMYQTCNIELRSAYWQORLLYENHRLANSYKMBELIRERHPRT 216
QY 190 IIVVIVVIVSPNNDKQYTLKINHDCVPEQVIAEAIKKTRSMILSSBQKLCVLEYQK 249
DB 217 FLIV---VKNEQDSTFLSYNEODTPPSLTSTLOKXNRSQMKXNR-----TSD 264
QY 250 YILKVCCEBEYLPKRYLOKYKIRSCIMLGMPNLMMAKSLYSQLPMDCFMPSYSR 309
DB 265 YILKVSGRDEYLDGDFPLQFLYIQEMLSDAVPNVL--QSVR--LESTINHNHQ 318
QY 310 RISTATPYMNGET-----STKSLMWINSALRIKILICATYVNVNTRDIDKIYVRTGIYHG 364
DB 319 AMYTKRPLRKRIYHLHKISLSIMDMGNFQLTLSISVNFQTKRALKGVAVCLYHG 378
QY 365 EPLCDNVNTRQVPCSPRNEMWL-----NYDIYFDLPPAARLCISIGV---KGRKG 414
DB 379 KKLCAQRSTD---SPGNEDTFLFNDLVMPFDIQMNLPRMTLCVIEEVTKSSKXS 435
QY 415 AKSEHC-----PLAMGNINLPDYDTLVSGKQALNLPVPHGLE--DLNPIGV 462
DB 436 SNKIDIALDVPYKNPRLAVNNTTIFDKDILFTGHTLTYYADDIGSEVFNHGLTI 485
QY 463 GSNPKETPCLLEDFMFS--VVKFPMDSVIEEHANMSVSRPAGESYSHAGISNRLAR 519
DB 496 EPRPRKE-ECALYVDLFLSSGTQVAPSEEVLYQA--ADREQ-----VNRQ 542
QY 520 DNEIRENDKQALPACTR---DPLSEITEOEKDFLMSHRHYCT-IPELIPKLLSVK 574
DB 543 QLAGPEKRIKELKELMANYGTGLRIYEMVQDNNAIWERNNDILRELPBELSILHCVW 602
QY 575 NSRDEVAQWCLYKDWPRIPKQAMELLDCNYPDPMVYGFVAVRCLEKYLTDKLSQYLQ 634
DB 603 KERDDVADMWYLLKQWFLISERSLELDYAFDPVARRAICQL-FLQDEBLLLYLQ 661
QY 635 LVQVLYKYEQYLIDNLVFLKALTNORIGHFFWHLKSEMHNTKVSQRFGLLESYGRA 694
DB 662 LVQAIKIESYLSLVLVFLERLARNORIGHFFWHLRSMQTPRFGLLLEVLYKG 721
QY 722 CKHHVAPLRQQLHVEFLKQGSLLAKKSKKEXKVTMLDPLRQDRNSAVF---QNTQNP 777
DB 755 LNPRAHQGNRLBECRIMSASAKPPLMNMENPDIMSELFPONNEIIFKNGDDLRODMLT 814
QY 778 LNPFRCSGVLPDRCKVWDSKMRPLVWVFENADVNA---SDVHIIFKNGDDLRODMLT 833
DB 815 QIRIMENIMONQSLDLRLMPLVGCSTIGDCVGLIEVVNRNSHTTMOICQGLKQALO-FN 873
QY 834 QMLRVMDQMKRGDMDRAMINYNISMEKSGIMIEVVRHAETIANIKKEKGMFSAIAPFK 893
DB 874 SHTLHQLKDKNK-GEIYDAIDLFTSCAGCYCATFTLIGIDRHNSINIMYKDDQGLFHI 932
DB 894 KGSLSMLKHNKADKLKAIINFTLSAGYCVATYVLGIDRHSNDIMWKRGOLFHI 953

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Db 694 -----LPIVGNKILISIFLPITQVTKLTLELNETADQFNRLFTKKYS 739
Qy 247 -----QGKILKVCGEDEFLEKYPISQYKIRSCIMLGRPMPLML-AKESLYQL 297
Db 740 KHLNPNVSNHPLIKVVGSSDFIHGPHDIRPESINHHIOGTQPLTIQRPKPELDOP 799
Qy 298 PMDCFTMPS---YSRISTATPYMNGETSTK-----SLAWINSALRIKI 338
Db 800 FKRPEDVPELLIDHSCSNAINCNNTNSTNNNNINPDMDQITHISIREIKKPRKXV 859
Qy 339 LCATYVNVN-IRID-KIYVRTGIYHGEPLCDNVNTQRP-----CSNPRNEML 387
Db 860 MGRTRIPLSCTIKIDSSSVIVISILYHGLECSKAFQPIIPPPAPLAETLSVWCWML 919
Qy 388 NY-DIYIPDLPRARALCLISCS-----VKRKAKEEHCHLANGINLPDYDTL 436
Db 920 VFTNIDVSNLPVDALISIVYSANETVDVEIKNLDATKPLPIGINVWITDFKYL 979
Qy 437 VSGKALMLMPVPHGLEDLNPIGVTSNP-NKETPCLEFPDMFSSVVKPPDMSVIEH 495
Db 980 RQGVNELSLMP-----SPFSNPLGCSNPNSSQSGVLTLEFEENLVLP----- 1026
Qy 496 ANMSVSRAGFSYSHAGLSN--RLARDNELENDKEQLRAICTRDPLSEITEQKDLMS 553
Db 1027 -----RTKFTSVSVIEQPPPTINSNEMRE-FEQITLAL--DPLDLKQEKYQMLT 1076
Qy 554 HRHICVTIPEILPKLLSVKANSRDEVAQWCLVNDMPPIKPEQAMELLDCNPPRMWG 613
Db 1077 LRHYSILRPPVLPRLMLSVPTQATAVDEAISLDLRMPKLPKYESLELLDLKHNARKRE 1136
Qy 614 FAVGCLBEVLTDDKLSQYLIDLVOLKYEYOYLDNLVFLKKAALTNORIGHFFMHLKS 673
Db 1137 FAVTCLLED-LSBEDELLDLQLVQLKYEPFHDSKLSFLRKALINNHIGHSFMYLKS 1195
Qy 674 EMHNKTVSQRFGLLLESYCRACGYLKLHNRQVEAMEKLIINTDLKQEK--KDETOKYO 731
Db 1196 DLHDSNLSBERGILLLESYLVACGARIETLQ--MEVINNLTEVAKKIKPLKQDDR-- 1250
Qy 732 MKFLVEQRRPDMALQGLSPLPNAHQNLRLIEBCRIMSARPLMLNENDIMSE 791
Db 1251 -EFMIKER---ESLEWPKRPHLTLPNRPESNGLIINKSKYMSKPLRLSLTNTDNMAD 1306
Qy 792 LLFONNEIFPKNGDRLQDMLTLQIIRIMENIMQOGLDRLMPLPGCLSIGPCVGLIEV 851
Db 1307 PI---EYIFKAGDDLQDMLTLQIRLMDKLMQEGDLKLSPIGCGISTGMIGIEV 1362
Qy 852 RNSHTIMOIO-CKGLKGLQFNSHTLQWMLKDKNGEI-YDAALDLFTRSCAGCVATF 909
Db 1363 LNSETTAKIOKSEGG--GAPRFQVGSFGQLIQHNKSDMEYQKAVDTFILSCAGCVATY 1420
Qy 910 ILIGIDRNSNINMVDQGLPHIDGPHLDHKKKKFYKREVPVLYODPLIYISKQAO 969
Db 1421 VLGIGDRHNDMLMYKRGRLPHIDGPHLGNYKKKFGFRERARPPVFPDFCYV--GQK 1478
Qy 970 ECTKREERFEREMCYKAYLAIROHANLFINFSWMLSGMPELQSPDIAVIRKTLAD 1029
Db 1479 ESFK--ISQFVNYCTGTINIVKNAKLPANLFAAMVSTGIPELQSMEDLNYLKESFSE 1535
Qy 1030 KTEQEALEYFMKONDAHGGWTTKMDWTFHTIKOHA 1066
Db 1536 LSDAKAREKVALIHES-LATKTQLNNPFHHL-AHA 1570

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## RESULT 8

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T18273
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 2 - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18273
R:Zhou, K.; Takegawa, K.; Takegawa, K.; Takegawa, K.; Takegawa, K.; Takegawa, K.;
Mol. Cell. Biol. 15, 5645-5656, 1995
A:Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Bid

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A:Reference number: 206411
A:Accession: T18273
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1858 <ZHO>
A:Cross-references: EMBL:U23477; NID:9733521; PID:9733522; PIDN:AAA85722.1
C:Genetics:
A:Gene: PIK2
C:Keywords: phosphotransferase

Query Match      22.1%; Score 1262.5; DB 2; Length 1858;
Best Local Similarity 28.7%; Pred. No. 1e-77;
Matches 366; Conservative 197; Mismatches 397; Indels 317; Gaps 42;

Qy 15 LMPRIIVECLIPNGMI--VTECLREATLITIGHELFKARKYP-LHOLQDESSYIF- 70
Db 657 LIPEHYELKUSVNSTISNELP-LRQOTLM---QACNISRLEPKHLILKSSSTIILD 711
Qy 71 -----VSVOAEERBEFFDETRLCLEL-----FOPELYIEPVGN 107
Db 712 GASTTTTTTTTTTTTANQSSNITTKNSSLDLTINNSNEIDVKCHIQALELIEFELIGT 771
Qy 108 REEKILNREIGFALGMVCEPDWKDEYODFRN-----ILNCKEAVLDRLDLSNHSR 162
Db 772 SFTVLD-----QGEVVSFRDPAQFRISNFTSTRNDL-----SQ 807
Qy 163 AMYVYPNVSSEPELPHKIVNKLDKGQIIVYIVVAPNNDKQYTLKINHDCVPEQVIA 222
Db 808 MIVY-----SSEPLPLTPRK-----ITIMWL- PGQDK-----IKKAVDCPPNSVG 849
Qy 223 EAIRKTRSMILSSEQLKCVLEYQK-----YILKVCCEBEYL-----EKYP 266
Db 850 DVKKEIFKXAMIDR-----VHQGKTODDFVLKATGFEYILICHELGNLTSRQFYF 903
Qy 267 -----LSQKIRSCIMLGRPMPLML----- 288
Db 904 TSGGDFSLMDYDIKQCVGNQVLELSTNNISLSLNOVEKVSFLDKILETSDPDYD 963
Qy 289 -----AKESLYSQLPMDCFPM----- 304
Db 964 EDDLINSNSFDLKQSIQOQOQOQIOTVINIKRTNKENKDNKENDSSNNNNNNNN 1023
Qy 305 -----PSYSRISTATPYMNGETS-----TKSLWYI- 330
Db 1024 NNNNNNNNNNNNNNNNNNNNNNNNNNSNSISGSLDEGNGSGSGSQOPTLIG 1083
Qy 331 -----NSALRIKILCATY-VNV-NIRID-----KIYVRGIY 361
Db 1084 VQNFSLPNNSKLPINIVGRLEFRVNIAGRLNLFNNNEDARKKPADGKNQGNVFMALY 1143
Qy 362 HGEPLCDNVNTQRPVPCSN-----PRNEMLVNDIYIPDLPRARALCLISCVGRK 413
Db 1144 YGGEILNTPVTPPIAQLASVDSGSEVPENMEKIAFTIPRIYLPRARASTVVTITSE 1203
Qy 414 GAKBE-----HCPLEAGNINLPDYDTTLVSGKALNLMPVPHGLEL--LNPITYGTS 464
Db 1204 ALESQMEVAVESKLPIGNSCNCLMNHKMLMGTAFLW-----DQGRANDIGTCVD 1257
Qy 465 NPNKETPCLEL-EFDWBSVVKFPDMSVIEEHAN--MSVSEAGFSYSHAGLSNRLARON 521
Db 1258 NOAKQOPILLVBESEFIRPIVYVDTALQSMKVDSSISISNGVESPIVSFSSAASS 1317
Qy 522 ELRE-----NDKEQLRAICTRDPDLSEITEQKDFLMSHRKYCVTIPEILPK 567
Db 1318 PLPSSPLSPVGLKLLDDEARRLKALMDSPLVOLSNEBKVLVYGRHIIYKSKPKALAK 1377
Qy 568 LLLSVKANSRDEVAQWCLVNDMPPIKPEQAMELLDCNYPDPVNRGAFAVRCLEKYLTDK 627
Db 1378 FLTSNWNIDPQVNDAYRQNDWMLKRYQALLETLDKAFABEHRNFAIKIINFS-SDAE 1436
Qy 628 LSOYIQLVQLKYEYOYLDNLVFLKKAALTNQ-RIGHFFMHLKSMEHNKTVSQRGL 686
Db 1437 FSDFLQTLQVLYKPEYNSDLTILIORALSNRSRIGHFFFWPLKSEMTPEIEBRYL 1496

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QY 687 LLESYCRACGMYLKHNRQVAMEKLIINTDILKQEKDETOQVQMKFLVEQNRPPDMD 746
DB 1497 LLEGYRSCGTHRODILKQNOVLKSLHTVAMAVKQTSSESRK---KYLEGSLKIFPD 1553
QY 747 ALGGFLSLNPAHQSLRLBECRIMSASRPMLMNPENDDIMSHLLFQNNELIFKXGDD 806
DB 1554 TFO---LPLDPRWEAKGLIIDCKRYMDSKLPMLVENVNPPHAKPL---TYIFKXGDD 1606
QY 807 LRQDMTLQIIRIMENIMQNGDLRLM.PYGLSLIGCVGLIEVYRSHNTIMOICKGL 866
DB 1607 LRQDILITQYLRIMDKRWKSGMDRLQPKCIATGSGIGMLEVYLNANITANINKDAG 1666
QY 867 KGLAQNSHTLHOMLKDKNKEI-YDAIDLFRSCAGCVATFIIGIDRHSNINWMD 925
DB 1667 TGLAL-LEEKTLVWMLKXCNKTEAEYNKAVETFLISGAGYVATYVMGIDGRHSNIMITK 1725
QY 926 DQGLPHIDEGHFLDHKKKKGYKREYRPFVLTDPLIVISKAQECTKTEFERFQEMCY 985
DB 1726 LGHLPHIDEGHFLGNKKYGFRRERAPFIETPOYMAIV--GGKD---SENFRKFVTTCC 1780
QY 986 KAVLAIRQHANLFINFSMMLGSGMPELQSFDDIAVIRKTLALDKTEQALVEFMKO--- 1042
DB 1781 SANNIRKNTDLFINLQMLSTGIPBLQVAEDIDYRKALAGLSDEBAABEFTKNISV 1840
QY 1043 -----NMDAHGGM 1051
DB 1841 ALNTKTVLINDIFH-GW 1856

RESULT 9
T18274
1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 3 - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18274
R:Zhou, K.; Takegawa, K.; Emr, S.D.; Fittell, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
A:Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Bic
A:Reference number: 206411
A:Accession: T18274
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1585 <ZHO>
A:Cross-references: EMBL:U23478; NID:G733523; PID:G733524; PIDN:AAA85723.1
C:Genetics:
A:Gene: PIK3
C:Keywords: phosphotransferase

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Query Match 19.4%; Score 1109; DB 2; Length 1585;
Best Local Similarity 30.7%; Pred. No. 2.6e-67;
Matches 301; Conservative 189; Mismatches 374; Indels 118; Gaps 30;

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QY 146 VCKE-AVDLRDLNPSHRAMTVYPPNVESSPELPKHIYNKLDKGQIIVITWIVSP--NN 202
DB 562 LCKERLVLDQSLERINNGR-----PSIWS-----HIDVLSFNRLKRLAMLAKQSNV 610
QY 203 DKQKYLTKINHDCVPEQVI--AAAIKRTS-----MLSSBQLCVLEYGQ 248
DB 611 PAARLTPYRPPKTIPEFYRHLFPKQTKSLCANNHFAISLMTILSEKTKNTTPEDP 670
QY 249 KYLLKVGCDDEVLEKPLSQYKYIRSCI-----MLGRPNMLMAKESLYSLPMD 300
DB 671 QYRFLITGNOYVDPVPLSVYIYVKRKKEIDLTVWELSLGIIQQQQQQQQQQQ 730
QY 301 CTTPMSYSRRISTAT-----PYNNGETSTKSLWINSALRIKILICATY 343
DB 731 QQQQQQOINIDENILKINGLINVLKIEKPIREKDNICSLTYTEN-LQYRLHAHE 789
QY 344 VVNV-----IRDD---KIYVRGIYHGEPLCDNNVTQVRPVSNNRMWMLNYDIYD 395
DB 790 IFASKASEIITGDSPTQILTEAIVYFGELLATQSSKLVSFODTYVMWEMWNIPLAVSN 849

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QY 396 LPRARICLSICGVKRGKAKEECPLAWGNINLPYTTDL-VSGKALNLMWPVHGLE 454
DB 850 IPNGARMCGL-----NARYGDI FINI GWYGRHLFPDSKGLINTFAPPSLLWP-----G 898
QY 455 LNPPIGVTSNPKKEPCLLELEFDMSSVYKFPDMSVIEHAWSVSREGFSYHAGLS 514
DB 899 KINPIGCVNLSKQOAILIAEFKDYVY--BKTIHYEDDLIELISKD----- 945
QY 515 NRLARNDL---RENKQELRAICTRDPPLSEITQEQKDFLMSRHHCVTIPILPKLLS 571
DB 946 ---ENGNELPVVTMEEMDRVQIILIDPLYSLKKEERLIMKSRFYCHTKPQLSKLOS 1002
QY 572 VKNSRDEVAQMYCLYKDWPPPIKPEQAMBLDNCYRPPM-VRGFAVCEKYVLTDDLSQ 630
DB 1003 VEWNTYKQVGEARQQLKIMPTTSLAVDALLEDLPKPAVCVEIRRYTKCLDQ-MSDELEI 1061
QY 631 YILQIVQLKYEGYLDNLVRFLLKALTN-QRIGFFFNHLKSEMANKTVSQRFGLLE 689
DB 1062 YILQIVQALKHDFNHSVLSLFLIGRWQMMOVLGHFFWHLRADIDNOECERFVTLSS 1121
QY 690 SYCR-ACGMVLYKHLNRQVAMEKLIINTDILKQEKDETOQVQMKFLVEQMRPDMFAL 748
DB 1122 GFLRYAPQOLMESFKKEITTLRLLENLAKVKEVPEKQYVENNLRBQSFPTEI--- 1178
QY 749 QGFLSLNPAHQSLRLBECRIMSASRPMLMNPENDDIMSELLFQNNELIFKNGDRL 808
DB 1179 ---FVFPDPSIRILNIIPECKSMDSAKVPLWTFKNADPAPPL-----QMIKTGDDL 1231
QY 809 QDMTLQIIRIMENIMQNGDLRLM.PYGLSLIGCVGLIEVYRSHNTIMOIC-KGGLK 867
DB 1232 QDILITQYLRIMDKRWKSGMDRLQPKCIATGSGIGMLEVYLNANITANINKDAG 1291
QY 868 GAGQNSHTLHOMLKDKNKEI-YDAIDLFRSCAGCVATFIIGIDRHSNINWMD 926
DB 1292 GA--FKQTPRANMLKHNQNTENSQKAVSKFTLSGAGYVATYVLIIGRHSNINWMD 1349
QY 927 GOLPHIDEGHFLDHKKKKGYKREYRPFVLTDPLIVISKAQECTKTEFERFQEMCY 986
DB 1350 GHLPHIDEGHFLGNKFTFAGFQREKAPFVLTTPFVVI--GGKD---SENFRKFVTTCC 1404
QY 987 AVLAIRQHANLFINFSMMLGSGMPELQSFDDIAVIRKTLALDKTEQALVEFMKOMDA 1046
DB 1405 AFNIIIRSNHAFVTFMPELMLSTGIPELRSENDIVYRDKRFLDTDAEASEYFKLIIHES 1464
QY 1047 HHGQWTKMDMIFHTIKOHALN 1068
DB 1465 -IGTLTTTINFAIH-IMAHKN 1484

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## RESULT 10

S71792

phosphatidylinositol-3-OH kinase AGE-1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C&gt;Date: 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 01-Dec-2000

C:Accession: S71792; T31476; T18707

R:Morris, J.Z.; Tissenbaum, H.A.; Ruvkun, G.

Nature 382, 536-539, 1996

A:Title: A phosphatidylinositol-3-OH kinase family member regulating longevity and diapause

A:Reference number: S71792; NCID:96320556; PMID:8700226

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1164 &lt;MOR&gt;

A:Cross-references: EMBL:U56101

R:Williams, L.

submitted to the EMBL Data Library, October 1999

A:Reference number: Z21038

A:Accession: T31476

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-263; 'YEMK', 270-285; 'L', 'Q', 289-307; 324-328; 'LESY', 332-1164 &lt;WIL&gt;

A:Cross-references: EMBL:AL110499; PIDN:CAM57914.1; CESP:BO334.8

A:Experimental source: clone Y62PSA



```

QY 298 --PMDCTM-----PSTSRRI-----STARPYNG-----320
D 512 HNEVDALFDGDFPLADRVQSVKAI CNALAAVEPTELSALNQLPPCPSRMQPKQK 571
QY 321 -----ESTSKLWYNSAL--RIKILCATYNNVIR-----349
D 572 DPSVLAVRENRKVEALTAIDLVELYCNTF--NADQTAVPGRKHDVLQEAChEARS 630
QY 350 -----DIDKIYRTGIYHGEPICDNVNTQVPCSNP-----WNEML 387
D 631 LAFTVATHRIPIWATSYEDFYLSCLSHOGKMCSPLOTRKAFSKYLPHLIWMOOI 690
QY 388 NYDIYIPDLPPAARLCUSICSV-----KGRKAKEHCN--IAMGNINLPDYDTLVSG 439
D 691 CFPQVNRRLPRETLICATVALPPIPPGSSSEANKQKRVPEALGVTTPLFNFRQVLTGC 750
QY 440 KMALNMPVPHGLEDLNPIGVTSNPNKTP--CLELEPDMFSVVKPPDMSVIEHA 496
D 751 RKLGLMPATQE-----NP--SARWASPNFQPPSVIIQIDPFTSAFDIKETS---PPGD 800
QY 497 NWSVSRAGFSYSHAGSNRLARDNELRENDKEQLRAICTRDPLSEITBOEKDFLMSRH 556
D 801 KFBPRYFEG-----SIREEDOKLKIMOKESLYWLTADKRLMEKRY 844
QY 557 YCATTEPILPKLLSV--KMSRDEVAQWYCIWKDMPPIKPEQAMELDCNYPDPWVRG 613
D 845 YCHSEVSSLPLVLASAPSMEMACLPDI--YVLLKQTHNHQDALCLLHATFPDQVVR 901
QY 614 FAIRCLEKYLTDKLSOYLQIYOVLKYBOYLDNLVRFLLKALTNQRIQHFFFWLKS 673
D 902 MAQWQIGS--LSDDELLADLYLPOLVQALYECYDLSPLRFLKRAVSLRYTHFFWLLKD 960
QY 674 EMHNKTVSQRFGLLSEYCRACGWYLK--HNRQVEAMEKLINTDILKQEKDQVQVM 732
D 961 GLKDSQESIRYOYLALALCCCKGRLBEPNRQC--WLVNALAKLAQOVRKAPASARQ 1016
QY 733 KPLVEQRRPDMALOGFLS--PLNPAHQGNRLBECRIMSSAKRPLMWNENPDIMS 791
D 1017 GILRTGLEEVKQFPALNGSCRLPLSPSLVKGIVPRCSYFNSNAPVLTKLSFQNVPLGE 1076
QY 792 LLFONNEIIFKNGDDLRODMTLQIIRIMENIMONQGLDRLMPLPYGLSIGDCVGLIEV 851
D 1077 ---NIRVIFPKCDDLRQDMTLQIRIMSKIRWOBELDMRWVIFRCFSGRGRGWEMI 1132
QY 852 RNSHTIMOIOCKGGLKALQFNSHTLHQWLKDKNKG--IYDAALDLFTSCAGCYATFI 910
D 1133 PNAETLRKIOVEHGVTS--FKDRPLADWLQKINPGDEYEKAVENFIYSACGCCVATYV 1190
QY 911 LGIGDRHNSNIMVKKDQGLPHIDFGHLDHKKKKFGYKREVRPFVLTDPLIVISKAQ 970
D 1191 LGICDRHNDIMLKTGMHFIIDFGHLDHKKKKFGYKREVRPFVLTDPLIVISKAQ 1250
QY 971 CTTTRFEFRFQEMCYAYLAIROHANLFINLFSMMLGSGMPELOSPDIAVIRKTLALD 1030
D 1251 SSR---FHDPEVDLCCQAYNLIRKHTHFLNLLIMLSGIPSELSEDLKYVDALRPQD 1307
QY 1031 TEOEALYFMKQMDAHGSGWTKMDMIFHTIKO 1064
D 1308 TEANATTTFTTR--LISSLSGIVATKLNPFHTINLAQ 1340

```

## RESULT 12

T42642  
phosphoinositide 3-kinase (EC 2.7.1.-) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Jan-2000 #sequence\_rev: 11-Jan-2000 #text\_change 11-May-2000  
C:Accession: T42642  
R.Molz, L.M.; Chen, Y.W.; Hirano, M.; Williams, L.T.  
J. Biol. Chem. 271, 13892-13899, 1996  
A:Title: Cpk is a novel class of Drosophila ptdlns 3-kinase containing a C2 domain.  
A:Reference number: Z17659; MUID:96278830; PMID:8662856  
A:Accession: T42642

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1658 <MOL>  
A:Cross-references: EMBL:US2193; NID:g1272421; PID:g1272422; PIDN:AAC52604.1  
A:Experimental source: strain balb c  
C:Genetics:  
A:Gene: cpk  
C:Superfamily: Hec2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology  
C:Keywords: phosphotransferase

Query Match 18.4%; Score 1049.5; DB 2; Length 1658;  
Best Local Similarity 33.1%; Pred. No. 3,2e-63;  
Matches 270; Conservative 141; Mismatches 297; Indels 107; Gaps 24;

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QY 296 QLPMDCTMSY-----SRISTATPTMNETSKLWVNSAIRIKILCATYNNV 347
D 614 QVSMIDLTTAIYOLLRLHANSRSCSTGCP--RSSRNKEMATTEOQFTVAAHGSSN 671
QY 348 -IRIDIKIYRTGIYHGEPICDNVNTQVPCSNP-----RWNEMINVDIYIPDLPPAAR 401
D 672 WSNVNEKYVILCSLSHNGDLFKPIQSKYTKNFYILKMDLIIFFIOISQPLESV 731
QY 402 LCUSICSV-----KGRKAKEHCNPLAMGNIN--LPDYDTLVSGKQALNMLP 447
D 732 LHLTLFGVLNQSSSSPDSNKKQKQ-----PEALGVSLTLFPFRFLTGTKLYLMT 785
QY 448 VPHGLDLNPIGVTSNPNK---ETPCLELEPDMFSVVKPPDMSVIEHANMSVRE 503
D 786 SSH-----TNSIPAIKPKSYMERIVLQVDF-----PSPAPDII-----820
QY 504 AGFSYSHAGSNRLARDNELR--END--KEQLRAICTRDPLSEITBOEKDFLMSRH 560
D 821 ---YTSPOIDRNIIOODKLETLESIDIKGLDIIHRDSSFGSKEDKPYLMENRYCLK 876
QY 561 IPEILPKLLSV--KMSRDEVAQWYCIWKDMPPIKPEQAMELDCNYPDPWVRGAVR 617
D 877 HPCPLKPIIASAPNMKMAN--LAKTYSLLHQPPPLCPALAEILLDAKFAQDQVRSIAMS 933
QY 618 CLEKYLTDKLSOYLQIYOVLKYBOYLDNLVRFLLKALTNQRIQHFFFWLKS 677
D 934 WMEA--ISDELLADLYLPOLVQALYECYDLSPLRFLKRAVSLRYTHFFWLLKD 992
QY 678 KTVSQRFGLLSEYCRACGWYLK--HNRQVEAMEKLINTDILKQEKDQVQVM 736
D 993 THGSRVHYVLGALLSVGKGLRELSKQMKVLQVLGVAEKVQKQSSGTROYVLOK---1049
QY 737 EQRRPDMALOGFL-----SPLNPAHQGNRLBECRIMSSAKRPLMWNENPDIMS 790
D 1050 -----SMERVOQSFILRKRCRLPLKPSLVAKELNIKSCSPSSNAMPKVTVMNADPLG 1102
QY 791 ELLFONNEIIFKNGDDLRODMTLQIIRIMENIMONQGLDRLMPLPYGLSIGDCVGLIEV 850
D 1103 EEI---NVMFKVGEDLRQDMALQWIKIMDIWLBEGDLRMVIFRCISTGDRGMVEL 1158
QY 851 VNSHTIMOIOCKGGLKALQFNSHTLHQWLKDKNKG--EYDAALDLFTSCAGCYAVFI 909
D 1159 VPASDTLRKIOVEHGVTS--FKDRPLAEMLKRNPESEYEAGSNNFIYSACGCCVATY 1216
QY 910 LGIGDRHNSNIMVKKDQGLPHIDFGHLDHKKKKFGYKREVRPFVLTDPLIVISKAQ 969
D 1217 VLGI CDRHNDIMLRTGMHFIIDFGHLDHKKKKFGYKREVRPFVLTDPLIVISKAQ 1276
QY 970 ECTTRFEFRFQEMCYAYLAIROHANLFINLFSMMLGSGMPELOSPDIAVIRKTLALD 1029
D 1277 ---FTIRFQLFVLDLCCQAYNLIRKQTNLFINLISIMBGELETLSDILKYVDALRPQ 1333
QY 1030 KTEOALYFMKQMDAHGSGWTKMDMIFHTIKO 1064
D 1334 TTDAETITFTTR--LISSLSGIATKFNPFHTINLAQ 1367

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## RESULT 13

JCS985

phosphoinositide 3-kinase C2gamma - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 06-May-1998 #sequence\_revision 29-May-1998 #text\_change 30-Apr-1999  
 C:Accession: J05985  
 R:Hisawa, H.; Ohtsubo, M.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Yoshimura, A.  
 Biochem. Biophys. Res. Commun. 244, 531-539, 1998  
 A:Title: Cloning and characterization of a novel class II phosphoinositide 3-kinase cont  
 A:Reference number: J05985; MUID:98189216; PMID:9514948  
 A:Accession: J05985  
 A:Molecule type: mRNA  
 A:Residues: 11506 <MUS>  
 A:Cross-references: DDBJ:AB008791  
 A:Experimental source: liver  
 C:Comment: This protein exclusively expressed in the liver, and a N-terminal truncated fo  
 A:Map position: 6  
 C:Superfamily: Hec2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology  
 F:978-1239/Domain: catalytic #status predicted <CAT>

Query Match 16.1%; Score 919; DB 2; Length 1506;  
 Best Local Similarity 24.7%; Pred. No. 2,4e-54;  
 Matches 308; Conservative 204; Mismatches 414; Indels 322; Gaps 44;

QY 4 PPSGELWGHLMPPRLVBECLPFGMIVTIECLREKATLITIKELFKKARKYPLHQ--L 61  
 DB 127 RNPSSGKHGIEY--PRF--DALPPSTGQECNPOQSGTKHNYCGE-----HEGNL 175  
 QY 62 LQDESSYIPVSVTOEARREFFEDTRRLCDLRLPOPLKY-----IEP 104  
 DB 176 PHHSSYSIDISIPNR-----EKRSQGVNLVPSLSEKDFLRTSNVSESTER 227  
 QY 105 VGNREKILNREIGFALGMPVCEPDVYKDPREVQDFRNILNVCEAVDLR-----DLNS 158  
 DB 228 IG-----CPRIEVEVP--QCSNKLASFCKNVKKIRRESYASDINS 266  
 QY 159 PHSAMTV--YPPNVSSPELPHKIYVKKLDKQIIVIVIVPBNNDKQYTKIKINDC 215  
 DB 267 NSGKIMATTAYPPRLPADTKFR-----XKISTENSAQLLLMPPHANY 309  
 QY 216 VPBOVIAEAIKKRSMILSSEOLKLCVLEYQKYLKVCSCDEFEFLKPYLSQKYI-- 273  
 DB 310 LVKDLIAITL-----LICANEPLS-----PKETILVSCSEFLQMDHSLGSHKIFQX 357  
 QY 274 -RSCIMLRMPNMLMAKESLYSQ-----LPMDCFT--MPSYSRRI 311  
 DB 358 NKSIVQHLQKNRDPKGLSRKSEDDHSPHNLQLEFTHIWKISRQCLSTVMKKYNLAH 417  
 QY 312 S-----TATPYM----- 318  
 DB 418 EHLTKPKQMEBKHLSSMVGNGQHTSOPHVNVLBEVYNICSVLGCIEFTKQVSDAVKELN 477  
 QY 319 -----NGESTTK-----SLWVINSALRKIKLCATYVNVNINDIKI 354  
 DB 478 LILQPSGNFHONSETSKKGLIERVATLSRSIYQ-----IDVYCSSECT--DPQPV 528  
 QY 355 YVRGTIVH-----GGEPLCDNVNTQV 376  
 DB 529 HTPGGSVHVAHAGLOHSLFTVCSLHNVPEYTAHSAKAFSCWLTGYAGKCLCOVASCPL 588  
 QY 377 PCSNP-----RWNEMLNIDYIPDLPPRAARCLSLCSYKRGAKAEHNPPLAWGINLFD 431  
 DB 589 PVTKEFSLLVNNNEIINFLPIKSLPBESEMLVIKLF--GISASHTNMLAMTCLPLFP 645  
 QY 432 YVDIVLSGGM-ALNLMPPVPHGLIEDLLNPIGVGNSPNKKTPLCELEFFQFSSVVKPPDMS 490  
 DB 646 ROESVLSGLSLFVTLQSEPP--IEMTAPVWDGSDSP--LTLDID-----PPD-- 690  
 QY 491 VIEEHNANVSREAGFSYSHAGLSNRLARDNELRENDKEQLPAICTRD--PLSE----- 542  
 DB 691 -----AGMEY-----LKPSESENRTRDHEPRECKLHIAKLSQKKSPLL 729  
 QY 543 ITEOEKDFLMSHRHVCVTIPEILPKLL-LSVKNNSDEVAQMYCLVXMDPPPIKPEQAMLL 601

DB 730 LSEKRRYLMFYRLVCNNENSSLPLVLGASPGMD--EEIVSEMHAILLRMTFSHPWEALQ 788  
 QY 602 LDCNVDPNVRGFAVRCLEKYLTDKLSQYLQIVQVLEQYLDNLVLYFLKKALTNQ 661  
 DB 789 LRSRFPDQDIREVAVQQLDILLTDE-LDCLPOLVQAVFEMNLSPELLVLRRLRLOSI 847  
 QY 662 RIGHFFFMHLK--SEMHKTVSOPRFGLLLESYCRACGMYLKHLNQVAMEKILNLTDI 718  
 DB 848 RVNHCILYMLRDAQSAYKSMYQELALQ-FCAG-----EALNELSKEQVLVLGD 901  
 QY 719 LKQEKDETQVQWKFLEWQ--RRDPFDALQGLFSLPAPAHQGLRLBECRIMSAR 777  
 DB 902 IGEKVASADPQRKVDLKEIGLESEFFFDIKTCHLPLPALCICKIDIDACSYFNSAS 961  
 QY 778 PLMLNENPDIMSELLFONNEIFKNGDDLRODMTLQIIRIMENIQNSGLDRLMPYG 837  
 DB 962 PLKITFINAPMG--KINISVIFKAGDDLRQMLAQIIVQNDNMLOBGLDMQMITTG 1017  
 QY 838 CLSIDGCVGLIEVVRNSHTIMQIQCKGKGLAQFNSHTLHOWLKDKNK-GEIYDAIDL 896  
 DB 1018 CLSTGAAQGIENVPDAVTLAKIHLSGLIGPLKEN--TIKKWFSQNHMLKEDYEKALRN 1075  
 QY 897 FTRSCAGYCVATPILIGIGRHNSINWKDQQLPHIDFGHFLDKKKKRGYKREVPVL 956  
 DB 1076 FVYSCAGWCVTFILGVCDRHNDNIMLTSGHMFHIDFGKFLGHAQTFGGIKRDAPIF 1135  
 QY 957 TQDFLIVISGAEBCIKTRFERFERQEMCYAYLAIRHANTFINLPSMMLGSGMPELOSF 1016  
 DB 1136 TSEMEYFITEGK--NIQHFQDFVELCCRAVIVRHSGLIISLEMLHAGLPRLGI 1192  
 QY 1017 DDIAVIRKTLALDKTEQEALEYFMKQNDNAHSGMTTKMDVPHITIKQ 1064  
 DB 1193 EDLKYVNNILRPQDITDEATSHFTKKIKESLE-CFVKANLNLJHTLAQ 1239

RESULT 14  
 T13801  
 phosphoinositide 3-kinase (EC 2.7.-.-) - fruit fly (Drosophila melanogaster)  
 C:Species: Drosophila melanogaster  
 C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 17-Nov-2000  
 C:Accession: T13801; T13351  
 R:MacDougall, L.K.; Domin, J.; Waterfield, M.D.  
 Curr. Biol. 5, 1404-1415, 1995  
 A:Title: A family of phosphoinositide 3-kinases in Drosophila identifies a new mediator  
 A:Reference number: Z17764; MUID:96362138; PMID:8749393  
 A:Accession: T13801  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1876 <MAC>  
 A:Cross-references: EMBL:X97892; NID:92113837; PIDN:CAA63485.1; PID:92113838  
 R:Moiz, L.M.; Chen, Y.W.; Hirano, M.; Williams, L.T.  
 J. Biol. Chem. 271, 13892-13899, 1996  
 A:Title: Cpk is a novel class of Drosophila ptdins 3-kinase containing a C2 domain.  
 A:Reference number: Z17659; MUID:96278830; PMID:8662856  
 A:Accession: T13351  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-295; 'P', 297-331, 'R', 333-576, 'T', 578-641, 'S', 643-1876 <MOU>  
 A:Cross-references: EMBL:U52192; NID:91272419; PID:91272420; PIDN:AAC47117.1  
 A:Gene: PI3K 68D; cpk  
 A:Cross-references: FlyBase:FBgn0015278  
 A:Map position: 3L  
 C:Keywords: phosphotransferase

Query Match 15.0%; Score 859; DB 2; Length 1876;  
 Best Local Similarity 31.2%; Pred. No. 4.3e-50;  
 Matches 230; Conservative 129; Mismatches 281; Indels 98; Gaps 27;

QY 378 CSN-----PRWN--EWLNIDYI-IPDLPPRAARCLSLCSYKRGAKAEH----- 419  
 DB 893 CSNDTSGLFPLNFSAMLTFDQHPICITLPPREARLTVL--YGRQASSEGPNDQNGE 949

Qy 420 -----CPLANGNINLEPYDTDTLVSGKALNLMVPYHGLEJDLINLTIGVTSNPNKE--TPCL 473  
 Db 950 RROVTELTGMCSTQLPDKFRWIMIGPYLLSLMPM--TDKMLGPAPARGCHPQDFCPVL 1007  
 Qy 474 ELEEDWSSVYKPFDMSVIEEHANWSVREAGFSYSHAGLSNRLARONELREN--DKEQL 531  
 Db 1008 SIEVPPYGRKIERFEHOBVPRAP-----HYDFASL-----DANLOEBELDPAEL 1052  
 Qy 532 RAICTRDPLSEITEOEKDFLMSHRHYCVTIPETLTKLLSY-KMNSRDEVQWYCLVDM 590  
 Db 1053 -----GYGATERREVEF--WEKELYQSYFNALPKYLHAHNSWDYAN-LIDIALHLSW 1103  
 Qy 591 PRPKEDAMELDONNYDDPMYRGAVRCLEKYLTDKLSQYLQYLVQVLYKYEOYLDNLIV 650  
 Db 1104 APSPLOSLBELLEPRYPDAKREKAVEMISK--MENDQLVDFLPQLOSLKHDTEGASMA 1162  
 Qy 651 RPLKALTLNORIGHFFW-----HLKSEMNK-----TVSQRFQ-----LLL 688  
 Db 1163 RFLSKCLSEPRFHHMYLWLSLPPDPHNSIGAMAVDQEDSDQVTVRYRNRKMTL 1222  
 Qy 689 ESYCRAGC-MYKHLNBOVEAMEKLINLTDLKOEKDETQVQMKFLVEQMRAPDMDA 747  
 Db 1223 RALMALIGCKMLQRFMYQHNMCKLTTIAESVKAESMRKSLAAGMDV--HODLLE- 1279  
 Qy 748 LQGLSLPNAHQNLRLBECRIMSSAKRPLMLNMPDIMSBLIFQNNELIFKNGDDL 807  
 Db 1280 -OPTCLPLGEBLEVTGVSVNCSYFNSNTLPLKINFPQDA-----ESLPAIFKCGDL 1332  
 Qy 808 ROMTLQIIRIMENINQNGCLDRLMYPYGLSTIGDCVGLIEVYRNSHTIMQICKGKL 867  
 Db 1333 QOQDLTIQLIRINKMLARLDRKMTFNCVPTGYKSGMELISEETLARKIQVEGGLT 1392  
 Qy 868 GALQFNHTHOMLKDKNKEI-YDAIDLFTSRSCAGYATFLLIGDRHNSIMYKDD 926  
 Db 1393 GS--FKORPLAEWNGKPNSELYQSAVRNFTLSACGYATVYLGICDRNDINIMKTS 1450  
 Qy 927 GOLPHIDFHFLLDKKKKFGYKREVRVPLTODELIVISKAQECTYTREREPOEMCYK 986  
 Db 1451 GHLPIDFPGKFLGDAQFNGFNRDRTPFVLSDMAVYINGDKPST--DHYVVDLCR 1507  
 Qy 987 AYLAIRHALLFINLFEMMLGSGMPELQSPDDIAYIKTLALDTEDEALEYFPKQMDA 1046  
 Db 1508 AFNIVRNADLLHTLHAMTACMPGVNS-NAVQYVRALLPSQSNDEAATFAKMIQSS 1566  
 Qy 1047 HHGGMTKMDMIFHTIKQ 1064  
 Db 1567 LK-SMTQFNPFLHNLAQ 1583

RESULT 15  
 T21982  
 hypothetical protein f39b1.1 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000  
 C/Accession: T21982; T22312  
 R/Lighting, J.  
 - submitted to the EMBL Data Library, February 1996  
 A/Reference number: Z19497  
 A/Accession: T21982  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-1607 <MIL>  
 A/Cross-references: EMBL:Z69660; PIDN:CAA93489.1; GSPDB:GN00028; CESP:F39B1.1  
 A/Experimental source: clone f39b1  
 R/Thomas, K.  
 submitted to the EMBL Data Library, March 1996  
 A/Reference number: Z19545  
 A/Accession: T22312  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-1607 <MIL>  
 A/Cross-references: EMBL:Z69903; PIDN:CAA93776.1; GSPDB:GN00028; CESP:F39B1.1  
 A/Experimental source: clone F46F2

C/Genetics:  
 A/Gene: CESP:F39B1.1  
 A/Map position: X  
 A/Introns: 15/2; 65/2; 134/1; 190/1; 261/3; 298/1; 374/2; 417/3; 472/2; 512/1; 661/3; 71  
 C/Superfamily: Hec2 phosphatidylinositol 3-kinase; protein kinase C C2 region homology

Query Match 13.24; Score 751; DB 2; Length 1607;  
 Best Local Similarity 22.84; Pred. No. 8.5e-43;  
 Matches 261; Conservative 213; Mismatches 429; Indels 240; Gaps 39;

Qy 35 ECLREATLITIKHLEFPAKRYPLHQLQDESSYTFVSTQEARREFPETRALCLRL 94  
 Db 300 ECVGAKLI-----QENIEFP-----SSSPCLIDCPNGIE-----EQVKLCRNL 340  
 Qy 95 FO-----PLKATIEPVGNREKIL-----NREIGALGVPCVEFDVVKDPEV 136  
 Db 341 IRKDMTPDFIAPLVDMVTASTAVKVVYKDSMKANKNGKAM--ICAIID-----EK 392  
 Qy 137 QDFERNILNVCKEAVDLRDLSNPSHR--AMVYVPPN--VESSPELPKHIN----- 183  
 Db 393 MDI-----ITQALSLFDESELPDKEGYGLKIGLQFLSSDLSGLNLTGHCLNGDD 446  
 Qy 184 -KLDKQIIVIVIVYSPN-----DKQYTLKINHDCVPEOV--IAAIR 226  
 Db 447 VKLDLG-----VFAPNSRIYEQTLESNMLKKSQVYKSTVVDKEDVENTLGHIAEWS 498  
 Qy 227 K-----KTRGMLSSSEQLKLVLEYGQYILKVGCC-----DEYF--LEKYPISQY 270  
 Db 499 QYELAFNDGSTLKLISSSQKVK-----QVIMLCKCLHGVPEKLYVEMQYTLASTT 550  
 Qy 271 K-----YIRSCIMLGRMNLMLAKESYSQLEPMDCTPMSYRR 310  
 Db 551 EDQLVHNRDPLRHSFLBYLCRCYTSRYNIPRQITIRPKYEVLSKJDFQI----- 604  
 Qy 311 ISTATPMMGSETSKSLAVYNSALRIKILCATYVNNIRIDIKIYATGTGIYHGSEPLCDN 370  
 Db 605 -----MLNSVHSIPEHMQ-----SQYSEFYMSLDLYHGTQVLDGF 639  
 Qy 371 VNTQGVPCSNPRNEMNLNVIY-----IPDLPRARLCLSTC-SYKGRKAKEHCPC- 421  
 Db 640 SNKVPKTIKDNHFFPRPLDLVAKFKRLNLCQYPRETRIVASISGVRNSAQAAENENPD 699  
 Qy 422 ---LAMGNINLPDYDTLVSGKALNLMVPYHGLEJDLINLTIGVTSNPNKETCLELEFD 478  
 Db 700 IWLGYCSVPLVDENLFMRGRLPLPLTLKK--QPLTKFPGYPRYIKQADRPILMSFK 757  
 Qy 479 WFSVVKFP---DMSVI--BEHANWSVREAGFSYSHAGLSNRLARDNLENDKEQLRA 533  
 Db 758 IWDTEIYFPNVVIDMOCIPQDFATLDIETQ-----EYLLE 792  
 Qy 534 ICTRDPLSEITEOEKDFLMSHRHYCVTIPETLTKLLSYKMNSRDEVQWYCLVDMPT 593  
 Db 793 LIENQDTSTLETDDQDLIMQKRLHLTNQRPALPLVSLSDWSFGFMRVYQILIEVAPL 852  
 Qy 594 KPEQAMELDONYPDDPMYRGFAVRCLEKYLTDKLSQYLQYLVQVLYKYEOYLDNLIVFL 653  
 Db 853 RPLIAMEFLPKRPDERIRAHAAQSLARGST-DPLVHTTIQPLBALRFEIYKESALADFI 911  
 Qy 654 LKRALTNORIGHFFWMLKSEMNKTVSQRFGLLESYCRACGMWYK-----HLNRQ 705  
 Db 912 LEISFVSLDFTFEIYMQLOQRVHCAVDD-----LPAIRCOMLQOQIMDEHENPNLKT 966  
 Qy 706 VEMEKULINLTDLKOEKDETQVQMKFLVEQMRAPDMDA--LQGLSL-PLNPAHQLG 762  
 Db 967 IKLQHEHLELDSIQDDEKSGSDSEIRHRLRTRIGLIDSKLQNKVLPICPAVDCT 1026  
 Qy 763 NLRLBECRIMSSAKRPLMLNMPDIMSBLIFQNNELIFKNGDDLRODMTLQIIRIMEN 822  
 Db 1027 GVARIECSVNSNAKL-----KIVFGKLNNVYSLIHRRDDMDQDAVVMGLMMDR 1079  
 Qy 823 IMQNGDLRLMLPYGCLSTIGDCVGLIEVYRNSHTIMQICKGKLKALQFNSTHTLQWLK 882  
 Db 1080 IMKNSGLDLRMLTFRIMPVGYRGMGEIYLCATLMEIQEBSGLRGVL--NDEILRKMLM 1137

QY 883 DKXGEL-YDAIDLFTSCAGYCVATFIIIGIDRANSNIWKGQLEFHDGFIIDHK 941  
Db 1138 KHNSDEFAYKEAQENFIRSCAGWCIVTVVLGIGDRHNDNILEFTXGHVFIHDFGKYMGDW 1197  
QY 942 KKKFGYREBVPFVLTODFLIVISKGAOECTKREPERFOEMCYKAYIAIROHANLFINL 1001  
Db 1198 QMAAGFRDRVPFVFTTEMFHINNRR--APTQYNQKFIDYCCKAFNHILRRNQTILTNL 1254  
QY 1002 FSNMIGSGMPELOSFDDIAYIRKTIALDKTEQBALLEYFMKQMDNAHHGGWTTKMDWIEHT 1061  
Db 1255 LRIMACSDIRGI-NMDSIAFVENNLMLDLSPTDATVOFTAMIONS-LGSAFVRLNFVAHT 1312  
QY 1062 IKQ 1064  
Db 1313 VAQ 1315

Search completed: November 6, 2003, 14:44:52  
Job time : 32 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 6, 2003, 14:42:46 ; Search time 35 Seconds

(without alignments)  
5245.714 Million cell updates/sec

Title: US-09-325-095-37

Perfect score: 5709  
Sequence: 1 MPPRPSGELMGJHMPRI.....GWTTKDWIHTIKQALNX 1069

Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA: \*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
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17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5657	99.1	1068	12	US-10-101-235A-8 Sequence 8, Appl1
2	1978.5	34.7	1044	12	US-10-337-192-2 Sequence 2, Appl1
3	1978.5	34.7	1044	12	US-10-027-591-2 Sequence 2, Appl1
4	1976.5	34.6	1044	15	US-10-162-160-1 Sequence 1, Appl1
5	1467	25.7	1110	12	US-10-101-235A-4 Sequence 4, Appl1
6	1465.5	25.7	1102	11	US-09-974-573-1 Sequence 1, Appl1
7	1322	23.2	1076	12	US-10-101-235A-6 Sequence 6, Appl1
8	1089	19.1	1167	9	US-09-205-658-48 Sequence 48, Appl1
9	1089	19.1	1167	9	US-09-844-353A-48 Sequence 48, Appl1
10	1089	19.1	1167	12	US-09-963-693-48 Sequence 48, Appl1
11	1014.5	17.8	1686	14	US-10-092-219-2 Sequence 2, Appl1
12	685	12.0	887	10	US-09-771-161A-192 Sequence 192, App
13	685	12.0	887	10	US-09-771-161A-193 Sequence 193, App
14	675.5	11.8	803	10	US-09-921-232-2 Sequence 2, Appl1
15	675.5	11.8	803	10	US-09-921-330-2 Sequence 2, Appl1

16	675.5	11.8	803	10	US-09-921-329-2	Sequence 2, Appl1
17	545.5	9.6	756	10	US-09-771-161A-101	Sequence 101, App
18	442	7.7	1900	10	US-09-801-368-390	Sequence 390, App
19	357	6.3	195	12	US-10-101-235A-9	Sequence 9, Appl1
20	357	6.3	204	12	US-10-101-235A-2	Sequence 2, Appl1
21	341.5	6.0	150	9	US-09-205-658-17	Sequence 17, Appl1
22	341.5	6.0	150	9	US-09-844-353A-17	Sequence 17, Appl1
23	341.5	6.0	150	12	US-09-963-693-17	Sequence 17, Appl1
24	314.5	5.5	508	10	US-09-771-161A-102	Sequence 102, App
25	304	5.3	816	12	US-10-205-219-3	Sequence 3, Appl1
26	283.5	5.0	817	12	US-09-976-165-28	Sequence 28, Appl1
27	283.5	5.0	817	12	US-10-342-276-28	Sequence 28, Appl1
28	283.5	5.0	829	10	US-09-976-165-31	Sequence 31, Appl1
29	283.5	5.0	829	12	US-10-342-276-31	Sequence 31, Appl1
30	278	4.9	113	9	US-09-205-658-18	Sequence 18, Appl1
31	278	4.9	113	9	US-09-844-353A-18	Sequence 18, Appl1
32	278	4.9	113	12	US-09-963-693-18	Sequence 18, Appl1
33	261.5	4.6	119	10	US-09-765-298A-14	Sequence 14, Appl1
34	202.5	3.5	2654	15	US-10-227-610-2	Sequence 2, Appl1
35	199.5	3.5	1140	11	US-09-950-634-4	Sequence 4, Appl1
36	196.5	3.4	2549	11	US-09-950-634-3	Sequence 3, Appl1
37	188.5	3.3	1710	12	US-10-032-585-7238	Sequence 7238, Ap
38	186	3.3	34	15	US-10-162-160-6	Sequence 6, Appl1
39	180.5	3.2	4128	9	US-10-205-194-1	Sequence 1, Appl1
40	165	2.9	106	9	US-09-205-658-19	Sequence 19, Appl1
41	165	2.9	106	9	US-09-844-353A-19	Sequence 19, Appl1
42	165	2.9	106	12	US-09-963-693-19	Sequence 19, Appl1
43	160.5	2.8	2644	12	US-10-300-453A-19	Sequence 39, Appl1
44	151	2.6	51	9	US-09-864-761-48478	Sequence 48478, A
45	145.5	2.5	3056	15	US-10-175-225-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1  
US-10-101-235A-8  
; Sequence 8, Application US/10101235A  
; Publication No. US20030182669A1  
; GENERAL INFORMATION:  
; APPLICANT: Rockman, Howard A.  
; APPLICANT: Naga Prasad, Sathyamangla V.  
; APPLICANT: Laporte, Stephanie A.  
; APPLICANT: Barak, Larry S.  
; APPLICANT: Caron, Marc G.  
; TITLE OF INVENTION: Phosphoinositide 3-Kinase Mediated Inhibition of GPCRS  
; FILE REFERENCE: 033072-064  
; CURRENT APPLICATION NUMBER: US/10/101,235A  
; CURRENT FILING DATE: 2002-03-19  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 1068  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-101-235A-8

Query Match 99.1%; Score 5657; DB 12; Length 1068;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1056; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY	1	MPPRPSGELMGJHMPRIIVLVECLIPNGMIVTLECLREATTITIGHELFKRKRYPLHQ	60
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QY	61	LLODESSYIFVSTQAEEREEFPDETRRLCDLRLFPFLKVIIEPVGNREKILNREIGRA	120
DB	61	LLODESSYIFVSTQAEEREEFPDETRRLCDLRLFPFLKVIIEPVGNREKILNREIGRA	120
QY	121	IGMPVEFPMVNDPEVODFRRLINLVNCKEAVDLRLDINSFHSRAMYYPVNVSSPELPGH	180
DB	121	IGMPVEFPMVNDPEVODFRRLINLVNCKEAVDLRLDINSFHSRAMYYPVNVSSPELPGH	180

181 IYKLDKGOIIVYIWIIVSPNNDKOKYTLKINHDCVEQVIAEAIKRTKTSMLLSROK 240  
181 IYKLDKGOIIVYIWIIVSPNNDKOKYTLKINHDCVEQVIAEAIKRTKTSMLLSROK 240  
241 LCYLEYQGXIIKVCQCDDEYFLEKYPISQYKTI RSCIMLRMPMLMAKESYLSQJLPM 300  
241 LCYLEYQGXIIKVCQCDDEYFLEKYPISQYKTI RSCIMLRMPMLMAKESYLSQJLPM 300  
241 LCYLEYQGXIIKVCQCDDEYFLEKYPISQYKTI RSCIMLRMPMLMAKESYLSQJLPM 300  
301 CFMPSSSRISRTATPYMNGESTSKSLMWINSAIRIKILCTAYVNAVNRIDIKIYRTGI 360  
301 CFMPSSSRISRTATPYMNGESTSKSLMWINSAIRIKILCTAYVNAVNRIDIKIYRTGI 360  
361 YHGEPLCDVNTQVPCSNFRNEMWLNVDIYIPDLPPAARLCISGVKRRKAKEHC 420  
361 YHGEPLCDVNTQVPCSNFRNEMWLNVDIYIPDLPPAARLCISGVKRRKAKEHC 420  
421 PLAMGNINLPDYTTTLVSGKALMLMPVPHGLIEDLNPIGVTSNPKETPCLELEDFMF 480  
421 PLAMGNINLPDYTTTLVSGKALMLMPVPHGLIEDLNPIGVTSNPKETPCLELEDFMF 480  
481 SSVKPPDMSVIEEHANMSVREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDP 540  
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541 SEITEOEKDFLMSHRHNCVTIPEILPKLLSVKMSRDEVAQWYCLVQWPPRIKPEQAME 600  
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601 LLDGNYPRPWRGFAVRCLERYITDDKLSOYLIOUVOLXYBOYLDNLVFLKKAALT 660  
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661 ORIGHFPMHLKSEHNKTVSQRFGILLESYCRACGMVTKHLNRQVEAMEKILNLTDLK 720  
661 ORIGHFPMHLKSEHNKTVSQRFGILLESYCRACGMVTKHLNRQVEAMEKILNLTDLK 720  
721 QEKDETOYKQKFLVEQNRPRDFMDALQGLSPINPAHOLGNLLESCRISSAKRPLM 780  
721 QEKDETOYKQKFLVEQNRPRDFMDALQGLSPINPAHOLGNLLESCRISSAKRPLM 780  
781 LNMENPDIIMSELLFONNEIIFKNGDLDROMLTLOIIRIMENIWMONOGDLRLMYGCL 840  
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841 IGDGGLLEVANSHTIMOIOCKGKGLAJOFSHTLHQLMDKNGKELIYDAIDLFTRS 900  
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901 CAGYCVATFIIIGIRHNSINWVWDOGLFHIIDFGHFLDHKKKKGKERYPVULTDF 960  
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961 LIVISGAOECTKTRFEFERFQEMCYAYALAIQHANLFTNLFSMMLGSMPELOSFDDA 1020  
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1021 YIRKTLALDKTBOALEYFMKQNDANHGAMTJMDMIFHTIKOHALN 1068  
1021 YIRKTLALDKTBOALEYFMKQNDANHGAMTJMDMIFHTIKOHALN 1068

PRIOR APPLICATION NUMBER: 60/238, 057  
PRIOR FILING DATE: 2000-10-25  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 1044  
TYPE: PRT  
ORGANISM: Human p10delta protein  
US-10-337-192-2  
Query Match 34.7%; Score 1978.5; DB 12; Length 1044;  
Best Local Similarity 39.9%; Pred. No. 1,3e-170;  
Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;  
16 MPP-----RIVGCLPNGMIVLVECLREATLTITIGHELPEKARXYPLHQ 60  
1 MPPGVDCPMEFWTKENQSVVDFLPTGYVLPVSRNANLSTIQQLMHRQYERLPH 60  
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61 MLSGPEAYVFTCINQTHAEQOELDEQRRLCDVQPLPYRLVARBGDRVKKLINSQISL 120  
121 IGMVCEFDVYKDEVDQFRNRLNVCKEAVDRLDINSPIRAMYYPVNVESSE- 176  
121 IKGILHEFDLCPDEVNDFRAKMCQCFEEAARQOLGWEAWLOQSPFLQLEPSAQTWGP 180  
177 ---LPHATNKLDKGOIIVYIWIIVSPNNDKOKYTLKINHDCVEQVIAEAIKRTKRS 232  
181 GTURLPFR-----ALLVNVKFGESSEFTTQVSTKQVPLALMACLRK- 224  
233 LLSSEQKLIVLEYQGYIILKVCQCDDEYFLEKYPISQYKTI RSCIMLRMPMLMAKES 292  
225 ---ATVRQPLVEPREDYTLQVNGRHELYLVGNVPLCQFOYICSLHGLPHLTMVSSS 281  
293 LYSQLPMDCFMPSYSRISTATPYMNGESTSKSLMWINSAIRIKILCTAYVNAVNRID 352  
282 ILAMRDSQNPAPQVQPRAKRPPIPAKKPSVSLMSLEQFRLLELQGSVANDER-M 339  
353 KIYRTGIIYHGEPLCDVNTQVRVP-CSNPRNEMWLNVDIYIPDLPPAARLCISGV- 409  
340 KLVVQAGLFHENEMLCTVSSSEVSCEPVRKORLEFDINICLPPMARICFPLVAVIE 399  
410 -----KGRKAKEHCPLAWGINLFPDYTTTLVSGKALMLMP-VPHGLEDLNPIGVT 462  
400 KAKARSTKSKSKADPRIMANLMLPDYKQOLTGEBCLYMPSPDEKELINPTGTV 459  
463 GSNPKERTP-----CLELEFDWISSVYKPEPMYSIEBHANMSVREAGFSYSHAGLSRL 517  
460 RSNPWTDSAAALLICLP---EVADHPVYYPALKEKIL- 494  
518 ARDNE---LRENDKEQLRAICTRDPISITQOEKDFLMSHRHNCVTI-IPETLPKLLSVK 573  
495 GRHSECVATVEEOQLLEILERRGSGELYHEBDLVKMLNHEVOENHPEALARILLVTK 554  
574 MNSREVAQWYCLVQWPPRIKPEQAMELIDCNVDPVWRGFAVRCLERYITDDKLSOYL 633  
555 WNKEDVAMQYLCSWPELVLSLDELDSFPCHGSAISLRK-LTDDELFQYLL 613  
634 QLVQVLKTEYOYLNLVFLKKAALTQRIHFFFWHLKSEHNKTVSQRFGILLESYCR 693  
614 QLVQVLKTESYLDCELTGFLDRALANRRIKGFLEWHLRSEHNVSVALRFGLLLEAOCR 673  
694 ACGMYLKLINROVEAMEKILNLTDLTKOEKDETOYKQKFLVEQNRPRDFMDALQGL 752  
674 GSTHMKVLMKQGEALSTKALNDVFKLSQ-KTPKPTKELMLCMKQOEAYLELSHQ 732  
753 SPLNPAHOLGNLLESCRISSAKRPLMNMENPDIIMSELLFONNEIIFKNGDLDROM 812  
733 SPLDSESTLAEVCVEQCTFMSKMPKPLMIMYNEBAGS---GSVGIFFKNGDLDROM 789  
813 TLQIIRIMENIWMONOGDLRLMYGCLSGDVGGLIEVVRNSHTIMOIOCKGKGLAJO 871  
790 TLQIIRIMENIWMONOGDLRLMYGCLSGDVGGLIEVVRNSHTIMOIOCKGKGLAJO 849

RESULT 2  
US-10-337-192-2  
Sequence 2, Application US/10337192  
Publication No. US20030195211A1  
GENERAL INFORMATION:  
APPLICANT: SADHU, Chanchal et al.  
TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA  
FILE REFERENCE: 27866/39033  
CURRENT APPLICATION NUMBER: US/10/337,192  
CURRENT FILING DATE: 2003-01-06  
PRIOR APPLICATION NUMBER: 60/199,655  
PRIOR FILING DATE: 2000-04-25



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Db 850 FNNKALLNMLKSKNPGALDBAIEEFTLSCAGCVATFVLGIDGRHSDNIMIRSGOLF 909
Qy 932 IDEGHFLDHKKKKGKGRERVPVLTODFLIVISKGAOECTKTRFEPFQEMCYKALAI 991
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Db 910 IDFGHFLGNFKTKGIRNRPVFLITDFVAVIOOG--KTNNSEKFFERFRGVCERAYTIL 967
Qy 992 ROHANLFINFSMMLGSGMPELOSFDIAVIRKTLALDKTEOBALXEYFMKQMDAHNGW 1051
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Qy 1052 TTKMDWIFHTIKQ 1064
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1028 KTKVNMILAHNVSK 1040

RESULT 3
US-10-027-591-2
; Sequence 2, Application US/10027591
; Publication No. US20020161014A1
; GENERAL INFORMATION:
; APPLICANT: SABHU, Chanchal et al.
; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
; FILE REFERENCE: 27866/36170C
; CURRENT APPLICATION NUMBER: US/10/027,591
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/841,341
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/199,655
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/238,057
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent version 3.0
; SEQ ID NO 2
; LENGTH: 1044
; TYPE: PRT
; ORGANISM: Human p110delta protein
US-10-027-591-2

Query Match 34.7%; Score 1978.5; DB 14; Length 1044;
Best Local Similarity 39.9%; Pred. No. 1.3e-170;
Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

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Qy 61 LLDDESSYIFVSVTQGAEREPFDETRRLCDLRFQFLVYIEPVGNREKILNREIGFA 120
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 MLSGPEAVYTCINQTAEOBLEDEQRLCDVQFPLVLRLVAREGGRVKKLINSQISL 120
Qy 121 IGMVCEFDVWKCPDEVDFRRNIIINVKEAVDLRLDLSPSHRAMYVVPVNESSPE--- 176
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 IKGKIHFDLSCPDEVVDFRAKMGQFCBEBAARQOUGMEWMLOYSFPLGLEBAQWGP 180
Qy 177 ----LPRKIYTKLDKGOIIVIVYIVSPNNDKQKTYLKHNDVCPEVOIVAIKKTTRSM 232
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 GTLRLPNR-----ALIVNVAFEGSEBSFTQVSTKDPVPLALMCAKREK--- 224
Qy 233 LLSSEQLKLCVLEVGKYLKVGCGDEYFLKRYLSQYKIRSCIMLGRPNMLMAKES 292
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 ----ATVTRQPLVEQPEYITLQVNGRHYLYGNVPLCOFYICSLHSGLTPHLTMVSSS 281
Qy 293 LYSQLPMDCEFTMPSYRRISTATPYMNGESTKSLWYINSALRIKITLCATYVNVNIRID 352
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 282 ILAWRDQSNPAPQVQKPAKAPPIPAKKPSVSLWLEQFRELTLQSGKVNADER--M 339
Qy 353 KIYVTRGIYHGGEPLCNVANTQRP--CSNPRANEMWLVYDIPLPRAARLCSTICSV-- 409
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 340 KLVVQAGLFFGNEMLCITVISSEVSCSEPVWKORLEFDINITCDLPRMARLCFALYAVIE 399
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Qy 410 -----KGRKAKBEECPILAMGNINLFDYTDTLVSGMALNLMP--VPHGLEDLNPIGV 462
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Db 400 KAKKARSTKXKSKKADCPIMANMLFDYDQOLKTGRCLYMPSPVDEKELLNPIGV 459
Qy 463 GSNPNKETP-----CLELEFDWSSVVKFPDMSVIEEHNAMSVSREAGFSYSHAGSNRL 517
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 460 RSNPNSTSAALLILCP---EVAHPYYPALKEILE-----L 494
Qy 518 ARDNE---LAEENKEDORAICTRDPLSEITOEKDPILMSHRHYCVT--IPEILPKYLLSYK 573
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 495 GRHSECVHVEEQLQRETLERRSGGELYEHKEDLVWKLRHVEQEHFPALRLLVTK 554
Qy 574 MNSRDEVAQMYCIVKDPPIKPEQAMELDCNYPDPVNRFAVRCLEKYLTDDKLSQYL 633
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 555 MNKHEDVAQVLYLLCSWPELPVLSALELDFSPDCHVGSAFKSLRK--LTDELFPYLL 613
Qy 634 QLVQVLKYEQYLDNLVFLKKAALTNQIRGHEFFMHLKSEMHNTKVSQRFGLLESYCR 693
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 614 QLVQVLKYESYLDCELTKFLDLRALNRKIGHFLFWHLRSEMHVPSVALRFGILLIAYCR 673
Qy 694 ACGMYLKHLYRQYEAEMKILNLDILKQEKDETQYKQMFVBO--MRREDPMDALOGFL 752
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 674 GSTHMKVLMKQGBALSKLALNDFVLSQ--KTPKQYTELMLHLCRQBAYLEALSHLQ 732
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| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 733 SPLDPSLTLAEVCVEQCTFMDSKKPLMIYNSBEAGS---GSVGIIFKNGDDLRODML 789
Qy 813 TLQIRIMENIMQNGDLMLRBYGLSIGDCVGLIEVVRNSHITMQIC--KGLKCALQ 871
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 790 TLQMIQLMDVLMKQGBALSKLALNDFVLSQ--KTPKQYTELMLHLCRQBAYLEALSHLQ 849
Qy 872 FNSHTLHOMLKDNKKGSIYDAIDLFTRSCAGCVATFIIGIDGRHNSNIWVXDGOLF 931
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 850 FNNKALLNMLKSKNPGALDBAIEEFTLSCAGCVATFVLGIDGRHSDNIMIRSGOLF 909
Qy 932 IDEGHFLDHKKKKGKGRERVPVLTODFLIVISKGAOECTKTRFEPFQEMCYKALAI 991
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 910 IDFGHFLGNFKTKGIRNRPVFLITDFVAVIOOG--KTNNSEKFFERFRGVCERAYTIL 967
Qy 992 ROHANLFINFSMMLGSGMPELOSFDIAVIRKTLALDKTEOBALXEYFMKQMDAHNGW 1051
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 968 RRHGLLHLFALMRAAGLPBLSCKDIQYLKDSLALGKTEBALKHFVKFNEALRESW 1027
Qy 1052 TTKMDWIFHTIKQ 1064
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1028 KTKVNMILAHNVSK 1040

RESULT 4
US-10-162-160-1
; Sequence 1, Application US/10162160
; Publication No. US20030099627A1
; GENERAL INFORMATION:
; APPLICANT: Van Hasebroeck, Bart
; TITLE OF INVENTION: No. US20030099627A1el Lipid Kinase
; FILE REFERENCE: 2332-1-002
; CURRENT APPLICATION NUMBER: US/10/162,160
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US/09/194,640
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: 9611460.8
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1044
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-160-1
```

Query Match 34.6%; Score 1976.5; DB 15; Length 1044;  
 Best Local Similarity 39.9%; Pred. No. 2e-170;  
 Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

16 MPP-----RIVECLPNGMIVTLECEATLITIKHELEKARKYPLHQ 60  
 1 MPPGVDCPMEWTEKEENOSVVDPLPGVYLNFPVSRNNALSTIKOLMHRBAQEYELFH 60

61 LLODESSYIFVSYTQABEREFEFDETRRLCDLRLFOPLKIEFVGNREKILNREIGFA 120  
 61 MLSPEAVYFTICINQTAEQLEDEQRRLCDVQFPLRLVAREGCRVKTLINSQISLL 120

121 IGMVCFDPMKDEVDQFRNINLVCKEAVDLDLNSPHRAMVYVPNVESPE---- 176  
 121 IKGKIHFEFDSLCDPEVNDFAKMOQCFEAAARQOLGWEMLQYSPFLQLEPSAQWGP 180

177 ----LPHNIVKLDKGOIIVIVIVIVSPNNKOKYTLKINHDCVPEQVIAIRKTRSM 232  
 181 GTLRPNR-----ALLVNVKREGSESEFTPOVSTKQVPLALMACALKK----- 224

223 LLSSEQLKLVLEYQGYILKYCGCDEYFLEKYPLOSQYKIRSCIMLGRPNMLMAKES 292  
 225 ---ATVRQPLVEQPEDYTLQVNGRHEYLGSYPLQFOYICSLHSGLTPLHLMVHSSS 281

293 LYSQLPMDCTFMPYSRIRISTATPYMNGESTKSLMVNSALRIKILCATVNNINRID 352  
 282 ILAMRDEQSNAPQVQKPRAPPRPIPAKPPSSVSLMLEOPFRLELQGSKYNDER--M 339

353 KIYVRTGIYHGGEPICDNVNTQVRP--GSPRNEMELNDIYIPDLPRARCLISCSY-- 409  
 340 KLIVQAGLFGHNMELCTVSSSESVSCSEPVWKORLEDDINICULPRARCLFALYANIE 399

410 -----KGRKAKEHECPKAMGNINLPDYITLVSGKALMLP--VPHGLEDLNPIGVT 462  
 400 KAKKARSTKKSKKADCPILAMNMLPDKQOLKTGERCLVWMPVPDEKCELLNPTGTV 459

463 GSNPKETP-----CLELEPDMFSSVYKFPDMSVLEENANMSVSEADGFSYSHAGLSRL 517  
 460 RSNPTDGAALLCLP---EVAHPVYVYPALKEKLE-----L 494

518 ARDNE---LRENDKEQLRAICTRDPLSEITEOEKDFLMSHRHYCVT--IPEILPKLLLSVK 573  
 495 GRHSCHAVTEBEQQLRIBLERROSSGELYEHKRLWKLNHEVQENHPEALARLLLVTK 554

574 WNSRDEVAQMYCLVXWMPRIKPEQAMBLDCNYPDMVRGFAVRCLKEYITDDKLSQYLI 633  
 555 WNKEDVAQMYCLVXWMPRIKPEQAMBLDCNYPDMVRGFAVRCLKEYITDDKLSQYLI 613

634 QLVQVLKTEBOYLDNLVRLKALTNQRIGFHFMHLKSEMNKTTVSGRFGELLLESYCR 693  
 614 QLVQVLKTESYLDCELTFELDRALANRKIGHFLWHLRSEMNVSVALRFGELLEAYCR 673

64 ACGWVLKLNROVEAMKELINTDLIKQEKDETOVKQKFLVEQ--MRPRDMDALOGFL 752  
 674 GRTHMKVLMKQGBALSKULANDVYKSSQ--KTRKPOKELMLHLCMQEALVLELSHQ 732

753 SPLNPAHQNLRLBECRIMSSAKRPLMLNMPDIMESELLFQNNELLIFKNGDDLRQDML 812  
 733 SPLDSTLLAEVCOCFTMDSKMPLWIMYNSNEAGSG--GSAVGIIFKNGDDLRQDML 789

813 TLQIIRIMENIWNQGLDRLMLPYGLSLIGDCVGLIEVVRNHTTMOJOC--KGGKGLAQ 871  
 790 TLQIOLMDVLMKQGBALSKULANDVYKSSQ--KTRKPOKELMLHLCMQEALVLELSHQ 849

872 FNSHTLHQLKDKNGEYIDAAIIDLFTSACAGCVATFLIGIDRNSNINWYDQOLPH 931  
 850 FKDALNLNLSKNPEALDRAIEFTLSCAGCAVATYVIGIDRNSDMMIMRESQOLH 909

932 IDFGHFLDKKKKFGYKREVPFVLTPQPLIVISKAQOECTKREFRPOEMCYAKYAI 991  
 910 IDFGHFLDKKKKFGYKREVPFVLTPQPLIVISKAQOECTKREFRPOEMCYAKYAI 967

992 ROHANLFINLFSNMLGSGMPELOSFDIAYIRKTLALDKTQEALEYFKQKNDANHGCM 1051

DB 968 RRRGLFLHFLALMRAAGIPELSCSKDIOYLKDSIALGKTEEBALGHFVKFNEALRESW 1027  
 QY 1052 TTKMDWIFHTIKQ 1064  
 DB 1028 KTKVNMILAHNVSK 1040

RESULT 5  
 US-101-235A-4  
 ; Sequence 4, Application US/10101235A  
 ; Publication No. US20030182669A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rockman, Howard A.  
 ; APPLICANT: Naga Praasad, Sathyamangla V.  
 ; APPLICANT: Laporte, Stephanie A.  
 ; APPLICANT: Barak, Larry S.  
 ; APPLICANT: Caron, Marc G.  
 ; TITLE OF INVENTION: Phosphonosticide 3-kinase mediated inhibition of GPCRs  
 ; FILE REFERENCE: 033072-064  
 ; CURRENT APPLICATION NUMBER: US/10/101,235A  
 ; CURRENT FILING DATE: 2002-03-19  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 1110  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-101-235A-4

Query Match 25.7%; Score 1467; DB 12; Length 1110;  
 Best Local Similarity 35.3%; Pred. No. 5.7e-124;  
 Matches 358; Conservative 179; Mismatches 352; Indels 126; Gaps 33;

107 NREKILNREIGFALGMPVCEPDVNDQEVODFRNINLVCKEAVDLDLNSPHRAMVY 166  
 143 SEESQAFORQLTALIGYDVTVDSNVHDELEFTRGVLTPRMAEVSARD-----PKLYA 196

167 YEPVSESSPELPHKIVNKLKGOIIVIVIVIVSPNNKOKYTLKINHDCVPEQVIAIR 226  
 197 MHPVWTSKP--LPEVLMKLIANNCFIYI-----HRSSTGTLIVSDPDTPGAILQSFPT 249

227 K--KTRSMILSSSEQLKLVLEYQGYILKYCGCDEYFLEKYPLOSQYKIRSCIMLGRPN 284  
 250 KMAKKKSLMDIPES-----QSEDDFVLAVCGREYLVGEFPIKQPMVRRCLKNGEIH 303

285 LML-----MAKESLYQLEP--DCFTMPYSRIRISTATPYMNGE---ISTKSLWYNS 332  
 304 VVLDTPPDPALEVRKEWEPVLVDCTGVTGHEQLT-----IHGKHESVFTVSLMCDR 358

333 ALRKILCATVNNINRID-----KIYVRTGIYHGGEPICDNVNTQVRPSCNPR 382  
 359 KFRVY-----IRGIDIPVLPNTDLTVFVLANIIGHQOVLCOARRISPKFTEVL 408

383 WNMENIYDIYIPDLPRARCLISCSYK--GKKAKEHCPLAMGNINLPDYITDLV-- 437  
 409 WNVHLEFISIKIDLPKGLNLMLQIYCGKAPALSKASAESSESSSKGVRLVYVNLILI 468

438 -----SGKALNIMVPVHGLE--LINPIGVT--GSPNKKE--TPCLELEFDMSSVYKF 486  
 469 DHRFLRGEYVULHWMQISGKGEQGSFNAKLTSAIATPDKENSISILNDNCHPIAL 528

487 PDMSTIEBHAWMSVREAGFSYHAGLSNRLARONEIRENDKEQLRAICTRDPLSEITEQ 546  
 529 PKHQPTPPEGRV-----RAMPRQLR-----KQLEALITADPLNPLTAE 569

547 EKDFLMSHRHYCVTIPILPKLLSVKNSSDEVAQMYCL-----VKDMPRIKPEQAMEL 601  
 570 DEELIMHRRYESIKHPKAYVPLFSSVKNQGOEYIAKTYQLARREVMQASLDVGLTMQL 629

602 LDCNVPDMVRGFAVRCLKEYITDDKLSQYLIQLVQVLKTEBOYLDNLVRLKALTNQ 661  
 630 LDCNFSDENVRALAVQKLES--LEDDDVHLHYLLQVQAVKFEYPHDSALARFLKRLGRLNK 688

QY 662 RIGHFFMHLKSEM-HNKTIVSQRFGLLLESYCRACGMYLKH-LNROYEAMEKLTINTL-DI 718  
 Db 689 RIGHFFLFWPLRSELSAQSRHYQGRFAVILEAVLRGCGTAMLHDFQQGVIVEMLOKVTLDI 748  
 QY 719 --LKQEKXDETOKV--QMKFLVEQMRPDPMDALQGLSPINPAHQUNLRECRINSS 774  
 Db 749 KSLSAEKYDVSSQVLSQKQKLENIQNSQLPES--FRVPYDPGLKAGALAEKCKYMAS 805  
 QY 775 AKRPLMNMW--NPDIMSELLFQNN--IFKNGDDLRQDMLTLQIIRIMENIMONGL 829  
 Db 806 KKKPLMEFKCADPTALS-----NETIGILFKHGDDLRQDMLTLQIIRIMESIMETESL 859  
 QY 830 DLRLMPLGCLSGIDGCVGLIEVVRNSHTIMQI-QCKGGLKGAQFNSHTLHOMLADKN-KG 887  
 Db 860 DLCLPLPGCISTGDKIGMIEIVDATTAKIQOSTVGNTGA--FKDEVLANMLKEKSPTE 917  
 QY 888 EIIYDAIDLFTRSAGAGCVATFIIIGIDRNSNIMVKGQOLPHIDRGHFLDHKKKKFY 947  
 Db 918 EKFOAAVERFYSCAGYCVATFVLIGIDRNDNIMITETGNLFHIDRGHILGNYSFGLI 977  
 QY 948 KREVRPVLNODFLIVISKAQECTKREPERQEMCYKAYLATIROMANLFINLFSMWLG 1007  
 Db 978 NKERVPVLPDPLFVMTGSKKTSF--HFQKPDICVKAYLATIASHHTNLILILFSMWLM 1035  
 QY 1008 SGMBELQSPDIAIYIRKTLALDKTEOBALIEYFMKQMDAHNGWTTKMDWIFHTI 1062  
 Db 1036 TGMPLQSLSKEDIEYIRDALTYGKNEBDAKKYFLDOIEVCRDKGTVQEPNMFHLV 1090

RESULT 6  
 US-09-974-573-1  
 ; Sequence 1, Application US/09974573  
 ; Publication No. US20030022344A1

; GENERAL INFORMATION:  
 ; APPLICANT: Williams, Roger  
 ; APPLICANT: Ried, Christian  
 ; APPLICANT: Walker, Edward H  
 ; APPLICANT: Stephens, Len  
 ; TITLE OF INVENTION: PHOSPHOINOSITIDE 3-KINASES  
 ; FILE REFERENCE: ONYX1048-US  
 ; CURRENT APPLICATION NUMBER: US/09/974,573  
 ; CURRENT FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: US 60/242,801  
 ; PRIOR FILING DATE: 2000-10-23  
 ; NUMBER OF SEQ ID NOS: 1  
 ; SOFTWARE: Patent version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1102  
 ; TYPE: PR1  
 ; ORGANISM: Porcine PI3K  
 US-09-974-573-1

Query Match 25.7%; Score 1465.5; DB 11; Length 1102;  
 Best Local Similarity 33.5%; Pred. No. 7.7e-14;  
 Matches 382; Conservative 204; Mismatches 405; Indels 149; Gaps 39;

QY 1 MPPRPSGELMGHTLMPPRIIVECLTNGMIVT-----LECLREALTITIKHELEKKA 53  
 Db 23 MKRPSTASLSSMELIP---IEFVLPTSORNTKTPETALHLVAGHGVQEMKQAVLRA 78  
 QY 54 RKYPL-----HOLLQDESSYIFVSVTOEAEREFEFDETRRLCDLRFQPF-----LKVI 102  
 Db 79 LETSVSADFHRRLGPDHFLLLYQKKGWYELDYKYQVAVOTLDCRLRYKVLHRSQGHV 138  
 QY 103 EPGVNGREKI-LNEIGFALGMPCFEDMVKDEPVQDFRNILNVCKEAYDLRLNSPHS 161  
 Db 139 QRHAPSEETLAFQRLNALIGYDVTVDSNVHDELEFRRLRLVPRMAEVAAGR-----192  
 QY 162 RAMVVPVNPVNESSPELRKHINUKLDKQIIVIVIVISPNNDKRYTLKLNHDCVPEQVI 221  
 Db 193 PKLYAMHPWYTSKP-LPEYLLKTKITNNCVFIVL-----HRSTTSQITKVSADDTPTIL 245

QY 222 AEAIRK--KTRSMLLSEQULCVLEYQGRYILKVCGCDEYFLEKPLSOYKIRSGIML 279  
 Db 246 QSFPTKAKKXKSLMIDIES-----QNERDFVLRYCGRDEYLVGETPIKPNQWVRQCLKN 299  
 QY 280 GRMPLML-----MAKESLYSQLP--DCFTMPSYRRJSTATPYMNGE---TSTKSL 327  
 Db 300 GEEIHLVLDTPPPALDEVRKEEWPVLDCTGVYGHQULT---IHKDHESVFVSL 354  
 QY 328 WVINSAIRIKILCATYNNVNRID-----KIVYTGTYHGGEPICDNNTQVRP 377  
 Db 355 WDCDKRRVK-----IRGIDIPVLPRTADLVFVEANIOYGQOVLQORTSKRP 404  
 QY 378 CSNPRNEMVNYDIYIPDLPPARLCLSI-C-----SVYGRKA-----KEEKPLAWG 425  
 Db 405 TEVLANVWVLEFSKIDLPKGLNLNQICGAPALSGTSAEMSPESGKQQLLYV 464  
 QY 426 NINLFYDTDLVSGKALNMPVPHGED--LNPICVT-GSNPNKE-TPLCLEFPMFS 481  
 Db 465 NLILIDRFLRGEYVLHNMOLSGKGDGSPFADKLTATNPDKENSMISILDNVC 524  
 QY 482 SVYKFPMSVIEBHANSVSRGAFSYSHAGLSNRRLARDNELRENDKEQRAICTRPLS 541  
 Db 525 HPILPGRHRTPDDEGRV-----RAEMPQLR---KOLEAITADPLN 565  
 QY 542 EITEOKDFLMSHRHYCVTIPEILLPKLLSVKNNSREVAQMYCL-----VKDMPPIKPE 596  
 Db 566 PLTAEDEKELMHFRYESLKDPRKAYPKLFSSVKNQOQRIVAKTQYLLAKREWDQSDALDV 625  
 QY 597 QAMELDCNYPDMWRGFAVRCLEKYITDCKLSQYLIQIVQVLYKYEOLYLDNLVRLKK 656  
 Db 626 LTMQLDLCNFSDEVRAIAVOKLES--LEDDVLYHYTLQIVQAVKFEFHYHSALARFLLKR 684  
 QY 657 ALTMORIGHFFPMHLKSEM-HNKTIVSORFGLLESYCRACGMYLKH-LNROYEAMEKLTIN 714  
 Db 685 GLRWKRIGHFLFWPLRSELSAQSRHYQGRFAVILEAVLRGCGTAMLHDFQQGVIVEMLOK 744  
 QY 715 LT-DI--LKQEKXDETOKV--QMKFLVEQMRPDPMDALQGLSPINPAHQUNLRECR 769  
 Db 745 VTIDIKSLSAEKYDVSSQVLSQKQKLENIQ--LNLPSFVRYPYGLKAGALVIEKC 801  
 QY 770 RINSSAKRPLMNMW--NPDIMSELLFQNN--IFKNGDDLRQDMLTLQIIRIMENIW 824  
 Db 802 KWMAKKKPLMEFKCADPTALS-----NETIGILFKHGDDLRQDMLTLQIIRIMESIW 855  
 QY 825 QNGCLDRMLPYGLSGIDGCVGLIEVVRNSHTIMQI-QCKGGLKGAQFNSHTLHOMLXD 883  
 Db 856 ETSBLDCLPLPGCISTGDKIGMIEIVDATTAKIQOSTVGNTGA--FKDEVLSHWLKE 913  
 QY 884 KNK-GEIYDAIDLFTRSAGAGCVATFIIIGIDRNSNIMVKGQOLPHIDRGHFLDHKK 942  
 Db 914 KCPLEKFOAAVERFYSCAGYCVATFVLIGIDRNDNIMISITGNLFHIDRGHILGNYK 973  
 QY 943 KKGYKREVRPVLNODFLIVISKAQECTKREPERQEMCYKAYLATIROMANLFINL 1002  
 Db 974 SFLGINERVPVLPDPLFVMTGSKK--TSLHFQFQOVQVAYLATIASHHTNLILIL 1031  
 QY 1003 SMMLGSMPLQSPDIAIYIRKTLALDKTEOBALIEYFMKQMDAHNGWTTKMDWIFHTI 1062  
 Db 1032 SMMLMTGMPLQSKEDIEYIRDALTYGKNEBDAKKYFLDOIEVCRDKGTVQEPNMFHLV 1091

RESULT 7  
 US-10-101-235A-6  
 ; Sequence 6, Application US/10101235A  
 ; Publication No. US20030182669A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rockman, Howard A.  
 ; APPLICANT: Naga Prasad, Sachyamangia V.  
 ; APPLICANT: Laporte, Stephanie A.  
 ; APPLICANT: Barak, Lary G.  
 ; APPLICANT: Caron, Marc G.  
 ; TITLE OF INVENTION: Phosphoinositide 3-kinase mediated inhibition of GPCRs  
 ; FILE REFERENCE: 033072-064

CURRENT APPLICATION NUMBER: US/10/101,235A  
CURRENT FILING DATE: 2002-03-19  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 1076  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-101-235A-6

Query Match 23.2%; Score 1322; DB 12; Length 1076;  
Best Local Similarity 33.4%; Pred. No. 8,7e-11;  
Matches 339; Conservative 175; Mismatches 340; Indels 162; Gaps 35;

107 NREKILNREIGFALGMPVCEPDWKCDEVDPRNIIINCKEAVDADLMSPHRAMYV 166  
143 SEESQAFGRQVLTALGYDVTDSNHDELEFTRGGLTPMAEYASD-----PKLYA 196  
167 YPPNVSSPELPKHIYNKLDKQQLIVVWIVSPNNQKQYTLKINHCVPEQVLAER 226  
197 MHPWTSKP-LPEYIMKRIANNCFIV-----HRSITSQTIKVSPPDTGALIQSF 249  
227 K-KTRSMULSSQIKLCVLEYQKYLKVCGCDEYELKYPPLSOYKITSICMLGRMN 284  
250 KMAKKKSLMDIPES-----QSEDFVLRCGRDEYLVGETPIKMFQWRHCLKKEEIH 303  
285 LML-----MAKESIYQLPM--DCFTMPSYRRISTATPYMNGE-----TSTKSLMVIS 332  
304 VLDTPPPALDEVRKEEMPLVDCTGYGHEQTL-----IHGDHESVFVLSIMDCR 358  
333 ALRIKILCATYVNVNIRID-----KIYVTGIYHGGEPLCDNVNTQVPCSNR 382  
359 KFRVX-----IRGIDIPVLPRNDLVFVNAVNIHQGOVLQCRRTSPKPTTEVL 408  
383 WNEWINDIYIPDLPRARLCLSTICSVK---GRKAKEBHCPLAMNINLPDYDTLV- 437  
409 WNVWLEFSIKIKDLPKGLALNLQIYCGKAPALSSKASSESSKGVRLIYYVNLII 468  
438 -----SGKALNIMPRPHGED--LNPICVT--GSMNKE--TFCLELEFDMFSYVKF 486  
469 DHRFLRGEYVLAHMQISGKEGDSFNADKLTISATNPDKENSISILDNVCHPAL 528  
487 PDMSVIEEHAMSVSREAGFSYSHAGLSNRLARDLEBNDEQRAICTRDPSEITEQ 546  
529 PKHQTPREGEDRV-----RAEMPNQLR-----KQLEALINDPLNPLAE 569  
547 EKDFLMSHRHYCVTIPETLPKLLSVKNSRDEVAQMYCL-----VKDWPIKEQAMEL 601  
570 DKELMHFRYESLKHPRKAYPKLFSYKVGQOEIVAKTYQLARREVMDQSALDVGLTNQL 629  
602 LDCNVPDMVWGAFAARCLEKYITDDKLSQYLILQVQVLYKBOYLDNLVRFLLKALTNQ 661  
630 LDCNVDENVRALIAVKLES--LEDDVLAHYLLQVQAKFEFYHDSALARFLKGLKNK 688  
662 RIGHEFFMHLKSEM-HNKTVSQRFGLLESYCRACGMVLRH-LNRQVAMEKLINLT-DI 718  
689 RIGHFLFPLASSELINQSHHYQORFAVILEAYIRGGTAMLDHFTQOVVIENTLOKVTLDI 748  
719 --LKOEKDETOKV--QMKFLVEQMRPDPMDALOGPLSPNLPAHOLGNLREECRISS 774  
749 KLSAEKYDVSSQVISOQKLENLQNSQLPES--FVVPYDPGLKAGALAIERCKVNAS 805  
775 AKRPLMLWE--NPINSELLFQNN-----IFKNGDDIROMULTIOIRIMENIQNG 829  
806 KKKPLMLPFKADPALSS-----NETIGILFRHDDIDRQDMLLIQILRIMESIWETSL 859  
830 DLRLMPLVYCLSGDCEVGLIEVVRNSHTIMQI-QCKGKLGALQFNSHTLHQMLKDN-KG 887  
860 DLCLLPYCIGISGDKIGMIEIVKATIAKTAKIOQSTVNGTGA--FDEVLVNHLKSKSTPE 917  
888 EYDAIDLPTRSCAGYCVATPILIGIRHNSNINVKDGOQLFHLDFGHLDHKKKKFGY 947  
918 EKFGAAVERFVYSCAGYCVATFVLGIGD----- 945

RESULT 8  
US-09-205-658-48  
Sequence 48, Application US/09205658  
Patent No. US20010029617A1  
GENERAL INFORMATION:  
APPLICANT: Ruvkun, Gary  
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
FILE REFERENCE: 00786/351004  
CURRENT APPLICATION NUMBER: US/09/205,658  
CURRENT FILING DATE: 1998-12-03  
EARLIER APPLICATION NUMBER: 08/857,076  
EARLIER FILING DATE: 1997-05-15  
EARLIER APPLICATION NUMBER: 08/888,534  
EARLIER FILING DATE: 1997-07-07  
EARLIER APPLICATION NUMBER: US98/10080  
EARLIER FILING DATE: 1998-05-15  
NUMBER OF SEQ ID NOS: 328  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 48  
LENGTH: 1167  
TYPE: PRT  
ORGANISM: Caenorhabditis elegans  
US-09-205-658-48

Query Match 19.1%; Score 1089; DB 9; Length 1167;  
Best Local Similarity 27.2%; Pred. No. 1,7e-89;  
Matches 311; Conservative 219; Mismatches 431; Indels 182; Gaps 39;

39 EATITTKHBLFK--EARKYPLHOLLDESSYIFVSTQEAEREFEFDETRRLCDLRLPQ 96  
91 EIKLSDPKHQLFELIAMKMGTVSVKPD--YVFRQLNNGEIEIVINDQPLSKELHG 148  
97 --PFLKVIPEVNGNEEKLIRBEIGFALGMPVCEPDWKCDEVDPRNIIINVCKEAVDLR 154  
149 TPEWLFYQPDGINRDKELMSDISHCIGYSLDKLEESLDELRFRASLWARTKTLTR 208  
155 DLNSPHSRAMVYVPPN--VSSPELPKHIYNKLDKQOI-IVIWIIVSPNNQKQYTLKI 211  
209 GL--EGTSHAFAFEEQYLCVGSCEPKDLESKYAAKLSQMFV-----RKRAEI 256  
212 NHDCVPEQVLAER---KTRSMULSS---EQKLKCVLEYQK---YILKVCGCDEYF 261  
257 NGVC--EKMMKIQIEFNPNEPSPKSLHTFLYEMKKLDDVYDTDDPADEGWELQAGRTTFV 314  
262 LE-KYPLSQYKIRSCIMLGMPLMLMAK-----ESLVS-----QLPMDC 301  
315 TNPVKLITSYDGVSELESTRCPGFVVRROSLVUKDYCRPKPLYEPIYRAHERKMLDV 374  
302 FTM-----PSYSRRISTATPYMNGESTK--SLWVINSALRIKILCATYVNVNIRID- 352  
375 LSVSISDTPKOSKSDWVMVDFRFASLKGSLMDLDANLIR-----PVNISGFDP 427  
353 ---KIYVRT--GIYHGGEPLCDNVNTQVPCSNRPN--EWLNDIYIPDLPRARLCLSI 406  
428 ADVDMYVRIEBSYVUGTLTJLASK-STTKVNAQFAKMKKEWYTFDLVYKMDWPPSA--VLSI 484  
407 CSVGRGAKAEHHPFLAMGNINLPDYDTLVSGMALNLW-PVPHGEDLNPICGV-TGS 464  
485 RVLYGKVKLSEBEFEVGMVNNSLTDMRDELROGQFLHLWABETPANSRIGENGARIGT 544  
465 NPNKETPCLLEPDMFWSVVFPMDS-----VIEEHAMSVSREAGFSYSHAGLSNRLARD 520

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Db      545 N-----AAVTIESSYSGVRMPGQGYTYLVKHSWTET-----LINIGDD 587
Qy      521 NELRENDKEQLRAICTRDPLSE-----TTEQKDFLWGHRYCVTIPILP 566
Db      588 YE-----SCIRDPGYKLOMLVKKHESGIVLEBDEQRVMMWRY---IQOEP 633
Qy      567 KLI-----LSVKNSRDEVAQMYCLVQWDPRIKPEQAMELLDCNYPDPWVGFAPVCLER 621
Db      634 DLLIVSELAFVWTDRENSELYMLEKKPSPVAALTLTGKRCCTDRVIRKFAVEKLE 693
Qy      622 YLTDDKLSQYLQVQLKYEOYLDNLVFLFKKALTNRIGHFFWHLKSEMH----- 676
Db      694 QLSVTFHFLFLPLIQALKYEPRAQSEVGMMLTRALCDYRIGHFLWMLRAETARLDC 753
Qy      677 --NKTVSQRFGLLESYCRACGMYLKHLNROVEAMEKLINLTDILKOEKD-ETQV--Q 731
Db      754 DLKSEBYRRLSLMEAYLRGNNEHIKITRQVDMVDELTRISTLVKGMPCVDATMKLRDE 813
Qy      732 MKFLVQMRPDPFMDALQGFLSPLNPAHOLGNLRECRIMSSAKRPLMNMENPDIMSE 791
Db      814 LRSISHMEMND-----SPLDPVYKLGEMIDKAIVLGSAKRPMLMHKKNPKSD 864
Qy      792 LLFQNNELIFKNGDDLRODMTLTQIIRIMENIMQNGDLRLMLPYGCLSIGCVGLEIV 851
Db      865 LHLPCAMIFKNGDDLRODMTLVQVLEVMDNIMKANIIDCLNPYAVLPMGEMIGILEV 924
Qy      852 RNSHTIMOIOCKGGLKGLAL--QFNSHTLHOWL-----KDKNKGEI----- 889
Db      925 PNCKTIFELIOVGTGFMTAVRSIDPSFMNWKIRKOCGIEDEKKSKSDSTKNPEKKIDN 984
Qy      890 -----YDAIDLFTSCAGYCVATFIIGIDRHSNINWKGDCQLFHDHFGHLDHKK 943
Db      985 TQMKKYCFEEDVDFVSCVSVATYIMGIDKXHSDDLMLTEQKYYHIDFGHILHGKGT 1044
Qy      944 KRFYKKEBVFVLTQDFLIYSKQAOECYKTRFEPEQEMCYAYLAIROHANLFINLFS 1003
Db      1045 KGIQDRDPFILTETHMTVIRSGKSYDGNSHLOKFKTLCVAEYEMNNRDLFVSLFT 1104
Qy      1004 MMGSGMPELQSDPDLAYIRKTLALD-KTEQELVFMKQMDAHGQWTKMDMIFHTI 1062
Db      1105 LMLGMLPELSTAKDDLHKLTLFCNGESKEERKFPAGIYEBAFNGSMTKTNWLFHAV 1164
Qy      1063 KOH 1065
Db      1165 KHY 1167

RESULT 9
US-09-844-353A-48
; Sequence 48, Application US/09844353A
; Patent No. US20020037585A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Kimura, Kouitarou
; APPLICANT: Patterson, Garth
; APPLICANT: Ogg, Scott
; APPLICANT: Paradis, Suzanne
; APPLICANT: Tisendaum, Heidi
; APPLICANT: Morris, Jason
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; FILE REFERENCE: 00786/351005
; CURRENT APPLICATION NUMBER: US/09/844,353A
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 08/857,076
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 1167
; TYPE: PRT

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; ORGANISM: Caenorhabditis elegans
US-09-844-353A-48

Query Match      19.1%; Score 1089; DB 9; Length 1167;
Best Local Similarity 27.2%; Pred. No. 1,7e-89;
Matches 311; Conservative 219; Mismatches 431; Indels 182; Gaps 39;

Qy      39 EATLITRKHLPLFK--EARKYPLHQLODESSYIFVSVTQAEERPEFDETRRLCDLTLFQ 96
Db      91 EILSLDFKHLPLFELIAPMKRGITSVKPD--VYFROLANGELIEVLPNDQPSKLELHG 148
Qy      97 --PFLKIEFVGNREKILNREIGFALGMPEVCEFDWYKBEVDFPRNINLVCKEAYDLR 154
Db      149 TFPMLFLYCPDGINRDKELMSDISHGCGYGLDKLESIDBELQFRASLWARTKCTLTR 208
Qy      155 DLSHPSRMYVPPN--VSSPELPRHLYNKLDKQI-IVVIVVIVSPNNDKOKYTLKI 211
Db      209 GL--EGTSHYAPPEEQYLCVGESCPRLDESCKVAAKLASYQMFV-----RKRVAEI 256
Qy      212 NHDCEPOVIAEAIR--KKTSMILSS--EQKLCVLEYQK--YILKYCGCEYF 261
Db      257 NGVC--EKMKKIOIEPNPNETPKSLHTFLYENRKLVDYTDTPADEGMFLDLAGRTTFV 314
Qy      262 LE-KYPLSQYKYIRSCIMLRMPNMLMAK-----ESTYS-----OLPMDC 301
Db      315 TNDPVKLTSDYGRSELESYRCGFVYRQSLVKDXYCRKPLREPHYVAHERKLALDV 374
Qy      302 FTM-----PSYGRISTATPYNNGESTK--SLWVINSALRIKILCATVYNNVIRID-- 352
Db      375 LSVSISTPQKSKNSDMWMTDFRPTASLKVSTLMDANIMIR-----PVNISGEFDP 427
Qy      353 ---KIYVRT--GIYHGEPICDQVNTQVPCSPRRN--EWLANDIYIPDLPRARLCLST 406
Db      428 ADVDMVRLREFSYVGTLLTLAG--STTKVNAQPAKANKKEVYTDLVKMDKPPA--VLST 484
Qy      407 CSYKRGKAKEEHCPLAMGNINLFDYTDPLVSGKALNLM--PVPHGLELDLNPV--TGS 464
Db      485 RVLVGYVKLSEFEFVGWVNMSTLDRDELROQGFPLHMAPEPTNRSRISGNGARIGT 544
Qy      465 NPKKTEPCLLEFEDMSSVYKPPDMG---VIEEHAWSVSRAGFSYSHAGLSNRLARD 520
Db      545 N-----AAVTIESSYSGVRMPGQGYTYLVKHSWTET-----LINIGDD 587
Qy      521 NELRENDKEQLRAICTRDPLSE-----ITQEKDFLWGHRYCVTIPILP 566
Db      588 YE-----SCIRDPGYKLOMLVKKHESGIVLEBDEQRVMMWRY---IQOEP 633
Qy      567 KLI-----LSVKNSRDEVAQMYCLVQWDPRIKPEQAMELLDCNYPDPWVGFAPVCLER 621
Db      634 DLLIVSELAFVWTDRENSELYMLEKKPSPVAALTLTGKRCCTDRVIRKFAVEKLE 693
Qy      622 YLTDDKLSQYLQVQLKYEOYLDNLVFLFKKALTNRIGHFFWHLKSEMH----- 676
Db      694 QLSVTFHFLFLPLIQALKYEPRAQSEVGMMLTRALCDYRIGHFLWMLRAETARLDC 753
Qy      677 --NKTVSQRFGLLESYCRACGMYLKHLNROVEAMEKLINLTDILKOEKD-ETQV--Q 731
Db      754 DLKSEBYRRLSLMEAYLRGNNEHIKITRQVDMVDELTRISTLVKGMPCVDATMKLRDE 813
Qy      732 MKFLVQMRPDPFMDALQGFLSPLNPAHOLGNLRECRIMSSAKRPLMNMENPDIMSE 791
Db      814 LRSISHMEMND-----SPLDPVYKLGEMIDKAIVLGSAKRPMLMHKKNPKSD 864
Qy      792 LLFQNNELIFKNGDDLRODMTLTQIIRIMENIMQNGDLRLMLPYGCLSIGCVGLEIV 851
Db      865 LHLPCAMIFKNGDDLRODMTLVQVLEVMDNIMKANIIDCLNPYAVLPMGEMIGILEV 924
Qy      852 RNSHTIMOIOCKGGLKGLAL--QFNSHTLHOWL-----KDKNKGEI----- 889
Db      925 PNCKTIFELIOVGTGFMTAVRSIDPSFMNWKIRKOCGIEDEKKSKSDSTKNPEKKIDN 984
Qy      890 -----YDAIDLFTSCAGYCVATFIIGIDRHSNINWKGDCQLFHDHFGHLDHKK 943

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Db 985 TOAMKKYFESVDRLFLYSCVGSVATYIMGIDKDRHSNLMLTENGKVVHIDFGHILGHGKT 1044

Qy 944 KFGYKREVPFVLTOPFLVIYSKGAOECTKTRREFEFQEMCYAYLAIRHANLFINLFS 1003

Db 1045 KLGIGDRQPFILTEHMTYIRSGKSVDSGSHLOKFKLTCVAEYVMMNNRDLFVSLFT 1104

Qy 1004 MMLGSGMPELQSPDDIAYIRKTLALD-KTQEOALEYFMKOMNDAHGCGTTKDWIHTI 1062

Db 1105 LMLGMELPELSTKADLHLKKTLCFNGESKEARKFAGIYEBAFNGSWSTKTNWLFHAV 1164

Qy 1063 KQH 1065

Db 1165 KHY 1167

RESULT 10

US-09-963-693-48

/ Sequence 48, Application US/09963693

/ Publication No. US20030181364A1

/ GENERAL INFORMATION:

/ APPLICANT: Ruvkun, Gary

/ APPLICANT: Osg, Scott

/ TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR

/ TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS

/ FILE REFERENCE: 00786/351004

/ CURRENT APPLICATION NUMBER: US/09/963,693

/ PRIOR FILING DATE: 2001-09-25

/ PRIOR APPLICATION NUMBER: US/09/205,658

/ PRIOR FILING DATE: 1998-12-03

/ PRIOR APPLICATION NUMBER: 08/857,076

/ PRIOR FILING DATE: 1997-05-15

/ PRIOR APPLICATION NUMBER: 08/888,534

/ PRIOR FILING DATE: 1997-07-07

/ PRIOR APPLICATION NUMBER: US98/10080

/ PRIOR FILING DATE: 1998-05-15

/ NUMBER OF SEQ ID NOS: 328

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 48

/ LENGTH: 1167

/ TYPE: PRT

/ ORGANISM: Caenorhabditis elegans

US-09-963-693-48

Query Match 19.1%; Score 1089; DB 12; Length 1167;

Best Local Similarity 27.2%; Pred. No. 1.7e-89;

Matches 311; Conservative 219; Mismatches 431; Indels 182; Gaps 39;

Qy 39 EATLITTKHLELFK--EARKYPLHQLLODESSITFVSVTQEARERFEDTRLCDLALFQ 96

Db 91 EIKLSDFGHQLFELIAPMKMGTSYVSPD--YVFQLNNGFGEIYEVTFNDDPLSKLELHG 148

Qy 97 --PFLKATIEPVGNREKILNREIGALGMVCEPFDMVDEPEODRRNILLNCKEAVDLR 154

Db 149 TFPMLFLVQPGINDKELMSDISHCLYSLDKLESIDBELROFRASIMARTKTCILTR 208

Qy 155 DLNSPHSAMVYVPPN--VESPPELPKHIYNNKLDKQI-IVYIWIIVSPNNDKQYTKI 211

Db 209 GL--EGSHAFPEQYLVCESECPKOLSEKVKAAKSYQMFW-----RKKAEI 256

Qy 212 NHDVPEQVIAEIR--KKTSMLLSS--EQLKLVLEYGK---YILKVCCEDEF 261

Db 257 NGVC--EKMMKIQIEFNPETPKSLHFLYEMRKLDVDTDDPADEGFIQLARITTFV 314

Qy 262 LE-KYPLSGYKIRSCINLGMKPNLMLAK-----ESTYS-----QLPMD 301

Db 315 TNPDKLTSYDGVSELESYRCGFVVRQSLVLKDYCPKPLYPHYRAHERKTLADV 374

Qy 302 FTM-----PSYSRRISTATPYNNGETSTK--SLWVINSALRIKILCATVYNNIRDID-- 352

Db 375 LSVSISDSTPKQSKNSDMWTDRPRASLKQVSLMDLALMLR-----PNTISGFDP 427

Qy 353 ---KIYVPT--GIYHGEPLCDNVNTQVRVPCSNPRNW-EMLVNDIYIPDLPPAARLCSTI 406

Db 428 ADVDMVRIEFSVYVYVLTLLASK-STTKVNAQFAKKMKEMTYFDLYMKDMPSA--VLSI 484

Qy 407 CSYKRRKAKKEHCPLAMNINLFDYDTLVSGKXALNW-VPPGLJEDLNPIDY-TSS 464

Db 485 RVLVGKVKLSEEFEGVWNMSLTDMRDELROGQPLFHLMADEPLANRRIENGARIGT 544

Qy 465 NPKETPCLEEFDMSSVYKFPDMS---VIEEHNMSVSEAGFSYSHAGLSNRLAD 520

Db 545 N-----AATTEISSGVGRVMPSSQOQYTVLKHSTWET-----LNIWGDD 587

Qy 521 NEIRENDKEQLRAICTRDLSE-----ITEQKDFLMSHHRYCVTIPELIP 566

Db 588 YE-----SCIRDPYKQLQMLYKHSIGVLEEDBQRHVMWERY--IQOBP 633

Qy 567 KLI-----LSVKNSRDEYAOYCLVKDMPPIKPEQAMELLDQNYDPDWRGFAVCEK 621

Db 634 DLLIVISELAFWTTDENFSELYVMLEKKRPSVAALTLTGKRCCTDRIVIRKFAVCKLB 693

Qy 622 YLTDDKLSOYLQYOVULKYEQYLDNLVRFLLKALTNQRIQHPFFMHLKSEMH----- 676

Db 694 QLSPTVPHLFLPLIALKTEPPAQSVEGMMLTRALCDYRIGHRFLFWLRAIARLRC 753

Qy 677 --NKTYSOREGLLESYCAQGYLRLNROVEAMEKLINLIDLKOEKD-ETQVY--Q 731

Db 754 DLKSEYBRISLMEAYLRGNEEHIKITROVDMVDELTRISTLVKGMPPDVATMKLRDE 813

Qy 732 MKFLVEGMRRPDMALQGLSPNLPAHQNLRLKECRIMSARPLMLNMENPMISE 791

Db 814 LRSISHMENMD-----SPLDPYKLGEMITDKATVLGSAKRPMLMHMKPKPSD 864

Qy 792 LLENNNEIIFKNGDDLRQDMLTQIIRIMENIQONOGDLRMLPYGCLSIGDCVGLIEV 851

Db 865 LHLRFCAITRKNDLRLQDMLVQVLEVMNITKANINDOCLNPAVYLPNGEMIGIIEV 924

Qy 852 RNSHTIMQIOCKGLKCAL--QENSHTLQWL-----KDKXKGI----- 889

Db 925 PNCKTIEIQTGVGMNTAVRISIDSPMNKIRKQCGIEDEKKSKXDSTKNIEKKIDN 984

Qy 890 -----YDAALDLFTRSCAGYATPILGIGDRHNSIMWKDDGOLPHIDFGHLDHKK 943

Db 985 TOAMKKYFESVDRLFLYSCVGSVATYIMGIDKDRHSNLMLTENGKVVHIDFGHILGHGKT 1044

Qy 944 KFGYKREVPFVLTOPFLVIYSKGAOECTKTRREFEFQEMCYAYLAIRHANLFINLFS 1003

Db 1045 KLGIGDRQPFILTEHMTYIRSGKSVDSGSHLOKFKLTCVAEYVMMNNRDLFVSLFT 1104

Qy 1004 MMLGSGMPELQSPDDIAYIRKTLALD-KTQEOALEYFMKOMNDAHGCGTTKDWIHTI 1062

Db 1105 LMLGMELPELSTKADLHLKKTLCFNGESKEARKFAGIYEBAFNGSWSTKTNWLFHAV 1164

Qy 1063 KQH 1065

Db 1165 KHY 1167

RESULT 11

US-10-092-219-2

/ Sequence 2, Application US/10092219

/ Publication No. US20020115114A1

/ GENERAL INFORMATION:

/ APPLICANT: Domin, Jan

/ TITLE OF INVENTION: No. US20020115114A1 Lipid Kinase

/ FILE REFERENCE: 1064HG/50947

/ CURRENT APPLICATION NUMBER: US/10/092,219

/ CURRENT FILING DATE: 2002-03-07

/ PRIOR APPLICATION NUMBER: PCT/GB98/00244

/ PRIOR FILING DATE: 1998-01-27

/ PRIOR APPLICATION NUMBER: 09/355,160

/ PRIOR FILING DATE: 1999-10-01

/ PRIOR APPLICATION NUMBER: 9701652.1

/ PRIOR FILING DATE: 1997-01-28

/ NUMBER OF SEQ ID NOS: 11

/ SOFTWARE: PatentIn version 3.1

```

; SEQ ID NO 2
; LENGTH: 1686
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-219-2

Query Match      17.8%; Score 1014.5; DB 14; Length 1686;
Best Local Similarity 32.5%; Pred. No. 1.8e-82;
Matches 263; Conservative 131; Mismatches 293; Indels 123; Gaps 23;

QY 298 PMDCFTMPSYSRIRISTATPYMNGSTSKSLMVINSALRIKILCTYNNV-IRIDIKIV 356
DB 666 PDC-----AQSSEVKEAMVTTTQLOFTTFAHGISSSMWSVYKYYL 709
QY 357 RTGIYHGEBELCDNVNTQRPVCSNP-----RWNEMLVNDIYIPDLPRARLCLISICSV-- 409
DB 710 ICSLSHNGKDLFPRIQSKYGVYNNFPYLLKMDLLIFPIQISDPLIESVILHLLPILN 769
QY 410 -----KGRKAKEEHCPILAMGNIN--LFDYDTLVSGKVALNLMVPVPHGLEDDL 457
DB 770 QSSGSSPDSNKKRG-----PEALGKVSPLCDFRFRLCGTYLALMTSSH----- 816
QY 458 PIVTGSNPKKP-----CLELEF--DMSSVVKFP--DMSVIEEHNMSVSREAG 505
DB 817 -----TNSVPECTVKGYMERIYLVQVPSAPFDIITTPQVDRSIIQOH----- 862
QY 506 FSYSHAGLSNRLARDNLEEND--KEOLRAICTRDPLEITEOEKDFLMSRHVCVTIPEI 564
DB 863 -----NLETLENDIKGKLLDLHKDSSLSGSKEDKAFMEKRYICFKHPNC 908
QY 565 LPLKLLSV--KNSRDEVAQMTCLVKDWPPIKEQAMELLDCNYPDMVRGFAVRCLK 621
DB 909 LPLILASAPMKWGN--LAKTYSLSLHQWPAVPLALLELLDSKFADQEVRLAVTWIEA 965
QY 622 YLDDDLSQLYLIQVLYQVLYKEQYLDNLVPLFKKALTNRIGHFFPMHLKSEHNKTVS 661
DB 966 -ISDDELTDLLPQVQALKEIYINSSLVQFLLSRAIGIQAIAHLYMLKDLHDFQS 1024
QY 682 QREGLLESYCRACGMILKHLNROVEAMEKILNLTDLKOEKDETQKQVMEFLVEQMR 741
DB 1025 TREHNVGALLSVG--KALREBELKQTLVOLLGGVAEKVAQSSASARQVVLQNSMER 1081
QY 742 PDFMDALQGLS-----PLNPAHQGNLLEECRIMSSAKRPLNWMENPDIMSELLFQ 795
DB 1082 -----VQSFQKMKCRLPLKPSLVAKEINIKSCSFSSNAVPLKVTWVADPLGEEL-- 1133
QY 796 NNEIIRKNGDRLQDMTLTLOIRIMENIMONOGIDMLPFGCLISGDCVGLIEVVRNSH 855
DB 1134 --NVMERKVGEDLQDMIALQMIKIMKIMLKEGLDIRMVFICKLSTGRDRGMVELVPSD 1191
QY 856 TIMQIOCKGGLKCALQFNSHTLHOWLKDKKKG--EIVDAATDLFTRSCAGYCAVTFILIG 914
DB 1192 TLRKIVGVGVTS--FKDKPRLAEWLRKINPSEEEKASENTIYSCAGCAVTVVLGIC 1249
QY 915 DRHNSIMVVDQQLPHIDGHEFLDHKKKKGYKREVRVFLTQDFELIVISKAQECTKT 974
DB 1250 DRNDNIMLRSTGMHFIIDGKFLGHAQMGSKFRBPAPVLSDMAYVINGEK---PT 1306
QY 975 REPERQEMCYKAYLAIROHANLFINPSMMLSGMPELOSFPDIAVIRKTALDKTEOE 1034
DB 1307 IRQQLTVDLCCQAYNIRKQTNLFNMLISLIMPSGPELTSIODEKVRDALQPTTDAE 1366
QY 1035 ALEYFMKONMDAHNGGATTKMDWIFPTIKQ 1064
DB 1367 ATIFFTR-LIESSLGIATKFNFINLQ 1395

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; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 192
; LENGTH: 887
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-192

Query Match      12.0%; Score 685; DB 10; Length 887;
Best Local Similarity 23.4%; Pred. No. 6.8e-53;
Matches 203; Conservative 158; Mismatches 312; Indels 194; Gaps 23;

QY 354 IYRTGIYHGEBELCDNVNTQRPVCSNP--RWNEMLVNDIYIPDLPRARLCLISICVGR 412
DB 57 LYVTCQVFAEGKPSALPVRTSYKAFSTRMWNEMLKLPVXPDLPRNAQVALLIMDYGP 116
QY 413 KGAKESHCPLAMGNINLFDYDTLVSGKVALNLMVP--VPHGLEDDLPIGVTSNPKKETP 471
DB 117 GKA-----VPVGGTVVLFQGYGMSRQGMHLKWPVNEADGSPPTPGFTSTLSDDQ 172
QY 472 CL-----EEFDFSSVVKFPDMSVIEEHNMSVSREAGFSY----- 508
DB 173 SRLAKLTKAHQGMWKMVMDRLT--FREIEMINE---SVKSSNFMILMGFRVCYKCD 227
QY 509 -----SHAGLSNRL--ARDNELR 524
DB 228 DKEYGIVYEEKODESSPILTSFELVVPDPQMSLENLVESKHNLRPSLRSGPSDHLK 287
QY 525 --ENDQOLRAICTRDPLEITEOEKDFLMSRHVCVTIPELLPKLLSVKNMSRDEVAQ 582
DB 288 PVPSPDQLKNIVSYPPSKPFTYEEDLVWEFRYYLTNODKATLKITLSVTIMDLPOGAKQ 347
QY 583 MYCLVMDWPPIKEQAMELLDCNYPDMVRGFAVRCLKEXLTBDKLSQYLIQVLYKYE 642
DB 348 ALALLKKNMPMDVEDSELISHTYTPYKRVAVARL--ROADDEDLMLYSOLVQALKYE 406
QY 643 QY----- 644
DB 407 NFDIDKNGLEPTKDSQSSVSGNVSNGINSAEIDSQIITSPLEVSPPASKTKEVP 466
QY 645 ----LDNLVRLPLKALTNORIGHFFPMHLKSEHNKTVSQRFGLLSYCRACGMYLK 700
DB 467 DGENLEQDICTFLISASKNSSTLANLYWYVIVECDODTOOGDPKTHETIYLVNMRFSQ 526
QY 701 HL--NRQYEAM-----EKLINLTDLKOEKDETQK--VOMKFLVEQMRPDEM 745
DB 527 ALLKPKSIVRWSLSLAAQOTFVDRVHLMKAVQKSGRKKKNKNELOALLGDNENQNIS 586
QY 746 DALQGLSPLNPAHQGNLLEECRIMSSAKRPLNWMENPDIMSELLPONNE----II 800
DB 587 D-VELIPLPLEPVQKIRGIIPEFATLFKSLMP-----AQLPFTKEDGKGYPI 634
QY 801 FKNQDRLQDMTLTLOIRIMENIMONOGIDMLPFGCLISGDCVGLIEVVRNSHTIMOJ 860
DB 635 FKHGDLRDQDLOLIQIISLMDKILRKENDLKLTPYKVATATSKHGFQFIOISVPAEVL 694
QY 861 QCKGGLKALQFNSHTLHOWLKDKKKGLEYDAIDLFTRSCAGYCAVTFILIGDRHNSN 920
DB 695 DTBGSIQNFRKRYABS-----ENGNNGISAEVMDTVYVSCAGYCVITIIIGVGRHLDN 748
QY 921 INWKDQGLPHIDGHEFLDHKKKKGYKREVRVFLTQDFLIVISKAQECTRTREPERF 980
DB 749 LVLTKTGKLPHIDFGYILGRDPKL-----PPMKLNKE--NVEGNGG--TQSEQYGEF 798

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RESULT 12
US-09-771-161A-192
; Sequence 192, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.

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QY 981 OEMCYKAYLAIROHANLFINLFSMMLGSGMPELOSPDD--IAVIRKTLALDKTEQALEY 1038  
Db 799 RKOCYTAFLHLRKXSNLILNLFSLMWDPNIPDIALBPDVKVKVQDKFRILDSDEAVHY 858  
QY 1039 FMKQMDAHHGWTTKXDWIETHIKOH 1065  
Db 859 MGSILIBESVHALPFAAVEQI-HKFAQY 884

RESULT 13  
US-09-771-161A-193  
; Sequence 193, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 193  
; LENGTH: 887  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-193

Query Match 12.0%; Score 685; DB 10; Length 887;  
Best Local Similarity 23.4%; Pred. No. 6,8e-53;  
Matches 203; Conservative 158; Mismatches 312; Indels 194; Gaps 23;

QY 354 IYVRTGIHGEPLCDNVNTRVPCSNP-RNMENLNYDIYIPDLPRARLCISCVKGR 412  
Db 57 LVYTCQVAEGPSALPRTSTYKAFSTKMNMMMLKLVKXPDDLPRNNQVALTIVDYGPR 116  
QY 413 KGAKEHEPLAMGNINLFDYDTTLVSGKALNLMP-VPHGLEDDLNPIGVTSNPKETP 471  
Db 117 GK A-----VPVGSTYSLFGKYGMSQGMNDLKVMNVNVEADGSEPTNTGRTSTLSEDM 172  
QY 472 CL-----ELEFDWESSVVKFPDMSYIEEHAWSVSRKGFST----- 508  
Db 173 SRLAKLTGAHRQGHVAVKVDMLDLRLT-FREIEMINE---SVKRSNFMYLWGGFRCVKCD 227  
QY 509-----SHAGLSNRL--ARDNEIR 524  
Db 228 DKEYGIVVEKDGDESSPILISFELVKKVPDPQMSLENLVESGHNLPRLBRSRGPBDHDX 287  
QY 525 --ENDKEQRLAICTRDPLSEITEOEKDFLMSHRHCVTIPEILPKLLSVKNSDEVAQ 582  
Db 288 PYPSPRDOAKNIVSYSPSKRPTEYEBDDLWMEFRYYVTNDQKALTKILTSTVIMDLPGAKQ 347  
QY 583 MYCLVNDWPPIKPEQAMELLDCNYPDMYRGFAVRCLEKYLITDDKLSQYLILQVQLKYE 642  
Db 348 AALALGKNMPDVEDLELISHYTNPTVRVAVARL-ROADDEDLMLYQLVQLKYE 406  
QY 643 QY----- 644  
Db 407 NFDPIKNGLEPTKKDSQSSVSGVNSGINSAEIDSSQIITSLPVSSEPPSPAKTKEVP 466  
QY 645 ----LDNLVRFLLKALTNORIGHPFMHLKSEMNKTVSGRGLLESYCRACGMYLK 700  
Db 467 DGENLEQDCLTFISAPSKNSTLANLYWVIVIECEDDQDQDPTHEWYLVNMMRFSQ 526  
QY 701 HL-----NROYEAM-----EKLINTDLIKQEKDETQK-VQMKFLVEQMKRRPDEM 745  
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QY 801 FKNGDDLRODMTLQIIRIMENIWONQDLEMLPYGLSICDVCGLIEVENSHTIMO 860  
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QY 861 QCKGKLGALQENSHTHOMLKDKNKGIYDAIDLFTSCGCGYCATFTILIGDBHNSN 920  
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RESULT 14  
US-09-921-232-2  
; Sequence 2, Application US/09921232  
; Patent No. US20020102681A1  
; GENERAL INFORMATION:  
; APPLICANT: Martino-Catt, Susan J.  
; APPLICANT: Wang, Hongyu  
; TITLE OF INVENTION: Polypeptides Controlling Phytate  
; TITLE OF INVENTION: Metabolism in Plants  
; FILE REFERENCE: 0706D4  
; CURRENT APPLICATION NUMBER: US/09/921,232  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: 60/055,446  
; PRIOR FILING DATE: 1997-08-11  
; PRIOR APPLICATION NUMBER: 60/055,526  
; PRIOR FILING DATE: 1997-08-08  
; PRIOR APPLICATION NUMBER: 60/053,944  
; PRIOR FILING DATE: 1997-07-28  
; PRIOR APPLICATION NUMBER: 09/118,442  
; PRIOR FILING DATE: 1998-07-17  
; PRIOR APPLICATION NUMBER: 09/677,064  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 2  
; LENGTH: 803  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(803)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-921-232-2

Query Match 11.8%; Score 675.5; DB 10; Length 803;  
Best Local Similarity 26.3%; Pred. No. 4,3e-52;  
Matches 215; Conservative 155; Mismatches 298; Indels 149; Gaps 30;

QY 330 INSARIKILCATYVNVNIRIDKIYVRTGIHGEPLCDNVNTRVPCSNR--WNEML 387  
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QY 388 NYDIYIPDLPRARLCISCVKGRKGAKEHEHCPLAMGNINLFDYDTTLVSGKALNLMP 447  
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QY 448 VPHGLEDLNPIGVTSNPKETPCLE-LE-----FDW-----FSSVVK-- 485
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Db 246 PSEHKQIKLAKSLTRGIVDRDLKPSNKRKLQTIIRKPPRTILEVDEKQIVMKFRPSLM 305
QY 560 TIEPIELKLLSVKMSRDEVAQMYCLVKMPPIKPEQAMLLDCNYPDMVAGFAVRCL 619
Db 306 SEKKALTKFVRSVMSDNOQAQAVELIGKEMIDVADALELSPDESDEVGAYAVSL 365
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QY 727 TOKVQMKFLVEQMR-----PDMFALQGLSPINPAHQLSNRLSECRIMSSAKR 777
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Db 748 DI-SADESGGLKLOEKFRLLDDDEAIIHFQDLINDS 783

RESULT 15
; Sequence 2, Application US/09921330
; Patent No. US20020102682A1
; GENERAL INFORMATION:
; APPLICANT: Martino-Catt, Susan J.
; APPLICANT: Wang, Hongyu
; APPLICANT: Beach, Larry R.
; TITLE OF INVENTION: Polypeptides Controlling Phytate
; TITLE OF INVENTION: Metabolism in Plants
; FILE REFERENCE: 0706D3
; CURRENT APPLICATION NUMBER: US/09/921,330
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/055,446
; PRIOR FILING DATE: 1997-08-11
; PRIOR APPLICATION NUMBER: 60/055,526
; PRIOR FILING DATE: 1997-08-08
; PRIOR APPLICATION NUMBER: 60/053,944
; PRIOR FILING DATE: 1997-07-28
; PRIOR APPLICATION NUMBER: 09/118,442
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: 08/677,064
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 31

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(803)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-921-330-2

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Query Match 11.8%; Score 675.5; DB 10; Length 803;
Best Local Similarity 26.3%; Pred. No. 4.3e-52;
Matches 215; Conservative 155; Mismatches 298; Indels 149; Gaps 30;

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QY 330 INSALRIKIIICATVNNINIDIDIKYRTGIYHGGEPLCONVNTQRPCCNPR--NMEWL 387
Db 16 ISHPLARVLAHEIITLTDKVPPELFVECKLYIDGIOFGLPVKTRLEP-SGPKYCWNELI 74
QY 388 NYDIYIPDLPPAARLCLISCVKGRKAKEHCPLAGNINLFDYDTLVSGKALNLMF 447
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QY 560 TIEPIELKLLSVKMSRDEVAQMYCLVKMPPIKPEQAMLLDCNYPDMVAGFAVRCL 619
Db 306 SEKKALTKFVRSVMSDNOQAQAVELIGKEMIDVADALELSPDESDEVGAYAVSL 365
QY 620 EKYITDKLSQYLQLOVULKYEOYLDNLVRFLLKALTNQRIIGHFFPHLKSSEMNKT 679
Db 366 ER-ADDELOCYLLQLOVALRFRSDKSRLLFLVNRALSNIEIASFLRMVILVELHSPA 424
QY 680 VSOR-----FGLLESYCRACG-----MYLKLNRQVAMEKILNLTDLIKOEKDE 726
Db 425 YARRIYGYDMLKMSMKLVGERDEDEGDFRLMOSLTRQDTLTAQLCSIMKDVANNVGS 484
QY 727 TOKVQMKFLVEQMR-----PDMFALQGLSPINPAHQLSNRLSECRIMSSAKR 777
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QY 778 PMLNMENPDMISLLEFQNNELIFKNGDDLRQDMLTLQIIRIMENIMQNGLDRLMLPYG 837
Db 536 PLRLTFETKAN-----GQTSKIYKKGDDLRQDQLVQTVSLMDRLKLEMLDLHLTPYR 589
QY 838 CLSIGDCVGLIEVNRSHITMOIQCKGKLGALQFNHSH-TLHOMLKDNKGE-----IYD 891
Db 590 VLTAGQDEGMLEFI-SSSSLAQI-----LSHRSTITSYLQKFRHDEDPFGIT 637
QY 892 AAILDFTRSCAGYCVATFIIIGIDRHNNSNIMVKDQGLFHIIDFGHLDHKKKFGYKRR 951
Db 638 QCELETFIKSCAGYSVITYILGVGDRHLDNLTDDGRLFHVDFAFILGRDPKPF-----P 692
QY 952 VPFVLTDPLIVISKAGQECTKTRFERFQEMCYKATLAIQHIANLFINLFSMMLGSGMP 1011
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Db 748 DI-SADESGGLKLOEKFRLLDDDEAIIHFQDLINDS 783

Search completed: November 6, 2003, 14:46:14

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Wed Nov 12 14:55:48 2003

us-09-325-095-37.rapb

Page 12

Job time : 39 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: November 6, 2003, 14:41:45 ; Search time 22 Seconds  
(without alignments)  
2055.923 Million cell updates/sec

Title: US-09-325-095-37  
Perfect score: 5709  
Sequence: 1 MPRPSSGELWGHLMPPRI.....GWTTKDWIPIIKQALNX 1069

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	5708	100.0	1069	2	US-08-780-872-37
3	5708	100.0	1069	3	US-09-085-957-37
4	5657	99.1	1080	2	US-08-162-081B-36
5	5657	99.1	1080	2	US-08-780-872-36
6	5657	99.1	1080	3	US-09-085-957-36
7	5645	98.9	1068	3	US-08-390-874C-11
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9	1978.5	34.7	1044	2	US-08-777-871A-2
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12	1978.5	34.7	1044	4	US-09-841-341-2
13	1976.5	34.6	1044	4	US-09-194-640A-1
14	1467	25.7	1101	2	US-08-916-917-14
15	1467	25.7	1101	3	US-09-225-170-4
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17	1466.5	25.7	1102	2	US-08-972-631-4
18	1466.5	25.7	1102	2	US-08-972-630-4
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25	1051.5	18.4	1658	2	US-08-609-049A-13
26	1051.5	18.4	1658	2	US-09-170-996-23
27	1048.5	18.4	1726	2	US-08-609-049A-30

28	1048.5	18.4	1726	3	US-09-170-996-30	Sequence 30, Appl
29	1014.5	17.8	1686	4	US-09-355-160D-2	Sequence 2, Appl
30	887.5	15.5	171	2	US-08-609-049A-21	Sequence 21, Appl
31	887.5	15.5	171	3	US-09-170-996-21	Sequence 21, Appl
32	859	15.0	1876	2	US-08-609-049A-12	Sequence 12, Appl
33	859	15.0	1876	3	US-09-170-996-12	Sequence 12, Appl
34	852	14.9	1876	2	US-08-609-049A-28	Sequence 28, Appl
35	852	14.9	1876	3	US-09-170-996-28	Sequence 28, Appl
36	675.5	11.8	803	3	US-09-118-442-2	Sequence 2, Appl
37	675.5	11.8	803	3	US-09-677-064-2	Sequence 2, Appl
38	648.5	11.4	868	2	US-08-162-081B-33	Sequence 3, Appl
39	648.5	11.4	868	2	US-08-780-872-33	Sequence 3, Appl
40	648.5	11.4	868	3	US-09-085-957-33	Sequence 3, Appl
41	537.5	9.4	171	2	US-08-609-049A-22	Sequence 22, Appl
42	537.5	9.4	171	3	US-09-170-996-22	Sequence 22, Appl
43	482.5	8.5	171	2	US-08-609-049A-23	Sequence 23, Appl
44	482.5	8.5	171	3	US-09-170-996-23	Sequence 23, Appl
45	456	8.0	85	2	US-08-162-081B-46	Sequence 46, Appl

## ALIGNMENTS

RESULT 1  
US-08-162-081B-37

Sequence 37, Application US/08162081B  
Patent No. 5824492

## GENERAL INFORMATION:

APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Balai, Watfield; Michael Derek; Parker, Peter  
APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefano; Gou, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
TITLE OF INVENTION: THEIR PREPARATION AND USE  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
City: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage  
COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,081B

FILING DATE: February 7, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB93/00761

FILING DATE: 13 April 1993

ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.

REGISTRATION NUMBER: 34,894

REFERENCE/DOCKET NUMBER: LUD 5256

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 838-3884

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 1069 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-162-081B-37

Query Match 100.0%; Score 5708; DB 2; Length 1069;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1068; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Sequence 37, Application US/08780872
; Patent No. 5846824
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volintia,
; APPLICANT: Stefano; Gout, Ivan Tarasovich
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pelfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,872
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paesqualini, Patricia A.
; REFERENCE/DOCKET NUMBER: 34,894
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEO ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1069 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-780-872-37

Query Match 100.0%; Score 5708; DB 2; Length 1069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1068; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPRPSGELMGTHLMPRLIVECLLPNGMIVTLECLREATLITIKHELFKEARKYPLHQ 60
DB 1 MPPRPSGELMGTHLMPRLIVECLLPNGMIVTLECLREATLITIKHELFKEARKYPLHQ 60
QY 61 LLODESSYIFVSVYQGEAREEFDETRRLCDLRFOPFLKIEBPVGNREKILNREIGFA 120
DB 61 LLODESSYIFVSVYQGEAREEFDETRRLCDLRFOPFLKIEBPVGNREKILNREIGFA 120
QY 121 IGMVPCFDMWKDEVDQFRNINLVNCKEAVDLRLDLSPHSRAMYVPPNVSSPELPLKH 180
DB 121 IGMVPCFDMWKDEVDQFRNINLVNCKEAVDLRLDLSPHSRAMYVPPNVSSPELPLKH 180
QY 181 IYKLDKGOIIVVIVVISPNNQKXTLKNHDCVPEQVIAEIRKKTSMILSSBOLK 240
DB 181 IYKLDKGOIIVVIVVISPNNQKXTLKNHDCVPEQVIAEIRKKTSMILSSBOLK 240
QY 241 LCVLEYOGKYLKVCGCDEYFLEKYPISOYKXIRSCIMLGMPNIMLAKESLYSOLPMD 300
DB 241 LCVLEYOGKYLKVCGCDEYFLEKYPISOYKXIRSCIMLGMPNIMLAKESLYSOLPMD 300
QY 301 CFTMPSYSRISTATPYNNGESTSKSLWVINSALRIKILCATYVNVNIRDIDKIYVPTGI 360

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Db      301 CFTMPSYRRISTATPYNNGETSTKSLWVINSALRIKILCATYVNVNIRIDIKIYVRTGI
Qy      361 YHGGEPLCDNVNTORVPCSNPRNEMWLNVDIYIPDLPRARLCLISYVGRKGAKEHC
Qy      361 YHGGEPLCDNVNTORVPCSNPRNEMWLNVDIYIPDLPRARLCLISYVGRKGAKEHC
Qy      421 PLAMGNINLFDYTDITLVSGKALNLMFVPHGEDLNPVIGVTSNPNKETPCLELEDFWF
Qy      421 PLAMGNINLFDYTDITLVSGKALNLMFVPHGEDLNPVIGVTSNPNKETPCLELEDFWF
Qy      481 SSVVKEPDMVSIEEHANMSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPL
Qy      481 SSVVKEPDMVSIEEHANMSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPL
Qy      541 SEITTEOKDFLMSHRHVCVTIPEILPKLLSVKMSNDEVAOMYCLVKDMPRIKPEQAME
Qy      541 SEITTEOKDFLMSHRHVCVTIPEILPKLLSVKMSNDEVAOMYCLVKDMPRIKPEQAME
Qy      601 LUDCNYPDPWVRGFAVRCLEKYLTDKLSQYLLQVVLKYEQYLDNLVPLKKAALTIN
Qy      601 LUDCNYPDPWVRGFAVRCLEKYLTDKLSQYLLQVVLKYEQYLDNLVPLKKAALTIN
Qy      661 QRTGHEFFPMLKSEMNKTVSQRFGLLBSYCRACGMVYLGHNLROYEAMEKILNTDILK
Qy      661 QRTGHEFFPMLKSEMNKTVSQRFGLLBSYCRACGMVYLGHNLROYEAMEKILNTDILK
Qy      721 QEKKDETOKVOMELVEQOMRPFMDALOGFLPPLNPAHOLGNLREECINSARPLM
Qy      721 QEKKDETOKVOMELVEQOMRPFMDALOGFLPPLNPAHOLGNLREECINSARPLM
Qy      781 LNMENPDIMSELLFONNEILFKNGDDLRODMTLQIIRIMENIMONQGLDRLMPLYCLS
Qy      781 LNMENPDIMSELLFONNEILFKNGDDLRODMTLQIIRIMENIMONQGLDRLMPLYCLS
Qy      841 IGGCVGLIEVNRSHITMOQCKGGLKALQFNSHTLHQWLKONKEIYDAIDLEFTRS
Qy      841 IGGCVGLIEVNRSHITMOQCKGGLKALQFNSHTLHQWLKONKEIYDAIDLEFTRS
Qy      901 CAGYCVATFLLGSDHNSINIMVKGDDGOLPHIDFGHFLDHKKKPGKREVPFVLTODF
Qy      901 CAGYCVATFLLGSDHNSINIMVKGDDGOLPHIDFGHFLDHKKKPGKREVPFVLTODF
Qy      961 LIVISGAOECTRTREPERQEMCYKAYLAIRQHANLFINLFSMUGSGMPELOSPDDIA
Qy      961 LIVISGAOECTRTREPERQEMCYKAYLAIRQHANLFINLFSMUGSGMPELOSPDDIA
Qy      1021 YIRKTLALDKTBOALEYFKQKQNDAHGCGWTTKMDMIFHTIKOHALN
Qy      1021 YIRKTLALDKTBOALEYFKQKQNDAHGCGWTTKMDMIFHTIKOHALN
Qy      1021 YIRKTLALDKTBOALEYFKQKQNDAHGCGWTTKMDMIFHTIKOHALN

```

## RESULT 3

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US-09-085-957-37
; Sequence 37, Application US/09085957
; Patent No. 6274327
; GENERAL INFORMATION:
; APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
; APPLICANT: Bala, Waterfield, Michael Derek; Parker, Peter
; APPLICANT: Joseph, Otsu, Masayuki; Panayotou, George; Volinia,
; APPLICANT: Stefano, Gout, Ivan Tarasovitch
; TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felle & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

```

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; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085, 957
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/780, 872
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: 08/162, 081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ. ID NO.: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1069 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-085-957-37

```

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Query Match      100.0%; Score 5708; DB 3; Length 1069;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1068; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MPRPSSGELMGHLMPPRLVBCLLPNGMIVTLECLREATLTITGHELFKEARKYPLHQ 60
Db      1 MPRPSSGELMGHLMPPRLVBCLLPNGMIVTLECLREATLTITGHELFKEARKYPLHQ 60
Qy      61 LLODESSYFVSVTOAEKEEFDETRLCDLRLPQPIKVIKVPVGNREBKILNREIGFA 120
Db      61 LLODESSYFVSVTOAEKEEFDETRLCDLRLPQPIKVIKVPVGNREBKILNREIGFA 120
Qy      121 IGMVCEPDMVQDEVDQRRNLIANVCKEAVDLRLNSPHSRAMVYYPNVSSPELPGH 180
Db      121 IGMVCEPDMVQDEVDQRRNLIANVCKEAVDLRLNSPHSRAMVYYPNVSSPELPGH 180
Qy      181 IYKLDKQIIVIVITVSPNNDKQYTLKINHDCVPEOVIKAIKRTKSMILSSQOLK 240
Db      181 IYKLDKQIIVIVITVSPNNDKQYTLKINHDCVPEOVIKAIKRTKSMILSSQOLK 240
Qy      241 LCVLEYQGYIILKVGCDEYPLEKYPLSOYKIRSCIMGRPNMLMAKESISQOLPMD 300
Db      241 LCVLEYQGYIILKVGCDEYPLEKYPLSOYKIRSCIMGRPNMLMAKESISQOLPMD 300
Qy      301 CFTMPSYRRISTATPYNNGETSTKSLWVINSALRIKILCATYVNVNIRIDIKIYVRTGI 360
Db      301 CFTMPSYRRISTATPYNNGETSTKSLWVINSALRIKILCATYVNVNIRIDIKIYVRTGI 360
Qy      361 YHGGEPLCDNVNTORVPCSNPRNEMWLNVDIYIPDLPRARLCLISYVGRKGAKEHC 420
Db      361 YHGGEPLCDNVNTORVPCSNPRNEMWLNVDIYIPDLPRARLCLISYVGRKGAKEHC 420
Qy      421 PLAMGNINLFDYTDITLVSGKALNLMFVPHGEDLNPVIGVTSNPNKETPCLELEDFWF 480
Db      421 PLAMGNINLFDYTDITLVSGKALNLMFVPHGEDLNPVIGVTSNPNKETPCLELEDFWF 480
Qy      481 SSVVKEPDMVSIEEHANMSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPL 540
Db      481 SSVVKEPDMVSIEEHANMSVSREAGFSYSHAGLSNRLARDNELRENDKEQLRAICTRDPL 540
Qy      541 SEITTEOKDFLMSHRHVCVTIPEILPKLLSVKMSNDEVAOMYCLVKDMPRIKPEQAME 600
Db      541 SEITTEOKDFLMSHRHVCVTIPEILPKLLSVKMSNDEVAOMYCLVKDMPRIKPEQAME 600

```

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QY 601 LLDGNYPDPMVGRFAVRCLEKYLTDKLSQYLLIQLVQVLYKEYOYLNDLVRFLKKAALTN 660
DB 601 LLDGNYPDPMVGRFAVRCLEKYLTDKLSQYLLIQLVQVLYKEYOYLNDLVRFLKKAALTN 660
QY 661 QRIQHFFPMHLKSEMHNTKVSQRFGLLLESYCRACGMYLKLNRQVEAMEKLIINTDILK 720
DB 661 QRIQHFFPMHLKSEMHNTKVSQRFGLLLESYCRACGMYLKLNRQVEAMEKLIINTDILK 720
QY 721 QEKKDETQYQKMFVLEQMRPDMALQGLSPINPAHQIQLRLEECRIMSASAKRPLW 780
DB 721 QEKKDETQYQKMFVLEQMRPDMALQGLSPINPAHQIQLRLEECRIMSASAKRPLW 780
QY 781 LNMENPDIMSELLFQNNELIFKNGDDLRQDMLTLQIRIMENIWONQGLDRLMLPYGCLS 840
DB 781 LNMENPDIMSELLFQNNELIFKNGDDLRQDMLTLQIRIMENIWONQGLDRLMLPYGCLS 840
QY 841 IGDGCVGLIEVVRNSHTIMQIQCKGKLGALQFNSHTLQWLKDKNKGSIYDAIDLFTRS 900
DB 841 IGDGCVGLIEVVRNSHTIMQIQCKGKLGALQFNSHTLQWLKDKNKGSIYDAIDLFTRS 900
QY 901 CAGYCVATFIIGIDRHSNIMVAKDQGLPHIDGHEFLDHKKKFGYKREVRVPVLTQDF 960
DB 901 CAGYCVATFIIGIDRHSNIMVAKDQGLPHIDGHEFLDHKKKFGYKREVRVPVLTQDF 960
QY 961 LIVISKAQOECTKTREFEFOEMCYKAYLAIRQHANLFINLPSMLCSGMBELSPDIA 1020
DB 961 LIVISKAQOECTKTREFEFOEMCYKAYLAIRQHANLFINLPSMLCSGMBELSPDIA 1020
QY 1021 YIRKTLALDKTEQALFEMKQNDAAHHGWTTKMDMIFHTIKOHANL 1068
DB 1021 YIRKTLALDKTEQALFEMKQNDAAHHGWTTKMDMIFHTIKOHANL 1068

RESULT 4
US-08-162-081B-36
Sequence 36, Application US/08162081B
Patent No. 5824492
GENERAL INFORMATION:
APPLICANT: Hillel, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bales, Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph, Otsu, Masayuki; Panayiotou, George; Volinia,
APPLICANT: Stefano, Gout, Ivan Tarabovich
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,081B
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasquallini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 1080 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-162-081B-36
Query Match 99.1%; Score 5657; DB 2; Length 1080;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1056; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPRPSSGSLMGHILMPRIIVLVECLIPNGMIYTLBELRATLITTHLELFKARAKYPLHQ 60
DB 1 MPRPSSGSLMGHILMPRIIVLVECLIPNGMIYTLBELRATLITTHLELFKARAKYPLHQ 60
QY 61 LLODESSYIFVSTQGAEREEPEDETRRLCDLRFQPLKVEPVGNREKILNREIGFA 120
DB 61 LLODESSYIFVSTQGAEREEPEDETRRLCDLRFQPLKVEPVGNREKILNREIGFA 120
QY 121 IGMVCEFDKVPVQDPRRNLIVCKEAVDLRLDLSPHSRAMVYYPVNESSPELPMH 180
DB 121 IGMVCEFDKVPVQDPRRNLIVCKEAVDLRLDLSPHSRAMVYYPVNESSPELPMH 180
QY 181 IYKLDKGOIIVYIWIYVSPNDKQYTLKINHCVPEQVYAAIRKTRSMILSSQOK 240
DB 181 IYKLDKGOIIVYIWIYVSPNDKQYTLKINHCVPEQVYAAIRKTRSMILSSQOK 240
QY 241 LCYLEQKTIILAVCCDEVELEKYPISOYKYRSCIMLRMNLKMAKESLYSQLPMD 300
DB 241 LCYLEQKTIILAVCCDEVELEKYPISOYKYRSCIMLRMNLKMAKESLYSQLPMD 300
QY 301 CFMPSSYRISTATPYMNGESTKSLMIVNSALRIKILCATYVNVNIRIDIKIYVRTGI 360
DB 301 CFMPSSYRISTATPYMNGESTKSLMIVNSALRIKILCATYVNVNIRIDIKIYVRTGI 360
QY 361 YHGEPLCDNVNTQVPCSNPRNEMLNVDIYIPDLPRARLCLISCVYGRGAKAEHC 420
DB 361 YHGEPLCDNVNTQVPCSNPRNEMLNVDIYIPDLPRARLCLISCVYGRGAKAEHC 420
QY 421 PLANGINLNDYDITLVSQKALNMPVPRGLDLNPIGVTSNPKETPCLELEDFWF 480
DB 421 PLANGINLNDYDITLVSQKALNMPVPRGLDLNPIGVTSNPKETPCLELEDFWF 480
QY 481 SSVYKFPDMSYIEEHAWSVSRAGFSYSHAGLSNRLARNDLRENDKEQLRAICTRDL 540
DB 481 SSVYKFPDMSYIEEHAWSVSRAGFSYSHAGLSNRLARNDLRENDKEQLRAICTRDL 540
QY 541 SEITEQEKDFLMSHRHYCVTIPETLPLKLLSVKNSRDEVAQNYCLVKDMPPIRPEQAME 600
DB 541 SEITEQEKDFLMSHRHYCVTIPETLPLKLLSVKNSRDEVAQNYCLVKDMPPIRPEQAME 600
QY 601 LLDGNYPDPMVGRFAVRCLEKYLTDKLSQYLLIQLVQVLYKEYOYLNDLVRFLKKAALTN 660
DB 601 LLDGNYPDPMVGRFAVRCLEKYLTDKLSQYLLIQLVQVLYKEYOYLNDLVRFLKKAALTN 660
QY 661 QRIQHFFPMHLKSEMHNTKVSQRFGLLLESYCRACGMYLKLNRQVEAMEKLIINTDILK 720
DB 661 QRIQHFFPMHLKSEMHNTKVSQRFGLLLESYCRACGMYLKLNRQVEAMEKLIINTDILK 720
QY 721 QEKKDETQYQKMFVLEQMRPDMALQGLSPINPAHQIQLRLEECRIMSASAKRPLW 780
DB 721 QEKKDETQYQKMFVLEQMRPDMALQGLSPINPAHQIQLRLEECRIMSASAKRPLW 780
QY 781 LNMENPDIMSELLFQNNELIFKNGDDLRQDMLTLQIRIMENIWONQGLDRLMLPYGCLS 840
DB 781 LNMENPDIMSELLFQNNELIFKNGDDLRQDMLTLQIRIMENIWONQGLDRLMLPYGCLS 840
QY 841 IGDGCVGLIEVVRNSHTIMQIQCKGKLGALQFNSHTLQWLKDKNKGSIYDAIDLFTRS 900
DB 841 IGDGCVGLIEVVRNSHTIMQIQCKGKLGALQFNSHTLQWLKDKNKGSIYDAIDLFTRS 900
QY 901 CAGYCVATFIIGIDRHSNIMVAKDQGLPHIDGHEFLDHKKKFGYKREVRVPVLTQDF 960
DB 901 CAGYCVATFIIGIDRHSNIMVAKDQGLPHIDGHEFLDHKKKFGYKREVRVPVLTQDF 960

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QY 961 LVIISGAOECTRTREFEFOEMCYKAYLAIRQHANI.FINLFSMILGSGMPELOSFDDIA 1020  
DB 961 LVIISGAOECTRTREFEFOEMCYKAYLAIRQHANI.FINLFSMILGSGMPELOSFDDIA 1020  
QY 1021 YIRKTLALDKTEOEALEYFMKQNDAAHGGMTTKMDI.FHTTIKOHANL 1068  
DB 1021 YIRKTLALDKTEOEALEYFMKQNDAAHGGMTTKMDI.FHTTIKOHANL 1068

RESULT 5  
US-08-780-872-36  
Sequence 36, Application US/08780872  
Patent No. 5846824  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefano; Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felte & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/780, 872  
FILING DATE: 09-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/162,081  
FILING DATE: February 7, 1994  
APPLICATION NUMBER: PCT/GB93/00761  
FILING DATE: 13 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pasqualini, Patricia A.  
REGISTRATION NUMBER: 34,894  
REFERENCE/DOCKET NUMBER: LUD 5256  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1080 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-780-872-36

Query Match 99.1%; Score 5657; DB 2; Length 1080;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1056; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPPRPSGSGELMGHLMPPRIIVLVECLLPNGMIVTLECLREATLTITIHLEFKKARKYPLHQ 60  
DB 1 MPPRPSGSGELMGHLMPPRIIVLVECLLPNGMIVTLECLREATLTITIHLEFKKARKYPLHQ 60  
QY 61 LIODESSYIFVSVYQAEEREEFFDETRRLCDLRLFQPFLLKVIIBPVGNREKKILNREIGFA 120  
DB 61 LIODESSYIFVSVYQAEEREEFFDETRRLCDLRLFQPFLLKVIIBPVGNREKKILNREIGFA 120  
QY 121 IGMPPCEPFMVDPEVODFRRLNLTNCKEAVLDRLNLSPHSRAMVYYPVIVSSPELPLKH 180  
DB 121 IGMPPCEPFMVDPEVODFRRLNLTNCKEAVLDRLNLSPHSRAMVYYPVIVSSPELPLKH 180

QY 181 IYNKLDKGOIIVIVIVISFNNNDKOKYTLKINHDCVPEQVIAEIRKTRSMILSSSEOLK 240  
DB 181 IYNKLDKGOIIVIVIVISFNNNDKOKYTLKINHDCVPEQVIAEIRKTRSMILSSSEOLK 240  
QY 241 LCYLEYQKYLKLVCCGDEFFLEKYPLOSQYKIRSCIMGRMNMLMAKESLYSQLPMD 300  
DB 241 LCYLEYQKYLKLVCCGDEFFLEKYPLOSQYKIRSCIMGRMNMLMAKESLYSQLPMD 300  
QY 301 CFTMPSYRRISATATPYNNGETSTKSLAWINSAARIKIIICATVNVNIRPIDIYRTGI 360  
DB 301 CFTMPSYRRISATATPYNNGETSTKSLAWINSAARIKIIICATVNVNIRPIDIYRTGI 360  
QY 361 YHGEPLCDNVNTQRPVCSNPRNEMLNVDIYIPDLPRARLCLASICYVGRKGAEEHC 420  
DB 361 YHGEPLCDNVNTQRPVCSNPRNEMLNVDIYIPDLPRARLCLASICYVGRKGAEEHC 420  
QY 421 PLAMGINLPDYDTLVSGMALNLPVPHGLEDLNPIGVTGSNPNKETPCLLEDFDW 480  
DB 421 PLAMGINLPDYDTLVSGMALNLPVPHGLEDLNPIGVTGSNPNKETPCLLEDFDW 480  
QY 481 SSVYKFPDMSVIEEHANWSVSREAGFSYSHAGISNRLARDNELRENDKQOLAICTRDP 540  
DB 481 SSVYKFPDMSVIEEHANWSVSREAGFSYSHAGISNRLARDNELRENDKQOLAICTRDP 540  
QY 541 SEITTEOKDFLMSHRHYCVTIPEILPKLLSVKMSRDEVAQWYCLVKMPPIKPCQAME 600  
DB 541 SEITTEOKDFLMSHRHYCVTIPEILPKLLSVKMSRDEVAQWYCLVKMPPIKPCQAME 600  
QY 601 LLDGNYPDMNVGFAVRCLEKYLTDKLSQYLIOLVOVLKYEQYLDNLVLFLLKALTN 660  
DB 601 LLDGNYPDMNVGFAVRCLEKYLTDKLSQYLIOLVOVLKYEQYLDNLVLFLLKALTN 660  
QY 661 QRTGHPFWMHLSSEMNKTVSOFGLLSYCACGMVYKHNRYQEAENEKILNLTDIK 720  
DB 661 QRTGHPFWMHLSSEMNKTVSOFGLLSYCACGMVYKHNRYQEAENEKILNLTDIK 720  
QY 721 QEKEDTOKYOMFLVEQMRPDPMDALQFSLPAPAHQNLGRLEGRINSASAKPLM 780  
DB 721 QEKEDTOKYOMFLVEQMRPDPMDALQFSLPAPAHQNLGRLEGRINSASAKPLM 780  
QY 781 LNMENPDIWNSHTIMQIOCKGGLKALQFNSHTLHQLMDKXNGEYDAIDFTS 900  
DB 781 LNMENPDIWNSHTIMQIOCKGGLKALQFNSHTLHQLMDKXNGEYDAIDFTS 900  
QY 841 IGDGVLIEVNRSHITMOIOCKGGLKALQFNSHTLHQLMDKXNGEYDAIDFTS 960  
DB 841 IGDGVLIEVNRSHITMOIOCKGGLKALQFNSHTLHQLMDKXNGEYDAIDFTS 960  
QY 901 CAGYCATFILIIGDRHNSINWYKDDGOLFHIIDFGHFLDHKKKKFGYKREVPFVLTDF 960  
DB 901 CAGYCATFILIIGDRHNSINWYKDDGOLFHIIDFGHFLDHKKKKFGYKREVPFVLTDF 960  
QY 961 LVIISGAOECTRTREFEFOEMCYKAYLAIRQHANI.FINLFSMILGSGMPELOSFDDIA 1020  
DB 961 LVIISGAOECTRTREFEFOEMCYKAYLAIRQHANI.FINLFSMILGSGMPELOSFDDIA 1020  
QY 1021 YIRKTLALDKTEOEALEYFMKQNDAAHGGMTTKMDI.FHTTIKOHANL 1068  
DB 1021 YIRKTLALDKTEOEALEYFMKQNDAAHGGMTTKMDI.FHTTIKOHANL 1068

RESULT 6  
US-09-085-957-36  
Sequence 36, Application US/09085957  
Patent No. 6274327  
GENERAL INFORMATION:  
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu  
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter  
APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,  
APPLICANT: Stefano; Gout, Ivan Tarasovitch  
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felte & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022

NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Felle & Lynch  
 STREET: 805 Third Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10022  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: WordPerfect  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/085,957  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/780,872  
 FILING DATE: 09-JAN-1997  
 APPLICATION NUMBER: 08/162,081  
 FILING DATE: February 7, 1994  
 APPLICATION NUMBER: PCT/GB93/00761  
 FILING DATE: 13 April 1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pasqualini, Patricia A.  
 REGISTRATION NUMBER: 34,894  
 REFERENCE/DOCKET NUMBER: LUD 5256  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 688-9200  
 TELEFAX: (212) 838-3884  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1080 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-085-957-36

Query Match 99.1%; Score 5657; DB 3; Length 1080;  
 Best Local Similarity 98.9%; Pred. No. 0;  
 Matches 1056; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPPRSSGELGIMHMPRIIVECLPNGMIITTECLREALTITIKHELFEKARKYPLHQ 60  
 DB 1 MPPRSSSELGIMHMPRIIVECLPNGMIITTECLREALTITIKHELFEKARKYPLHQ 60  
 QY 61 LLODESSYIFVSVTGEAREEFDETRRLCDLRFQPLKVIETPGNREBEKILNEIGFA 120  
 DB 61 LLODESSYIFVSVTGEAREEFDETRRLCDLRFQPLKVIETPGNREBEKILNEIGFA 120  
 QY 121 IGMPCVEFDMVYDEPVOFRRIILNVCKEAVDLRLNSPHSAMVYPPNVESSELPELPH 180  
 DB 121 IGMPCVEFDMVYDEPVOFRRIILNVCKEAVDLRLNSPHSAMVYPPNVESSELPELPH 180  
 QY 181 IYNNKLDKGOIIVIVWIVSPNNDKOKYTLKINHDCVPEQVIAEAIKRTKTRSMLSSEQIK 240  
 DB 181 IYNNKLDKGOIIVIVWIVSPNNDKOKYTLKINHDCVPEQVIAEAIKRTKTRSMLSSEQIK 240  
 QY 241 LCVLEVOGKYILKVGCGDEYFLKXPPLSQYKIRSCIMGRPNMLMAKESLYSQLPMD 300  
 DB 241 LCVLEVOGKYILKVGCGDEYFLKXPPLSQYKIRSCIMGRPNMLMAKESLYSQLPMD 300  
 QY 301 CFTMPSYSRISTATPYNMGETSTSLWVINGALRIKILCATYVWVNNIRIDIKIYRTGI 360  
 DB 301 CFTMPSYSRISTATPYNMGETSTSLWVINGALRIKILCATYVWVNNIRIDIKIYRTGI 360  
 QY 361 YHGGEPICNNVNTORVPCSNPRNENLNDIYIPDLPRARLCLISICSVKRGKANEHC 420  
 DB 361 YHGGEPICNNVNTORVPCSNPRNENLNDIYIPDLPRARLCLISICSVKRGKANEHC 420  
 QY 421 PLAMGNINFDYTDITLVSGKMLNLMPVPHGLEDLNIPIGVTGSNNPKETPCLELEFDWF 480

DB 421 PLAMGNINFDYTDITLVSGKMLNLMPVPHGLEDLNIPIGVTGSNNPKETPCLELEFDWF 480  
 QY 481 SSVKRPDMSVIEBHANSVSRAGSVSHAGLSNRILARDNELRENDKQLRAICTRDL 540  
 DB 481 SSVKRPDMSVIEBHANSVSRAGSVSHAGLSNRILARDNELRENDKQLRAICTRDL 540  
 QY 541 SETTEOKDFLMSHRHYCTTIPILPKLLSVKMSRDEVAQMYCLVKDMPPIKEQAME 600  
 DB 541 SETTEOKDFLMSHRHYCTTIPILPKLLSVKMSRDEVAQMYCLVKDMPPIKEQAME 600  
 QY 601 LLDONYPDMVVRGFAVRCLEKYLTDKLSQYLIQVQVTKYECYLDNLVRLFKALTN 660  
 DB 601 LLDONYPDMVVRGFAVRCLEKYLTDKLSQYLIQVQVTKYECYLDNLVRLFKALTN 660  
 QY 661 QRTGHPFPHLKSEMNKTVSOFGLLESYCRACGMVYKHLNRQVEAMEKILNLTDLK 720  
 DB 661 QRTGHPFPHLKSEMNKTVSOFGLLESYCRACGMVYKHLNRQVEAMEKILNLTDLK 720  
 QY 721 QEKKDETOKVQMFLEVRMRPDMALOGFLSPINPAHQNLRLSECRIMSSAKRPLW 780  
 DB 721 QEKKDETOKVQMFLEVRMRPDMALOGFLSPINPAHQNLRLSECRIMSSAKRPLW 780  
 QY 781 LNMENPDIMSELLFONNEIIFKNGDDLRODMLTLQIIRIMENIWOQGLDLRLPYGLS 840  
 DB 781 LNMENPDIMSELLFONNEIIFKNGDDLRODMLTLQIIRIMENIWOQGLDLRLPYGLS 840  
 QY 841 IGDVGLIEVVRSHITMOIQCKGGLKGAOFNSHTLHOWLKDNKGEIYDAADLFTFS 900  
 DB 841 IGDVGLIEVVRSHITMOIQCKGGLKGAOFNSHTLHOWLKDNKGEIYDAADLFTFS 900  
 QY 901 CAGYCATFIIIGIDRHSNINMYKDCQLEFHIDFGHLDHKKKFGYKRERVPVLTQDF 960  
 DB 901 CAGYCATFIIIGIDRHSNINMYKDCQLEFHIDFGHLDHKKKFGYKRERVPVLTQDF 960  
 QY 961 LIVISKAQECTKREFERFQEMCYKAYLAIRQHANFIVLFSMGLSSGPELOSFDIA 1020  
 DB 961 LIVISKAQECTKREFERFQEMCYKAYLAIRQHANFIVLFSMGLSSGPELOSFDIA 1020  
 QY 1021 YIRKTLALDKTEQALIEFMKQMDAHNGMTTKMDIIFHTIKOHALN 1068  
 DB 1021 YIRKTLALDKTEQALIEFMKQMDAHNGMTTKMDIIFHTIKOHALN 1068

RESULT 7  
 US-08-390-874C-11  
 ; Sequence 11, Application US/08390874C  
 ; Patent No. 6043062  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Klippel, Anke  
 ; TITLE OF INVENTION: A Constitutively Active  
 ; TITLE OF INVENTION: Phosphatidylinositol 3-kinase and Uses Thereof  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/390,874C  
 ; FILING DATE: 17-FEB-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dow, Karen B.  
 ; REGISTRATION NUMBER: 29,684  
 ; REFERENCE/DOCKET NUMBER: 02307K-057000US



TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 576-0200  
 TELEFAX: (415) 576-0300  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1068 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-390-874C-11

Query Match 98.8%; Score 5645; DB 3; Length 1068;  
 Best Local Similarity 98.8%; Pred. No. 0;  
 Matches 1055; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

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QY 1 MPPRPSGELMGHLMPPRLIVECLLPNGMIVTLECLREATLTITIKHELFKEARKYPLHQ 60
DB 1 MPPRPSGELMGHLMPPRLIVECLLPNGMIVTLECLREATLTITIKHELFKEARKYPLHQ 60
QY 61 LLODESSYIFVSTQGAEREFEFDETRRLCDLRFQPLKVIIEPVGNREKILNREIGFA 120
DB 61 LLODESSYIFVSTQGAEREFEFDETRRLCDLRFQPLKVIIEPVGNREKILNREIGFA 120
QY 121 IGMPCFEDMVKDPEVODFFRRNLTNCKEAVDLRLDLSPSHRAMYVPVNESSPELPKH 180
DB 121 IGMPCFEDMVKDPEVODFFRRNLTNCKEAVDLRLDLSPSHRAMYVPVNESSPELPKH 180
QY 181 IYKRLDGOIIVIVWVSPNNOKOYTLKINHCEVOYIAERIKKTSMLSSFOLK 240
DB 181 IYKRLDGOIIVIVWVSPNNOKOYTLKINHCEVOYIAERIKKTSMLSSFOLK 240
QY 241 LCVLEYOGKYLIVYVSPNDQKYLKINHCEVOYIAERIKKTSMLSSFOLK 240
DB 241 LCVLEYOGKYLIVYVSPNDQKYLKINHCEVOYIAERIKKTSMLSSFOLK 240
QY 301 CFMPYSRISITATPYMNGESTKSLWVINSALRIKILCATYVNVNIRIDIKIYVATGI 360
DB 301 CFMPYSRISITATPYMNGESTKSLWVINSALRIKILCATYVNVNIRIDIKIYVATGI 360
QY 361 YHGGEPLCDNVNORVPCSNPRNEMLVNDIYIPDLPRARLCISGVGRGAKKEHC 420
DB 361 YHGGEPLCDNVNORVPCSNPRNEMLVNDIYIPDLPRARLCISGVGRGAKKEHC 420
QY 421 PLAMGNINLFYDITLVSGKALNIMPVPHGLEDLNIPIGVTSNPKETPCLELEDFWF 480
DB 421 PLAMGNINLFYDITLVSGKALNIMPVPHGLEDLNIPIGVTSNPKETPCLELEDFWF 480
QY 481 SSYVKEPDMSVIEBHANVSREAGFSYSHAGLSNRLARDNELENDKEQLRALCTEDPL 540
DB 481 SSYVKEPDMSVIEBHANVSREAGFSYSHAGLSNRLARDNELENDKEQLRALCTEDPL 540
QY 541 SETTEBOKDPLMNGHRYCVTIPILLPLLLSVKNSNDEVAQWCLYKDMPIKPEQAME 600
DB 541 SETTEBOKDPLMNGHRYCVTIPILLPLLLSVKNSNDEVAQWCLYKDMPIKPEQAME 600
QY 601 ILDCNYPDPWVRGFAVRCLEKYLTDKLSOYLLOLVOLKYEOYLDNLVRFLLKKAULTN 660
DB 601 ILDCNYPDPWVRGFAVRCLEKYLTDKLSOYLLOLVOLKYEOYLDNLVRFLLKKAULTN 660
QY 661 QRIQHEFFMHLKSEMINKTVSQRFGLLESYCRACGMVYLGLNRYVAMEKILNLTDLK 720
DB 661 QRIQHEFFMHLKSEMINKTVSQRFGLLESYCRACGMVYLGLNRYVAMEKILNLTDLK 720
QY 721 QEKXDTOKYQMFIVQOMRRPDMALOGFLSPINAHQLGUNRLKECGINSSAKRPLM 780
DB 721 QEKXDTOKYQMFIVQOMRRPDMALOGFLSPINAHQLGUNRLKECGINSSAKRPLM 780
QY 781 LNNENPDIINSELLFONNEIIFKNGDDLRODMLTLOIRIMENIMONOGLLRMLPYCCL 840
DB 781 LNNENPDIINSELLFONNEIIFKNGDDLRODMLTLOIRIMENIMONOGLLRMLPYCCL 840
QY 841 IGDVGLIEVVRNSHTIMOICKGGLKGLAQFNSHTLHQLKDKNGEIVDAAIDLETRS 900
  
```

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DB 841 IGDVGLIEVVRNSHTIMOICKGGLKGLAQFNSHTLHQLKDKNGEIVDAAIDLETRS 900
QY 901 CAGYCVATFLLIGDRHNSNIMWDDGQLPHIDPGLHDKKKKFKRREVPVLNODF 960
DB 901 CAGYCVATFLLIGDRHNSNIMWDDGQLPHIDPGLHDKKKKFKRREVPVLNODF 960
QY 961 LIVISGADECTKTRERFERQEMCYKAYLAIRQHANLFINLPSMMLGSGMPELOSFDIA 1020
DB 961 LIVISGADECTKTRERFERQEMCYKAYLAIRQHANLFINLPSMMLGSGMPELOSFDIA 1020
QY 1021 YIRKTLALDKTEOBALFEPKQWMDAHGGMVTRKMDIFFTIIOHALN 1068
DB 1021 YIRKTLALDKTEOBALFEPKQWMDAHGGMVTRKMDIFFTIIOHALN 1068
  
```

## RESULT 8

```

US-09-265-772-11
Sequence 11, Application US/09265772
Patent No. 6300111
GENERAL INFORMATION:
APPLICANT: Klippel, Anke
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: A Constitutively Active
NUMBER OF INVENTION: Phosphatidylinositol 3-kinase and uses thereof
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265, 772
FILING DATE: 10-MAR-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/390, 874
FILING DATE: 17-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 02307K-057010US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-265-772-11
  
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Query Match 98.8%; Score 5645; DB 4; Length 1068;  
 Best Local Similarity 98.8%; Pred. No. 0;  
 Matches 1055; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

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QY 1 MPPRPSGELMGHLMPPRLIVECLLPNGMIVTLECLREATLTITIKHELFKEARKYPLHQ 60
DB 1 MPPRPSGELMGHLMPPRLIVECLLPNGMIVTLECLREATLTITIKHELFKEARKYPLHQ 60
QY 61 LLODESSYIFVSTQGAEREFEFDETRRLCDLRFQPLKVIIEPVGNREKILNREIGFA 120
DB 61 LLODESSYIFVSTQGAEREFEFDETRRLCDLRFQPLKVIIEPVGNREKILNREIGFA 120
  
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QY 121 IGMVCEFDWVDEVDOPFRNINLVCKEAVDLRLDLSPSHRAMVYVPPNVSSPELPHK 180
DB 121 IGMVCEFDWVDEVDOPFRNINLVCKEAVDLRLDLSPSHRAMVYVPPNVSSPELPHK 180
QY 181 IYNNLDKGOIIVIVWIVSPNNDKOKYTLKINHDCVBEQVIAEAIIRKTRSMILSSQOLK 240
DB 181 IYNNLDKGOIIVIVWIVSPNNDKOKYTLKINHDCVBEQVIAEAIIRKTRSMILSSQOLK 240
QY 241 LCYLEYQSGKYLKVCQDEYFLEKYPISQYKYITSCIMGRMPLMLMAKESLYSQPLMD 300
DB 241 LCYLEYQSGKYLKVCQDEYFLEKYPISQYKYITSCIMGRMPLMLMAKESLYSQPLMD 300
QY 301 CFMPSPSRISTATPYMNGESTSKSLMWINSALRIKILCATYVNVNIRIDIKIYVETGI 360
DB 301 CFMPSPSRISTATPYMNGESTSKSLMWINSALRIKILCATYVNVNIRIDIKIYVETGI 360
QY 361 YHGEPLCDNVNTOQVPCSNPRNEMWINDIYIPDLPRARLCLISCSVGRKKAKEBHC 420
DB 361 YHGEPLCDNVNTOQVPCSNPRNEMWINDIYIPDLPRARLCLISCSVGRKKAKEBHC 420
QY 421 PLWGNINLPDYTTTLVSGKALMLVPYHGLEDLNLPICVTGSPNPKETPCLELEPWF 480
DB 421 PLWGNINLPDYTTTLVSGKALMLVPYHGLEDLNLPICVTGSPNPKETPCLELEPWF 480
QY 481 SSVVKPDMQSYIEEHAMMSVSRGAFSGYSHAGLSNRLARDELRENDKEQLRAICTRDP 540
DB 481 SSVVKPDMQSYIEEHAMMSVSRGAFSGYSHAGLSNRLARDELRENDKEQLRAICTRDP 540
QY 541 SEITEQEKDPLMSHRHYCVTIPILPKLLSVKNNSRDEVQMYCLVQWMPPIRQEQAME 600
DB 541 SEITEQEKDPLMSHRHYCVTIPILPKLLSVKNNSRDEVQMYCLVQWMPPIRQEQAME 600
QY 601 LLDGNYPDPMYRGAIVNRCLEKYLTDCKLSOYLIOLVQYKLEQYLDNLVFLKKAALT 660
DB 601 LLDGNYPDPMYRGAIVNRCLEKYLTDCKLSOYLIOLVQYKLEQYLDNLVFLKKAALT 660
QY 661 ORIGHFFPMHLKSEMHNTKVSQRFGLLESYCRACGMVLEKILNVOEAMEKILNLTDLK 720
DB 661 ORIGHFFPMHLKSEMHNTKVSQRFGLLESYCRACGMVLEKILNVOEAMEKILNLTDLK 720
QY 721 QEKDETOQVOMKFLVEQMRBPDMDALQGFSLPNAHOLGNLRLBECRIMSSAKRPLW 780
DB 721 QEKDETOQVOMKFLVEQMRBPDMDALQGFSLPNAHOLGNLRLBECRIMSSAKRPLW 780
QY 781 LNMENPDIMSEBLFQNNELIFKNGDILFQDMLTLOIIRIMENIQONQGLDRLMLPYGCLS 840
DB 781 LNMENPDIMSEBLFQNNELIFKNGDILFQDMLTLOIIRIMENIQONQGLDRLMLPYGCLS 840
QY 841 IGDVGGLIEVVRNHSHTIWOICKGSLKGLAOFNSHTLQWLKDKXKGEIYDAIDLFTRS 900
DB 841 IGDVGGLIEVVRNHSHTIWOICKGSLKGLAOFNSHTLQWLKDKXKGEIYDAIDLFTRS 900
QY 901 CAGYCVATPILIGIDRHSNINMVKDQGLFIHDFSHFLDHKKKFKYGRERVPVLTQDF 960
DB 901 CAGYCVATPILIGIDRHSNINMVKDQGLFIHDFSHFLDHKKKFKYGRERVPVLTQDF 960
QY 961 LIVISKAQECTKTREFFERFQDMCYKAYLAIRQHANLFINLFSMVLGSGMBELQSFDDIA 1020
DB 961 LIVISKAQECTKTREFFERFQDMCYKAYLAIRQHANLFINLFSMVLGSGMBELQSFDDIA 1020
QY 1021 YIRKTLADKTEQOEALFEMKOMDAHHGWTCKDWIFHTIKQALN 1068
DB 1021 YIRKTLADKTEQOEALFEMKOMDAHHGWTCKDWIFHTIKQALN 1068

```

## RESULT 9

US-08-777-405A-2

Sequence 2, Application US/08777405A

Patent No. 5858753

GENERAL INFORMATION:

APPLICANT: Chantry, David

APPLICANT: Hoeckera, Merl F.

APPLICANT: Holtzman, Douglas A

```

TITLE OF INVENTION: No. 5858753el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5858753and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1044 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-777-405A-2

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Query Match 34.7%; Score 1978.5; DE 2; Length 1044;

Best Local Similarity 39.9%; Pred. No. 3.1e-195;

Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

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QY 16 MPP-----RLVECLPNGMIVTLECREATLTIKHELFKARKYPLHQ 60
DB 1 MPPGVDCPMEFWTKENQSVVVDLPTGYLNPVSRNANLSTIKOLLHRAQYELFH 60
QY 61 LLDSESYIFVSVTQEAERSEFPDETRLCDLRFOPFLVYIEBVNGREEKILNREIGFA 120
DB 61 MLSGPEAVVFTCINQTAEQLEDEQRRLCDVQFPLVLRVAREGDRVKKLINSQSL 120
QY 121 IGMVCEFDWVDEVDOPFRNINLVCKEAVDLRLDLSPSHRAMVYVPPNVSSPE 176
DB 121 IGMVCEFDWVDEVDOPFRNINLVCKEAVDLRLDLSPSHRAMVYVPPNVSSPE 176
QY 177 -----LPHIYNNLDKGOIIVIVWIVSPNNDKOKYTLKINHDCVBEQVIAEAIIRKTRSM 232
DB 177 -----LPHIYNNLDKGOIIVIVWIVSPNNDKOKYTLKINHDCVBEQVIAEAIIRKTRSM 232
QY 223 LLSSEQLKLCVLEYQGYKYLKVCQDEYFLEKYPISQYKYITSCIMGRMPLMLMAKES 292
DB 223 LLSSEQLKLCVLEYQGYKYLKVCQDEYFLEKYPISQYKYITSCIMGRMPLMLMAKES 292
QY 225 ---ATVFRQPLVEBPEDYTLQVNRHLYLGNVYLCQFOYICSLHSGTLTMVHSS 281
DB 225 ---ATVFRQPLVEBPEDYTLQVNRHLYLGNVYLCQFOYICSLHSGTLTMVHSS 281
QY 293 LYSQPLMDCFTMPSYRISTATPYMNGESTSKSLMWINSALRIKILCATYVNVNIRIDID 352
DB 293 LYSQPLMDCFTMPSYRISTATPYMNGESTSKSLMWINSALRIKILCATYVNVNIRIDID 352
QY 328 ILARDEQSNAPQVQPRAKPPIPAKKESVSLMSLEQFFRIELIGSVYNADER--M 339
DB 328 ILARDEQSNAPQVQPRAKPPIPAKKESVSLMSLEQFFRIELIGSVYNADER--M 339
QY 340 KLIVQAGLFHGENMLCKTVSSSEVSCSEPVAKORLEFDINICDLPRAKCFPLAYVIE 399
DB 340 KLIVQAGLFHGENMLCKTVSSSEVSCSEPVAKORLEFDINICDLPRAKCFPLAYVIE 399
QY 410 -----KGRKAKSEHCPILWGNINLPDYTTTLVSGKALMLVPYHGLEDLNLPICVT 462
DB 410 -----KGRKAKSEHCPILWGNINLPDYTTTLVSGKALMLVPYHGLEDLNLPICVT 462
QY 400 KAKARSTKKSADCPDIAMANLMLFDYKQOLKTGERCLYMWSSVPEKELLNPTGT 459
DB 400 KAKARSTKKSADCPDIAMANLMLFDYKQOLKTGERCLYMWSSVPEKELLNPTGT 459
QY 463 GSNPNKETP-----CLELEFPWFSSVVKFPMMSVIEEHAMMSVSRGAFSGYSHAGLSNRL 517
DB 463 GSNPNKETP-----CLELEFPWFSSVVKFPMMSVIEEHAMMSVSRGAFSGYSHAGLSNRL 517
QY 460 RSNPNTDAAALLICLP---EVAPHPVYYPALKEILE-----L 494
DB 460 RSNPNTDAAALLICLP---EVAPHPVYYPALKEILE-----L 494

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QY 518 ARDNE---LRNDKEQLRAICTRDPLESEITEOEKDFIMSHRYCVT-IPEILPKLLLSVK 573
D 495 GRHSECVHYTEBEOLOREILERRSGSEIYEHEKDLVWKLREHVEQHEPPEALRLLVTK 554
QY 574 WNSRDEVAQMYCLVMDWPIKPEQAMELLDCNYDPMPVNGAVRCLEKYLITDDKLSQYL 633
D 555 WNKHEBVAQMYLLCSWPPELVLSALBLLDFSPDCHGVSAFKSLRK-LTDBELFYLL 613
QY 634 QLVQVLYKESYLDNLVRLFLKALTNORIGHFFFWHLKSEMHNTVSORFGLLESYCR 693
D 614 QLVQVLYKESYLDNLVRLFLKALTNORIGHFFFWHLKSEMHNTVSORFGLLESYCR 673
QY 694 ACGMYLKLHNRQVAMEKILNTDILKOEKKDETQVOMKFLVBO-MRRPDMDLQGL 752
D 674 GSTHMKVLMKQGBALSKLALNDFVLLSSQ-KTRPKQTKELMHLCMROEAVYLEASHIQ 732
QY 753 SPLNPAHQNLRLBECRIMSSAKRPLMLMWNENDIMSELLFQNNELIFKNGDDLRODML 812
D 733 SPLDSTLLAEVCEQCTFMDSKMKPLMIMYSNEEAGS---GSVGIIFKNGDDLRODML 789
QY 813 TLQIIRIMENIQNOGLDRLMLPYGCLSIGDVCGLIEVRNSHTIMQIQ-KGGLKGLQ 871
D 790 TLQMIQMDVLMKQGBALSKLALNDFVLLSSQ-KTRPKQTKELMHLCMROEAVYLEASHIQ 849
QY 872 FNSHTLHQLKDKNKGRIYDAIDLFTSCAGYCVATFLLIGDRHNSIMVXDDGLFH 931
D 850 FNDKALNMLKSKNPGALDRAIEEFTLSCAGYCVATYVIGDRHNSIMVXDDGLFH 909
QY 932 IDGHLFDHKKKFGYKREVPVLTODFLIVISKAOECTKRIHREFQEMCYKAYLAI 991
D 910 IDGHLFDHKKKFGYKREVPVLTODFLIVISKAOECTKRIHREFQEMCYKAYLAI 967
QY 992 ROHANIPLNFSAWMLGSGMPELOSPDIAIYIRKTLADKTEOEALXEFMKNMDAHNGW 1051
D 968 RRGGLFLHFLALMRAAGLPELSCSDIYQIKOSLALGKTEEBELKHFVKEALRESW 1027
QY 1052 TTYMDWIFHTIKQ 1064
D 1028 KTKVNLVLAHVSK 1040

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RESULT 10
US-08-977-871A-2
; Sequence 2, Application US/08977871A
; Patent No. 5882910
;
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5882910el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borum
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/977, 871A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/777,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5882910and, Greta E.

```

```

;
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1044 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-977-871A-2
;
Query Match      34.7%; Score 1978.5; DB 2; Length 1044;
Best Local Similarity 39.9%; Pred. No. 3.1e-195;
Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;
;
QY 16 MPD-----RILVECLLPNGMIVTLAECLREATLITIKHELFKEARKYPLHQ 60
D 1 MPPGVDCEPMEFWTKENQSVVDFLLPTGVYLNFPVSRNANLSTIKQLMHRNQYERLFH 60
QY 61 LLODESSYIFVSTQAEERBEFFDETRRLCDRLFPQFLKVIKBPVGNREKILNREIGFA 120
D 61 MLSGPAAYFTCINQTAEOOLEDEQRRLCDVQFPFLVRLVAREGDRVKKLINSQISLL 120
QY 121 IGMVCEPMPVMDPEVODRRNRLNLANCYKCAVLDRLNLSHRAAMYPPRVSSPE---- 176
D 121 IKGGLHEPFLSCPEVNDPRACKQCFCEBAARQOLGWEAMLYQFPQLEPSAQTWGP 180
QY 177 ----LRKHLYNKLKDKQIIVIVIVISPNNDKQKYLKINHDCVPQVIAEAIRKTRSM 232
D 181 GLRLPLNR-----ALLVNVKFEGBESSEFTFOYSTDVPLALMAALARK----- 224
QY 233 LLSSEDLKLCVLEYQKYLKVCDCDEYFLKYPYSQYVIRSCINLGMPPMLMAKES 292
D 225 ---ATVRFQPLVEQPEDYTLQVNGRHEVLYGNVPLCQFYICSLHSGTLPHLTVHSSS 281
QY 293 LYSQLPMDCTMPSYRRISTATPYNNGSTSTKSLMIVINSALRIKILCATYVNVNRID 352
D 282 ILAMRDEQSNPAVOVKPRAPKEPPIPAKPPSSVLSLSLPFRILDIQSKVADDER--M 339
QY 353 KIYVRTGIYHGEPLLDNVNTOVRP-CSNPRNEMLNTYDIYIPDLPRARLCLISGV-- 409
D 340 KLVQNGKLGNGEMLCKTVSSSEVSVCSPEVWKQRIEPIINICDLPRMARLCPALYAV 399
QY 410 -----KGRKGAKEBHCPLAMGNINLFDYTDLVSGKMLNIMP-VPHGLJEDLNPIGVT 462
D 400 KAKKARSTKKSADKADCPIAMANLMLFDYDQDKTGERCLTVMPVSPDEKGLNPTGV 459
QY 463 GSNPNKETP-----CLELEFDMFPSSVYKPPDMSVIEEHNAMSVSREAGFSYHAGLSNRL 517
D 460 RSNPNTDSAAALLICLP---EVAHPHVYVPALEKLE-----L 494
QY 518 ARDNE---LRNDKEQLRAICTRDPLESEITEOEKDFIMSHRYCVT-IPEILPKLLLSVK 573
D 495 GRHSECVHYTEBEOLOREILERRSGSEIYEHEKDLVWKLREHVEQHEPPEALRLLVTK 554
QY 574 WNSRDEVAQMYCLVMDWPIKPEQAMELLDCNYDPMPVNGAVRCLEKYLITDDKLSQYL 633
D 555 WNKHEBVAQMYLLCSWPPELVLSALBLLDFSPDCHGVSAFKSLRK-LTDBELFYLL 613
QY 634 QLVQVLYKESYLDNLVRLFLKALTNORIGHFFFWHLKSEMHNTVSORFGLLESYCR 693
D 614 QLVQVLYKESYLDNLVRLFLKALTNORIGHFFFWHLKSEMHNTVSORFGLLESYCR 673
QY 694 ACGMYLKLHNRQVAMEKILNTDILKOEKKDETQVOMKFLVBO-MRRPDMDLQGL 752
D 674 GSTHMKVLMKQGBALSKLALNDFVLLSSQ-KTRPKQTKELMHLCMROEAVYLEASHIQ 732
QY 753 SPLNPAHQNLRLBECRIMSSAKRPLMLMWNENDIMSELLFQNNELIFKNGDDLRODML 812
D 733 SPLDSTLLAEVCEQCTFMDSKMKPLMIMYSNEEAGS---GSVGIIFKNGDDLRODML 789

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QY 813 TLQIIRIMENIMONOGDLRLMLPYGCLISGDCVGLIEVVRNSHTIMQIC-KGGLKALQ 871  
 DB 790 TLQMIQMDVLMKQEBGLDRLMTYGLPTGDRGLIEVLRSDTIANIQLNKSNAATAA 849  
 QY 872 FNSHTLHOMLKDKNKEIYDAIDLPTRSCAGYCVATFIIIGDRHNSNIMVKDQGLF 931  
 DB 850 FNDALMLNLMKSKNPGELDRAIEEFTLSCAGYCVATYVIGIDRHSNDIMIRESGQLF 909  
 QY 932 IDFGHFLDHKKKFGYKREVPVLTODFLIVISKAGQECTKTREPERFOEMCYKAYLAI 991  
 DB 910 IDFGHFLGNFKTFGINREVPFLITYDFVAVIQG--KTNNSEKFERFRGECERAYTIL 967  
 QY 992 ROHANLFINLFSMMLGSGMPELOSFDDIAYIRKTLALDKTEOALEYFMKQMDAHNGW 1051  
 DB 968 RRGGLFLHLFLALMRAAGLPELSCSKDIQYLKDSLALGKTEEBALKHFRVKFNEALRESW 1027  
 QY 1052 TTKMDWIFHTIKQ 1064  
 DB 1028 KTKVNLMLAHNVSK 1040

RESULT 11  
 US-09-225-951-2  
 ; Sequence 2, Application US/09225951  
 ; Patent No. 5985589  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chantry, David  
 ; APPLICANT: Hoeckstra, Merl F.  
 ; APPLICANT: Holtzman, Douglas A  
 ; TITLE OF INVENTION: No. 5985589e1 Lipid Kinase  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSES: Marshall O'Toole Gerstein Murray & Borun  
 ; STREET: 6300 Sears Tower/233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Parentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/225,951  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: No. 5985589and, Greta E.  
 ; REGISTRATION NUMBER: 35,302  
 ; REFERENCE/DOCKET NUMBER: 27866/33441  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (312) 474-6300  
 ; TELEFAX: (312) 474-0448  
 ; TELEX: 25-3856  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1044 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-225-951-2

Query Match 34.7%; Score 1978.5; DB 2; Length 1044;  
 Best Local Similarity 39.9%; Pred. No. 3.1e-195;  
 Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;  
 QY 16 MPP-----RLIVECLPNGMIVLVLECLREATLTITIGHELPEKREKRYPLHQ 60  
 DB 1 MPPGVDCPMEFWTKENOSVVDPLPTGVYLVNFPVSRNANLSTIQQLMHRAQYEPLEH 60  
 QY 61 LLDDESSYIFVSVTQEAEREPEFDETRRLCDRLFLQFPLKVLIEPVGNREBEKILNREIGFA 120

DB 61 MLSGEAYVFTCTINGTATQEBQLEDEQRRLCDVQPPVLRLVARBGRVKKLINSQISLL 120  
 QY 121 ICMPECFDMVKDPEVQDFRNNILNVCKEAVLDRLNSHSAAMYVPPNVSSPE---- 176  
 DB 121 IKGGLHFDLSLCPDEVNDFRAKQCFCEEAARROQLGWEALQYSFPQIDPSPQATWGP 180  
 QY 177 ----LPKXLYNLDKQIIVVIMVIVSPNNNDOKYTLKINHCPVEQVIAEAIKRTKSM 232  
 DB 181 GTLRPLNR-----ALLVVKFEGSESEFTFOYSTQDVPLALMACLRKK---- 224  
 QY 233 LLSSEQLKLCVLEYQKYLKVGCDDEYLEKRYPSQYKIRSCIMLGMPULMAKKS 292  
 DB 225 ---ATVFRQVIVQBPEDYTLQVNGRHELYGVNPLQCFYICSLHSGLTPLHLMVHSSS 281  
 QY 293 LYSQLEMDCTFMPYSRRISTATPYMNGSTSKSLNVLNVALRIKILCTVYNNVNRDID 352  
 DB 282 ILMRDEQSNPAFQVQKPRAPKPPPIPAKPRSSVSLSLQPRFIELIQSKVADDER--M 339  
 QY 353 KIYVRTGIYHGGEPICDNVNTQRP--CSNPRNEMVNTYDIYIPDLPRARLCLTICSV-- 409  
 DB 340 KLVVQAGLFGHGMELCKTVSSSEVSVCEBPWKQRLFPDINICDLPRMARLCPALAVIE 399  
 QY 410 -----KGRKAKEHCPLAMGNINLPDYTDLVSGMALNIMP-VPHGLELIDLPICVT 462  
 DB 400 KAKKASTKKSKKADCPIMANMLPDKDQDKTGRCILYMPSPVDEKGEILNPTGV 459  
 QY 463 GSNPNKETP-----CLELEFDFWFSVYKPPDMGVIEEHANMVSRRAGFSYHAGLSNRL 517  
 DB 460 RSNPNTDSAAALILCP---EVAPHPVYPALKEIE-----L 494  
 QY 518 ARDNE---LRNDKEOLRAICTRDPLEIPEOKDFMFSHRHYCVT-IPILPKLLSVK 573  
 DB 495 GRHSECVHTEESQLOREILERRGSELYEHKKDLVWKLHVEQHEFFPALRLLLVTK 554  
 QY 574 WNSRDEVAQYCVLWKDMPPIKPEQAMELDCNYPDPVWRCFAVRCLEKYLTDKLSOYL 633  
 DB 555 WNKHEDYAOVLVILYLCSPRELPVLSALELDPSFDCVGSFAIKSLRK-LTDELFPQYLL 613  
 QY 634 QLVQVLKYEQYLDNLVFLIKKALTNQRIGHFFFWHLKSEMNKTYSQRFGLLESYCR 693  
 DB 614 QLVQVLKYESYLDDELTKFLDRALANRXIGHFLRSEMHVPVALRFGLLIEAYCR 673  
 QY 694 ACGMYLKLHNRQVAMKILNLTDLKQEKKEDEQYQKMFVLRQ-WRRDPFMDALQGL 752  
 DB 674 GSTHMKVLMKQGBALSKLALNDFVLSGQ-KTRKQTEKLMHLCKRQEAYLEALSHLQ 732  
 QY 753 SPLPAHQNLRLBECRIMSSAKRPMLNWNENDIMSELLFONNEIIFKNGDDLRODML 812  
 DB 733 SPLDPSTLAEVCYEQCTFMDSKKPLMIVSNBEAGSG--GSVGIIIFKNGDDLRODML 789  
 QY 813 TLQIIRIMENIMONOGDLRLMLPYGCLISGDCVGLIEVVRNSHTIMQIC-KGGLKALQ 871  
 DB 790 TLQMIQMDVLMKQEBGLDRLMTYGLPTGDRGLIEVLRSDTIANIQLNKSNAATAA 849  
 QY 872 FNSHTLHOMLKDKNKEIYDAIDLPTRSCAGYCVATFIIIGDRHNSNIMVKDQGLF 931  
 DB 850 FNDALMLNLMKSKNPGELDRAIEEFTLSCAGYCVATYVIGIDRHSNDIMIRESGQLF 909  
 QY 932 IDFGHFLDHKKKFGYKREVPVLTODFLIVISKAGQECTKTREPERFOEMCYKAYLAI 991  
 DB 910 IDFGHFLGNFKTFGINREVPFLITYDFVAVIQG--KTNNSEKFERFRGECERAYTIL 967  
 QY 992 ROHANLFINLFSMMLGSGMPELOSFDDIAYIRKTLALDKTEOALEYFMKQMDAHNGW 1051  
 DB 968 RRGGLFLHLFLALMRAAGLPELSCSKDIQYLKDSLALGKTEEBALKHFRVKFNEALRESW 1027  
 QY 1052 TTKMDWIFHTIKQ 1064  
 DB 1028 KTKVNLMLAHNVSK 1040

RESULT 12

US-09-841-341-2  
 ; Sequence 2, Application US/09841341  
 ; Patent No. 6518277  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SADBHU, Chanchal et al.  
 ; TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA  
 ; FILE REFERENCE: 27866/361708  
 ; CURRENT APPLICATION NUMBER: US/09/841.341  
 ; CURRENT FILING DATE: 2001-04-24  
 ; PRIOR APPLICATION NUMBER: 60/199,655  
 ; PRIOR FILING DATE: 2000-04-25  
 ; PRIOR APPLICATION NUMBER: 60/238,057  
 ; PRIOR FILING DATE: 2000-10-25  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1044  
 ; TYPE: PRT  
 ; ORGANISM: Human p110delta protein  
 US-09-841-341-2

Query Match 34.7%; Score 1978.5; DB 4; Length 1044;  
 Best Local Similarity 39.9%; Pred. No. 3.1e-195;

Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

QY 16 MPD-----RILVECLLPNGMIVTLECLREATLITIKHELFKARKYPLHQ 60  
 DB 1 MPGVDCPMEFWTKEENOSVVDVFLPTGYVLPVSRNANLSTIKQLMHRQAQYELFH 60  
 QY 61 LLODESSYIFVSTOAEAREEFPEDETRRLCDRLPOFLVIEVGNREKILNREIGFA 120  
 DB 61 MMSGPEAYVFTCTINOTAEQOELEDEQRRLCDVOPFLVRLVARREGDRAVKKLINSQISLL 120  
 QY 121 IGMVCEFDVVKDPEVODFRRNILLNVCKEAVDLRLDINSFHSRAMVYVPPNVESSE 176  
 DB 121 IGGHIEFBSLCPDEVNDFRAKWCQCEEAARQOLGWEAMLOYSFPLQLEPSAQTWGP 180  
 QY 121 IGGHIEFBSLCPDEVNDFRAKWCQCEEAARQOLGWEAMLOYSFPLQLEPSAQTWGP 180  
 DB 121 IGGHIEFBSLCPDEVNDFRAKWCQCEEAARQOLGWEAMLOYSFPLQLEPSAQTWGP 180  
 QY 177 ----LPKHLYNKLDKGOIIVIVWIVSPNNDKOKYTLKINHDCPEQVIAEAIKRTKRS 232  
 DB 181 GTLRLPNR-----ALLVNVKFESESESFTOVSTKVPPLALMACALARKK---- 224  
 QY 233 LLSSEQLKLCVLEYGQKYLKVCGCDEYFLKYPPLSOYKIRSCIMLGRMPLIMAKES 292  
 DB 225 ---ATVFRPQLPQEDYTLQVNGRHEYLGNYPPLCOFYICSLHSGLTPHLTMVHSS 281  
 QY 293 LVSGQLMDCFTMSYARRISATPYNNGESTKSLWVINALIKILCATVYVNVNRDID 352  
 DB 282 ILLMRDEQSNPAQOVQEPRAKPPPIPAKPPSSVSLMSLEQPFRIELIQSKVADNR--M 339  
 QY 353 KIIVRTGIYHGBEPLCDNVNTQRP--CSNPRMNMWINDYDIYIPDLPPAALCLSGSV-- 409  
 DB 340 KLVVQGLPFGNMLCKTVSSSEVSCSEPVWKQRLFDINTCDLPRMARLCCALAVIE 399  
 QY 410 ----KRRKGAKEHCPLAMGININFDTYTLVSGMALNLMP--VPHGLEDLNPIGYV 462  
 DB 400 KAKKASTYKKSKKACCPIMANMLFDYDQKLTGSRCLYMPBPVYDEKGEGLNPTGT 459  
 QY 463 GSNPNKETP-----CLELEFDWSSVVKPPDMVIEBHANMWSRAGPSYAGLSNRL 517  
 DB 460 RSNPNDSAAALLICRP--EVAHPVYYPALKEILE-----L 494  
 QY 518 ARDNE---LRNDKEOLRAICTRDPLEITEOKDFLMSHRHYCVT--IPETLPKLLLSYK 573  
 DB 495 GRHSECVHTTEEQOLRLRELRSGGELYEHKDLVWKLRHEVQHFPAALRLLLVTK 554  
 QY 574 WNSRDEVAQNYCLVKKWPIPKQEAELLDCNYPDEWVRGFAVRCLEKYLITDCKLSQYLI 633  
 DB 555 WNGHEVVAQMYLLICSMPELPVLSALELDFSPDCGVGSFAIKSLRK--LTDEDELFOYLL 613  
 QY 634 QLVQVLYKVEQYLDNLVRLFKKALTNORIGHFFPHLKSSEMNKTVSQRFGLLESYCR 693  
 DB 614 QLVQVLYKVESYLDLCELTFLDLRALNARKIGHFLFWHLRSEMHVPVALRFGILLEYCR 673

QY 694 ACQWYLKHLNROYEAMEKLIINTDILKOEKDETOKVOMKFLVEQ--NRBDFMALOGFL 752  
 DB 674 GSTHMKVLMKQGEALSKLKALNDFVYKLSQ--KTPKPQTEKLEHLNLCRGQAVYLEALSHLQ 732  
 QY 753 SPLNPAHQNLNLEECRIYSSAKRPLYMWEPPDIMSSELLFONNEIIFKNGDLDRODM 812  
 DB 733 SPLDPSTLLAEVVEECTFMDSTOKPLMIMYSNEAGSG---GSVGIIFFKNGDLDLQMDL 789  
 QY 813 TLQIIRMENTINONOGDLRMLPYGCLSGDCCGLLEVRNNSHTIQIOG--KGLKGLALQ 871  
 DB 790 TLOMIQMDVLMKQGBGLDRLMTYGLPTGDRGLLEVLRSTPIANIQKSNMATAA 849  
 QY 872 FNSHTLHOMLKDKNKEIYDAIDLEFTRSCAGYCVATFIIIGDRHNSNIMVXDDGLFH 931  
 DB 850 FNKDALNMLKSNKPEALDRAIEEFTLSCAGYCVATYVIGIDRRSDNIMRESGLFH 909  
 QY 932 IDFGHFLDHKKKKFGYKREVPFVLTQDPLIVISKAQOECTKREPERFOEMCYKAYLAI 991  
 DB 910 IDFGHFLGNFKTKFGINREVPFILTYPFVHVIQOG--KTNNSEKEFERFGYCERAVTIL 967  
 QY 992 ROHANLFINLFSMMLSGSMPELOSFDIAYIRKTLALDKTEDEALEFMKQMDAHNGW 1051  
 DB 968 RRGGLFLHLFLMRAAGPELSCSKDIQYLKDSLALGTEBEALKHFRVKEALRESW 1027  
 QY 1052 TTKMDWIFHTIKQ 1064  
 DB 1028 KTKVMMLANVSK 1040

RESULT 13  
 US-09-194-640A-1  
 ; Sequence 1, Application US/09194640A  
 ; Patent No. 6482623

; GENERAL INFORMATION:  
 ; APPLICANT: Van Hasebroeck, Bart  
 ; APPLICANT: Waterfield, Michael D.  
 ; TITLE OF INVENTION: No. 6482623el Lipid Kinase  
 ; FILE REFERENCE: 2332-1-002  
 ; CURRENT APPLICATION NUMBER: US/09/194,640A  
 ; CURRENT FILING DATE: 1998-12-01  
 ; PRIOR APPLICATION NUMBER: PCT/GB97/01471  
 ; PRIOR FILING DATE: 1997-05-30  
 ; PRIOR APPLICATION NUMBER: 9611460.8  
 ; PRIOR FILING DATE: 1996-06-01  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1044  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-194-640A-1

Query Match 34.6%; Score 1976.5; DB 4; Length 1044;  
 Best Local Similarity 39.9%; Pred. No. 5e-195;  
 Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

QY 16 MPD-----RILVECLLPNGMIVTLECLREATLITIKHELFKARKYPLHQ 60  
 DB 1 MPGVDCPMEFWTKEENOSVVDVFLPTGYVLPVSRNANLSTIKQLMHRQAQYELFH 60  
 QY 61 LLODESSYIFVSTOAEAREEFPEDETRRLCDRLPOFLVIEVGNREKILNREIGFA 120  
 DB 61 MMSGPEAYVFTCTINOTAEQOELEDEQRRLCDVOPFLVRLVARREGDRAVKKLINSQISLL 120  
 QY 121 IGMVCEFDVVKDPEVODFRRNILLNVCKEAVDLRLDINSFHSRAMVYVPPNVESSE 176  
 DB 121 IGGHIEFBSLCPDEVNDFRAKWCQCEEAARQOLGWEAMLOYSFPLQLEPSAQTWGP 180  
 QY 121 IGGHIEFBSLCPDEVNDFRAKWCQCEEAARQOLGWEAMLOYSFPLQLEPSAQTWGP 180  
 DB 121 IGGHIEFBSLCPDEVNDFRAKWCQCEEAARQOLGWEAMLOYSFPLQLEPSAQTWGP 180  
 QY 177 ----LPKHLYNKLDKGOIIVIVWIVSPNNDKOKYTLKINHDCPEQVIAEAIKRTKRS 232  
 DB 181 GTLRLPNR-----ALLVNVKFESESESFTOVSTKVPPLALMACALARKK---- 224  
 QY 233 LLSSEQLKLCVLEYGQKYLKVCGCDEYFLKYPPLSOYKIRSCIMLGRMPLIMAKES 292

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Db 225 ---ATVFRQIVBQPDYTLQVNGRHEVLYGSYPLCGFYICSLHSGLTPLHLMWSSS 281
Qy 293 LYSQLEPMDCTFMSYSRRISTATFPMNGETSTSLWVINALIKLCAVYVNVIRID 352
Db 282 ILAMDEQSNPAQOVQFPAKPPPIPAKSSSVLSLEQPFRIELIQSKVADER--M 339
Qy 353 KIYVRGIYHGEPLCDNVTORV--CSNPRMWMINVDIYIPDLPRARLCLSTGCV-- 409
Db 340 KLVVQAGLEFGNEMLCTVSSSEVSVSEVWVQORLEFDINICDLPRMARLCAVAVIE 399
Qy 410 -----KGRKAKEBHCPLAMGNINLPDYDTIVSGMALNMP--VPHGEDILNPIGVT 462
Db 400 KAKKASTKKSKKADCPRIAMNLMFDYKQKKTGERCLYMPSPVDEKGEILNPGTV 459
Qy 463 GSNPNKTEP-----CLELEFDWSSSVYKFPDMSTIEEHAMWSREAGFSYHAGLSNRL 517
Db 460 RSNPNTDSAAALLICLP---EVAHPYYPALKEKILB-----L 494
Qy 518 ARDNE--LAENDKEQJRAICTRDPLEITEOEKDFLMSHRHYCVT-1PEILPCLLSVK 573
Db 495 GRHSECVHVEEEOJQREILERSGSELYHEKOLVYKLRHVEQHPPEALRALLVTK 554
Qy 574 WNSDEVAOMYCYKDMPPIKPEQAMELLDCNYPDPVVRGFAVRCLEKYITDYLQSYLI 633
Db 555 WNKEDVAMOMLYLCSMBELPVLSALBELDPSFPDCHVGFALIKLRK-LTDDLEFOYLL 613
Qy 634 QLVOLKYEBOYLDNLVRFELKALVYNORIGHFFFMHLSKSMNKYTSQREGLLESYCR 693
Db 614 QLVOLKYESYDELTEFLDLRALANKIGHFLFWHLRSEMHVSVALARGLLEAVCR 673
Qy 694 ACGMYLKLHNOVAMEKILNLTILKQEKDETOXOMKFLVQO-MRRPDMALQOGL 752
Db 674 GRTHMKVLMQGEALSLKALNDFVLSQ-KTPKPTKELMHLCHQGEAVLELSHQ 732
Qy 753 SPLNPAHQNLRLSECRIMSASAKPLMINNPDIMSELLFONNEIIFKNGDDIRQML 812
Db 733 SPLDBSTILAVCVCQCTFMSXMKPLMIMWSNEAGSG--GSVGIIFKNGDDIRQML 789
Qy 813 TLQIIRIMENIWQNGLDIRMLPYCCLSIGDCVGLIEVVRNSHTIMOQC-KGGLKALQ 871
Db 790 TLQMIQLMDVLMKQGLDLMTPYGLPTGDRGTGLEIVLRSDTIANIQLNKSNAATPA 849
Qy 872 FNSHTLQMLKDKNGEYIDAIDLFTSCAGYCATFLIGDRHNSINIMWQDGOFLH 931
Db 850 FNKDALMLWLSKNGEALDRAIEFTLSCAGYCATVYLGIDRHSNIMIRESGQLFH 909
Qy 932 IDFGHFLDHKKKFGKERVFPVLTODFLVYSKGAOECTKTRFEFERQEMCYAYLAI 991
Db 910 IDFGHFLGFKTRFGINRERVPFILTYDFVHVIQGS-KTNNSKEREFRGYCERAYTIL 967
Qy 992 ROHANLFINLFSMILSGMPELOSPDDIAYIRKTLALDTEQDALEYFMKQNDADHGM 1051
Db 968 RHGGLLEHFLPALMRAAGPELSCSKDIQYLDKSLALGKTEBBALMGFVKNENALRESW 1027
Qy 1052 TTKMDWTFHTIKO 1064
Db 1028 KTKVMMLAHNVSK 1040

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RESULT 14
US-08-916-917-14
Sequence 14, Application US/08916917
Patent No. 5856132
GENERAL INFORMATION:
APPLICANT: Stephens, Ien
APPLICANT: Braxelmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP

```

```

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: Fastseq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,917
FILING DATE: 15-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/672,211
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8549-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1101 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5856132e
US-08-916-917-14
Query Match 25.7%; Score 1467; DB 2; Length 1101;
Best Local Similarity 35.3%; Pred. No. 3,7e-142;
Matches 358; Conservative 179; Mismatches 352; Indels 126; Gaps 33;
Qy 107 NREKIILREIGFALGMPVCEFDVNVKDPVEODPPRRINLNVCKEAVDRLDLSPRHMYV 166
Db 143 SEESQAFQROLTALIGYDVVDVSNVHDELEFTRGLVTPRMAEVASRD-----PKLYA 196
Qy 167 YRPVNESPELPHKINVKLDKGOIIVYIYVIVSPNNDKQYTKLKHNDVCVEQVIAAIR 226
Db 197 MHPWTSKP-LPEYLMKKIANNCIFVI-----HRTSQTIVKSPDDPGALLOSGFFT 249
Qy 227 K-KTRSMILSSEQDKLVLEYQGYLIKVCDEYELEKYPISQYKYNISCMIGMKN 284
Db 250 KMAKKKSLMDIPES-----QSEQDFVLRCGRDEYLVGETPIKNFQVVRHCLNNGEIRH 303
Qy 285 LML-----MAKESLYSQLPM--DCTMPSYSRRISTATPYMNGE---TSTKSLMVINS 332
Db 304 VVLDTPPPALDEVYKEEMPLVDDCTGVTGYHEQULT-----IHGDHESVFTSLMDCR 358
Qy 333 ALRITLCAVYVNVNIRID-----KIYVRTGIYHGEPELCDNVNTQRPVCSNPR 382
Db 359 KFRVK-----IRGIDIPVLPRNTDLVYVEANIOHQOQVLCQRTSPKPFTEVYL 408
Qy 383 WNEMLNVDIYIPDLPRARLCLSTGCVK-----GKRGAKEBHCPLAMGNINLPDYDTIV- 437
Db 409 WNVVLEFSIKIDLPKGLALNLIQYCGKAPALSSAESAESSSESGKGYRLLYVNNLLI 468
Qy 438 -----SGKALNLMVPVPHGED--LNPICVYTG-SNPNKE-TPCLELEFPWFSSVXF 486
Db 469 DHRFLLRGEYVLHMQWISGKGEDQSFNADLTLSATPDKENSISITLLNCHPPLAL 528
Qy 487 PMSVSTIEEHAMWSVREAGFSYHAGLSNRLARNDKEQJRAICTRDPLEITEQ 546
Db 529 PKHQPTPDEGDRV-----RAEMPQQR---KQLEPAITATPPLNPLVNE 569
Qy 547 EKDFLMSHHYCVTPEILPCLLSYKMSRDEVAQMYCL-----VKDMPPIKPEQAMEL 601
Db 570 DKELMHRFYESLKHKAPKPLFSSVYKQCGEIVAKTYQLARREVWDQSALDVGITMQL 629

```



Wed Nov 12 14:55:48 2003

us-09-325-095-37.rai

Page 14

[illegible]

Search completed: November 6, 2003, 14:45:26  
Job time : 26 secs



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: November 6, 2003, 14:36:45 ; Search time 47 Seconds

(without alignments)  
3610.185 million cell updates/sec

Title: US-09-325-095-37

Perfect score: 5709  
Sequence: 1 MPPRRSGSLWGIHLMPPRI.....GWTTKDWTFHTIKOHALNX 1069

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

A\_Geneseq.16Jun03.\*  
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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
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6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	5708	100.0	1068	14	AA43341
2	5696	99.8	1068	15	AA46294
3	5657	99.1	1068	14	AA43342
4	5657	99.1	1068	23	AAU09687
5	1978.5	34.7	1044	19	AAW58570
6	1978.5	34.7	1044	20	AAW57390
7	1978.5	34.7	1044	21	AAW50179
8	1976.5	34.6	1044	19	AAW46625
9	1976.5	34.6	1044	21	AAW8372

10	1976.5	34.6	1044	23	AAU09685	Human p110delta is
11	1966	34.4	1070	21	AA11124	Human PI3 kinase p
12	1966	34.4	1070	23	ABP65170	Hypoxia-regulated
13	1966	34.4	1070	23	AAU09688	Human p110beta iso
14	1677.5	29.4	1088	22	ABP60424	Drosophila melanog
15	1467	25.7	1101	20	AAW90089	Human G-protein re
16	1467	25.7	1101	21	AAU76803	Human p110gamma re
17	1467	25.7	1101	21	AAU09689	Human p110gamma is
18	1466.5	25.7	1102	19	AAW23948	Porcine phosphoino
19	1466.5	25.7	1102	20	AAW90083	Porcine G-protein
20	1465.5	25.7	1102	21	AAU76802	Pig p120 regulator
21	1445	25.3	1101	19	AAW23947	Human phosphoinosi
22	1428	25.0	1049	17	AAW11576	Human phosphatidy1
23	1428	25.0	1050	17	AAW11577	Human phosphatidy1
24	1089	19.1	1146	19	AAW47544	Caenorhabditis ele
25	1089	19.1	1167	21	AAW60722	Caenorhabditis ele
26	1049.5	18.4	1176	21	AAW38756	Phosphatidy1 inosi
27	1014.5	17.8	1686	18	AAW70991	Human class II PI3
28	1014.5	17.8	1686	24	ABU19811	Androgen-independe
29	881.5	15.4	1445	23	ABU97312	Novel human protei
30	881.5	15.4	1450	22	ABG04173	Novel human diagno
31	881.5	15.4	1450	22	ABG07330	Novel human diagno
32	870.5	15.2	1462	22	AAW25582	Human protein sequ
33	870.5	15.2	1475	22	ABU11449	Human PI3-Kinase h
34	859	15.0	1876	22	ABU61970	Drosophila melanog
35	859	15.0	1876	22	ABU66876	Drosophila melanog
36	852	14.9	1876	18	AAW38757	Phosphatidy1 inosi
37	815	14.3	311	22	ABG09801	Novel human diagno
38	717	12.6	887	24	ABU54626	Human NOVX polypep
39	717	12.6	913	24	ABU54625	Human NOVX polypep
40	714	12.5	887	22	AAW39431	Human polypeptide
41	697	12.2	901	22	AAW41217	Human polypeptide
42	675.5	11.8	803	20	AAW97880	Maize phosphatidy1
43	657	11.5	1157	22	ABU61471	Drosophila melanog
44	547.5	9.6	818	24	ABU54627	Human NOVX polypep
45	465	8.1	2113	22	ABU64885	Drosophila melanog

## ALIGNMENTS

RESULT 1	
AA43341	AA43341 standard; Protein; 1068 AA.
XX	
XX	AA43341:
AC	
XX	
DT	25-MAR-2003 (updated)
DT	09-JAN-2003 (updated)
DT	12-APR-1994 (first entry)
XX	
DE	p110.
XX	
KW	Phosphoinositide kinase; PI, p85 subunit; screening; agonist;
KW	antagonist; cell proliferation; inhibition; prophylaxis; therapy;
KM	platelets; neurophil activity; 3-phosphorylated phosphoinositides.
XX	
OS	Homo sapiens.
XX	
PN	WO9321328-A1.
XX	
PD	28-OCT-1993.
XX	
PF	13-APR-1993; 93WO-GB00761.
XX	
PR	13-APR-1992; 92GB-0008135.
XX	
PA	(LUDW-) LUDWIG INST CANCER RES.
XX	
PI	Hiles ID, Fry MJ, Dhand R, Waterfield MD, Parker PJ, Otsu M;
XX	Panayotou G, Volinia S, Gout I;
XX	WPI; 1993-351738/44.

DR N-PSDB; AAC51155.

XX Recombinant polypeptide(s) - with phosphoinositide-3 kinase  
PT activity, useful for controlling cell proliferation

PS  
XX Claim 4; Fig 9; 146pp; English.

CC Southern blot analysis was performed using a bovine cDNA probe contg.  
CC a fragment of a p13-kinase-encoding sequence and human cDNA isolated  
CC from a cDNA library constructed from mRNA isolated from the human  
CC cell line K562. Positive clones were sequenced to give a human  
CC p13 kinase p10 sequence. This sequence has 95 percent  
CC homology with the bovine sequence. The domain encoding residues 19-  
CC 100 of human p10 is sufficient to encode the kinase which will  
CC associate with the p85 kinase subunit. The gene may be used to  
CC provide a protein with p13 kinase activity, and is useful for  
CC screening for (anti)agonists of p13 kinase activity which could be  
CC useful for stimulation or inhibition of cell proliferation and hence  
CC prophylaxis or therapy. Platelet or neutrophil activity or blood  
CC glucose levels can be controlled using the kinase.

CC See also AAR43342 and AAR46552-3.

CC (Updated on 09-JAN-2003 to add missing OS field.)

CC (Updated on 25-MAR-2003 to correct FN field.)

CC (Updated on 25-MAR-2003 to correct PI field.)

CC Sequence 1068 AA:

Query Match 100.0%; Score 5708; DB 14; Length 1068;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1068; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPRSSGELGIMHMPRIIVECLIPNGMIVTTECLREATLITIKHELFKEARKYPLHQ 60  
DB 1 MPPRSSGELGIMHMPRIIVECLIPNGMIVTTECLREATLITIKHELFKEARKYPLHQ 60  
QY 61 LLODESSYIFVSVTQEARREEFFDETRRLCDLRLFOPLKYTEPVGNKEKILNREIGFA 120  
DB 61 LLODESSYIFVSVTQEARREEFFDETRRLCDLRLFOPLKYTEPVGNKEKILNREIGFA 120  
QY 121 IGMVCEEDMVKDEPVODFRRIILNVCKEAVDLRLNPSHRAMVYVPNESSPELPKH 180  
DB 121 IGMVCEEDMVKDEPVODFRRIILNVCKEAVDLRLNPSHRAMVYVPNESSPELPKH 180  
QY 181 IYNKLDKQOIIIVWIVISPNNDKOKYTLKINHDCVPEQVIAEAIKRTKRLSSBQLX 240  
DB 181 IYNKLDKQOIIIVWIVISPNNDKOKYTLKINHDCVPEQVIAEAIKRTKRLSSBQLX 240  
QY 241 LCVLEYOGKYTLKVCGCDEYFLEKYPISQYKXIRSCIMLGMPNIMLMAKESLYSQLPMD 300  
DB 241 LCVLEYOGKYTLKVCGCDEYFLEKYPISQYKXIRSCIMLGMPNIMLMAKESLYSQLPMD 300  
QY 301 CFTHMSYSRRISTATPPYNGGETSTSLWVINSALIKILICATYVAVNIRDDIKIVYRGI 360  
DB 301 CFTHMSYSRRISTATPPYNGGETSTSLWVINSALIKILICATYVAVNIRDDIKIVYRGI 360  
QY 361 YHGGEPICDNVTOVPCSNPRMNEMLNNDIYIPDLFRAARCLISCSYKGRKGAKEHC 420  
DB 361 YHGGEPICDNVTOVPCSNPRMNEMLNNDIYIPDLFRAARCLISCSYKGRKGAKEHC 420  
QY 421 PLAMGNINLFDTDTLVSGKMLNIMPVHGEDLLNPIGVTSNPNKETPCLELEFDMF 480  
DB 421 PLAMGNINLFDTDTLVSGKMLNIMPVHGEDLLNPIGVTSNPNKETPCLELEFDMF 480  
QY 481 SSVVVFPPDMSVIEEHANMSVSRAGSYSHAGISNPLARDNELRENDKQLRAICTRDPL 540  
DB 481 SSVVVFPPDMSVIEEHANMSVSRAGSYSHAGISNPLARDNELRENDKQLRAICTRDPL 540  
QY 541 SSITTEOKPFLMSHRHYCTIPEILPKLLSVKMSRDEVAQMYCLVKDMPRIKPEQAME 600  
DB 541 SSITTEOKPFLMSHRHYCTIPEILPKLLSVKMSRDEVAQMYCLVKDMPRIKPEQAME 600  
QY 601 LLDGNYPDPMVGRFAVRCLEKYLTDCLKSOYLIIQIVOVAKYEQYLDNLLVRFLLKALTN 660  
DB 601 LLDGNYPDPMVGRFAVRCLEKYLTDCLKSOYLIIQIVOVAKYEQYLDNLLVRFLLKALTN 660

DB 601 LLDGNYPDPMVGRFAVRCLEKYLTDCLKSOYLIIQIVOVAKYEQYLDNLLVRFLLKALTN 660  
QY 661 ORIGHFFFWHLKSEHANKTVSORFGLLESYCRACGMVTKHINROVEAMEKILNTDLIX 720  
DB 661 ORIGHFFFWHLKSEHANKTVSORFGLLESYCRACGMVTKHINROVEAMEKILNTDLIX 720  
QY 721 QEKKECTOKVOKKFLVEQMRPDMALOGFSLPNAHQNLRLSECRINSSAKRPLM 780  
DB 721 QEKKECTOKVOKKFLVEQMRPDMALOGFSLPNAHQNLRLSECRINSSAKRPLM 780  
QY 781 LMWENEDINSELLFONNEIIFKNGDDLRODMTLTOIRIMENINQNGIUDMLPFGCIS 840  
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QY 841 IGCVCGLIEVNRSHITMOIQCGGKGLQPNRSHLQWLKDKNGEYDAIDPFTS 900  
DB 841 IGCVCGLIEVNRSHITMOIQCGGKGLQPNRSHLQWLKDKNGEYDAIDPFTS 900  
QY 901 CAGYCVATPFLIGDHNNSINWKDDGOLFHDGFLDHKKKKFGYKGERVPVLTDF 960  
DB 901 CAGYCVATPFLIGDHNNSINWKDDGOLFHDGFLDHKKKKFGYKGERVPVLTDF 960  
QY 961 LIVISGAOECTYTRFEERFOEMCYRAYLAIRQHANLFINLSWMLGSGMPELOSTDDIA 1020  
DB 961 LIVISGAOECTYTRFEERFOEMCYRAYLAIRQHANLFINLSWMLGSGMPELOSTDDIA 1020  
QY 1021 YIRKTLALDKTEBOALEYFMKQNDANHGGMWTKMDIIFHTIKQHALN 1068  
DB 1021 YIRKTLALDKTEBOALEYFMKQNDANHGGMWTKMDIIFHTIKQHALN 1068

# RESULT 2

AAR46294  
ID AAR46294 standard; Protein: 1068 AA.

XX AAR46294;

XX AC 25-MAR-2003 (updated)  
DT 31-AUG-1994 (first entry)

XX DE Pcdins 3-kinase 110 kD catalytic subnit.

XX KM 110 kD catalytic subunit; phosphatidylinositol 3-kinase;  
KM transformation; Schizosaccharomyces pombe; nmc promoter; thiamine;  
KM Pcdins 3-kinase; assay; detection; cell growth; regulation; cancer;  
XX KW blood vessel plaques.

XX OS Bos taurus.

XX FH Location/Qualifiers

FT Key

FT Peptide

FT /note= "Peptide A"

FT 163..175

FT Peptide

FT /note= "Peptide B"

FT 326..337

FT Peptide

FT /note= "Peptide C"

FT 441..464

FT Peptide

FT /note= "Peptide D"

FT 622..648

FT Peptide

FT /note= "Peptide E"

FT 657..672

FT Peptide

FT /note= "Peptide F"

FT 679..699

FT Peptide

FT /note= "Peptide G"

FT 712..720

FT Peptide

FT /note= "Peptide H"

FT 868..882

FT Peptide

FT /note= "Peptide I"

FT 885..908

FT Peptide

FT /note= "Peptide J"

FT 925..941

FT Peptide

FT /note= "Peptide K"

FT 949..966

FT Peptide

FT /note= "Peptide L"

FT 987..1010

FT Peptide /note="Peptide L"  
 FT 1031..1040 /note="Peptide M"  
 FT 1055..1063 /note="Peptide N"  
 FT /note="Peptide N"  
 PN W09403609-A1.  
 XX 17-FEB-1994.  
 PD 05-AUG-1993; 93WO-GB01651.  
 PF 05-AUG-1992; 92GB-0016654.  
 PR (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.  
 PA Goode NT, Nurse PM, Parker PJU, Waterfield MD;  
 PI WPI, 1994-065697/08.  
 DR N-PSDB, AA057012.  
 XX Bkaryotic cells transformed with mammalian phospholipid or  
 PT protein kinase DNA - useful in assays for compounds involved in  
 PT cell growth regulation and for treating cancers  
 XX Disclosure; Fig 1; 71pp; English.  
 XX This sequence represents the 110 kD catalytic subunit of the  
 CC phosphatidyl inositol (PtdIns) 3-kinase. The cDNA encoding this  
 CC sequence was transformed into Schistosaccharomyces pombe cells under  
 CC the regulatory control of the nmt promoter in an embodiment of the  
 CC invention. In the presence of thiamine the promoter is inactive and  
 CC the cells carrying the PtdIns catalytic subunit plasmid grow as the  
 CC parental strain. In the absence of thiamine the nmt promoter functions  
 CC and the PtdIns 3-kinase catalytic subunit is induced. PtdIns activity  
 CC is substantially increased under these conditions. Cells containing  
 CC constructs such as this, are useful in assays for detecting compounds  
 CC involved in cell growth regulation. It is also used as the basis for  
 CC detecting compounds for treating cancers and the formation of blood  
 CC vessel plaques.  
 CC (updated on 25-MAR-2003 to correct PN field.)  
 CC  
 SQ Sequence 1068 AA;  
 Query Match 99.8%; Score 5696; DB 15; Length 1068;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1066; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 361 YHGSEPLCDNVNTQVRVPCSNPRNEMWLNVDIYIPDLPRARLCLISGVKGRGAKEEHC 420  
 QY PLAMGINLPDPTDLVSGKMLNLMPPVHGLEDLNP:IGVGSNNKSTPCLELEFDMW 480  
 QY 421 PLAMGINLPDPTDLVSGKMLNLMPPVHGLEDLNP:IGVGSNNKSTPCLELEFDMW 480  
 DB 421 PLAMGINLPDPTDLVSGKMLNLMPPVHGLEDLNP:IGVGSNNKSTPCLELEFDMW 480  
 QY 481 SSVYKPEPMSVIEEHNAMSVSREAGFSYSHAGLSNRLADNELRENDKQLRAICTRDP 540  
 DB 481 SSVYKPEPMSVIEEHNAMSVSREAGFSYSHAGLSNRLADNELRENDKQLRAICTRDP 540  
 QY 541 SEITTEQKDFLWSHRHYCTTPEILPKLLSYKMSRDEVAQMYCLVKDMPPIKPEQAME 600  
 DB 541 SEITTEQKDFLWSHRHYCTTPEILPKLLSYKMSRDEVAQMYCLVKDMPPIKPEQAME 600  
 QY 601 LDDCNYPDMWGFARCLKYLTDKLSOYLILQVQLKYEQYLDNLLVRLFKKALTN 660  
 DB 601 LDDCNYPDMWGFARCLKYLTDKLSOYLILQVQLKYEQYLDNLLVRLFKKALTN 660  
 QY 661 ORIGHFFFWHLKSEMHNKTVSQRFGLLSEYCRACGMYLKHLNROYEAMEKILNTDILK 720  
 DB 661 ORIGHFFFWHLKSEMHNKTVSQRFGLLSEYCRACGMYLKHLNROYEAMEKILNTDILK 720  
 QY 721 QEKKESTQRYQKFLVEQMRPRPMDALOGFLSPINPAHQNLRLSECRIMSSAKRPLM 780  
 DB 721 QEKKESTQRYQKFLVEQMRPRPMDALOGFLSPINPAHQNLRLSECRIMSSAKRPLM 780  
 QY 781 LWMENPDINSELPFQNEIIFPKGGDLRODMITLQIRIMENINWQNGIDMLPFGCIS 840  
 DB 781 LWMENPDINSELPFQNEIIFPKGGDLRODMITLQIRIMENINWQNGIDMLPFGCIS 840  
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 DB 841 IDDCVGLIEVNSHTIMOIOCKGGLKALQFNSHTIHOWLKDKNGETYDAIDPFTS 900  
 QY 901 CAGYCVATFILDIGDRHNSNIWYKDGQLEFHDGFLDHHKKKFGYKREVPVLTQDF 960  
 DB 901 CAGYCVATFILDIGDRHNSNIWYKDGQLEFHDGFLDHHKKKFGYKREVPVLTQDF 960  
 QY 961 LIVISKGAQECTRTREPERFQEMCYKAYLAIQHANLPINLFMSMLGSMPELQSFDDIA 1020  
 DB 961 LIVISKGAQECTRTREPERFQEMCYKAYLAIQHANLPINLFMSMLGSMPELQSFDDIA 1020  
 QY 1021 YIRKTLALDPTQEALVEYFMKONDAHHGGWTTKMDMIFHTIKOHALN 1068  
 DB 1021 YIRKTLALDPTQEALVEYFMKONDAHHGGWTTKMDMIFHTIKOHALN 1068

RESULT 3  
 AAR43342  
 ID AAR43342 standard; Protein; 1068 AA.  
 AC AAR43342;  
 AC  
 DT 12-MAR-2003 (updated)  
 DT 12-APR-1994 (first entry)  
 DE Human p110.  
 XX  
 XX phosphoinositide kinase; PI; p85 subunit; screening; agonist;  
 KW antagonist; cell proliferation; inhibition; prophylaxis; therapy;  
 KW platelets; neutrophil activity; 3-phosphorylated phosphoinositides.  
 OS Homo sapiens.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 FT Domain 19..100  
 FT /note="binds with p85 subunit"  
 PN W09321328-A1.  
 XX  
 XX 28-OCT-1993.  
 PD

PF 13-APR-1993; 93W0-GB00761.  
 XX 13-APR-1992; 92GB-0008135.  
 PR (LUDW-) LUDWIG INST CANCER RES.  
 PA Hille ID, Fry MJ, Dhand R, Waterfield MD, Parker PJ, Otsu M;  
 PI Panayotou G, Volinia S, Gout I;  
 XX N-PSDB; AA051156.  
 DR WPI; 1993-351738/44.  
 XX Recombinant polypeptide(s) - with phosphoinositide-3 kinase  
 PT activity, useful for controlling cell proliferation  
 PS Claim 24; Fig 16; 146pp; English.  
 CC Southern blot analysis was performed using a bovine cDNA probe contg.  
 CC a fragment of a p13-kinase-encoding sequence and human cDNA isolated  
 CC from a cDNA library constructed from mRNA isolated from the human  
 CC cell line K562. Positive clones were sequenced to give the human  
 CC p13 kinase p130 sequence. This sequence has 95 percent homology  
 CC with the bovine sequence. The domain contg. residues 19-100 of human  
 CC p130 is sufficient to associate with the p85 kinase subunit. The  
 CC protein with p13 kinase activity is useful for screening for  
 CC (ant)agonists of p13 kinase activity which could be useful for  
 CC stimulation or inhibition of cell proliferation and hence  
 CC prophylaxis or therapy. Platelet or neutrophil activity or blood  
 CC glucose levels can be controlled using the kinase.  
 CC See also AAR43341 and AAR46552-3.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 CC  
 SQ Sequence 1068 AA:  
 Query Match 99.1%; Score 5657; DB 14; Length 1068;  
 Best Local Similarity 98.9%; Pred. No. 0;  
 Matches 1056; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

DB 481 SSVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKQOLRAICTRDP 540  
 QY SEITQOEKDFLMSHHNYCTTIPETLKLSTVKNMSRDEVAOMCYGVDMPPIKEQAME 600  
 DB SEITQOEKDFLMSHHNYCTTIPETLKLSTVKNMSRDEVAOMCYGVDMPPIKEQAME 600  
 QY LDDCNYPDPNVRGFAVRCLEKYLTDKLSQYLIQVQVLYKTEQYLDNLVRFLLKALTN 660  
 DB LDDCNYPDPNVRGFAVRCLEKYLTDKLSQYLIQVQVLYKTEQYLDNLVRFLLKALTN 660  
 QY ORIGHFFFWHLKSEMNKTVSQRFGLLLESYCRACGMVLYKLNROVEAMEKLIINTDILX 720  
 DB ORIGHFFFWHLKSEMNKTVSQRFGLLLESYCRACGMVLYKLNROVEAMEKLIINTDILX 720  
 QY QEKDETQVQMKFLVEQNRPRDPMALOGFLSPNPAHQNLRLRECRIMSASAKRPLM 780  
 DB QEKDETQVQMKFLVEQNRPRDPMALOGFLSPNPAHQNLRLRECRIMSASAKRPLM 780  
 QY QERKDETQVQMKFLVEQNRPRDPMALOGFLSPNPAHQNLRLRECRIMSASAKRPLM 780  
 DB QERKDETQVQMKFLVEQNRPRDPMALOGFLSPNPAHQNLRLRECRIMSASAKRPLM 780  
 QY LNMENPDIMSELFONNEIIFKNGDRLRQDMLTLQIRIMENIMQNGIDLRLPYGLS 840  
 DB LNMENPDIMSELFONNEIIFKNGDRLRQDMLTLQIRIMENIMQNGIDLRLPYGLS 840  
 QY IGDVGLIEVNRNSHTIMQIOCKGKGLKALQFNSTHQLKDKNGEITYDAIDLFTTS 900  
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 DB CAGYCATPILIGIDHNSNINWKDQGLPHIDFGHLDHKKKPKGYKXERVPVLTDPF 960  
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 DB LIYISGAOECTREPERFOECYKAYLAIRQANLFTNPSMVLGSGMPELQSFDDIA 1020  
 QY YIRKTLADKTEQDALEYFMKQNDAHGSGTTKQDMITHTITQAHALN 1068  
 DB YIRKTLADKTEQDALEYFMKQNDAHGSGTTKQDMITHTITQAHALN 1068

RESULT 4  
 AAU09687  
 ID AAU09687 standard; Protein: 1068 AA.  
 AC AAU09687;  
 DT 12-MAR-2002 (first entry)  
 XX Human p130alpha isoform of p13-kinase.  
 DE Human p130alpha isoform of p13-kinase.  
 XX Human; phosphatidylinositol 3-kinase; p13K; p130alpha isoform;  
 KW LASP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;  
 KW autoimmune disease; inflammatory bowel disease; bacterial pneumonia;  
 KW Type 1 diabetes mellitus; cytosolic; immunosuppressive.  
 OS Homo sapiens.  
 GN WO200185986-A2.  
 XX 15-NOV-2001.  
 PD 10-MAY-2001; 2001WO-US15065.  
 PF 10-MAY-2000; 2000US-203346P.  
 PR 10-MAY-2000; 2000US-203346P.  
 XX (ICOS-) ICOS CORP.  
 PA Sadhu C;  
 PI WPI; 2002-075252/10.  
 XX N-PSDB; AAS14365.  
 DR Identifying a modulator of p130delta polypeptide binding to SH3  
 PT domain-containing polypeptides e.g. LASP-1, comprising allowing the

PT binding partners to interact in the presence and absence of a test compound -

Example 1; Page 60-63; 85pp; English.

The present invention relates to identifying a modulator of the phosphatidylinositol 3-kinase (PI3k; p10delta) enzyme that binds to the catalytic subunit via a SH3 domain-containing polypeptide such as LAMP-1. Also described are methods of assaying the specific binding affinity of the PI3-kinase binding partner. Such modulators are useful for the treatment of diseases characterised by the undesirable or excessive activity of PI3kdelta. For example the modulators can be used for inhibiting the growth or proliferation of cancer cells (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues, Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid arthritis), ophthalmic disorders (e.g. allergic conjunctivitis), autoimmune diseases (e.g. systemic lupus erythematosus), inflammatory bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory dermatoses (e.g. contact dermatitis), central or peripheral nervous system inflammatory disorders (e.g. meningitis), bacterial pneumonia, and Type I diabetes mellitus. The present sequence represents human p10alpha isoform of PI3k.

Sequence 1068 AA:

Query Match 99.1%; Score 5657; DB 23; Length 1068;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 1056; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

```

QY 1 MPRPSSGELMGHLMPPRLVLECLLPNGMIVTECLRENTLTITKHELFKEARKYPLHQ 60
DB 1 MPRPSSGELMGHLMPPRLVLECLLPNGMIVTECLRENTLTITKHELFKEARKYPLHQ 60
QY LLODESSYIVSVYTOEAREBEFDETRRLCDLRFQPLVTEBVGREKTIINREIGFA 120
DB LLODESSYIVSVYTOEAREBEFDETRRLCDLRFQPLVTEBVGREKTIINREIGFA 120
QY 121 IGVNPFCDWVKQDEVDFFRNILNVCKEAVDLRLDLSPPSRAMYVPPNVSSPELPKH 180
DB 121 IGVNPFCDWVKQDEVDFFRNILNVCKEAVDLRLDLSPPSRAMYVPPNVSSPELPKH 180
QY 181 IYKLDKGQIIVIVWVSPNDKOKYTLKINHDCVEQVIAEIRKRTSMILSSBOLK 240
DB 181 IYKLDKGQIIVIVWVSPNDKOKYTLKINHDCVEQVIAEIRKRTSMILSSBOLK 240
QY 241 LCVLEVOGKYLKVCQDEGFLEKYPISOYKTIKSCMLGRMPLMKAKESLYSQPMD 300
DB 241 LCVLEVOGKYLKVCQDEGFLEKYPISOYKTIKSCMLGRMPLMKAKESLYSQPMD 300
QY 301 CFTMPYSRRISTATPYMNGESTSKSLMVISALRIKILCATYVNVNIRIDIKIYRTGI 360
DB 301 CFTMPYSRRISTATPYMNGESTSKSLMVISALRIKILCATYVNVNIRIDIKIYRTGI 360
QY 361 YHGGEPICDWNVNTQRPVCSNPRNEMINVDIYIPDLPRARLCLISGVKRGKAKEHC 420
DB 361 YHGGEPICDWNVNTQRPVCSNPRNEMINVDIYIPDLPRARLCLISGVKRGKAKEHC 420
QY 421 PLAMGNINLPDYDTLVSGKALNLMVPBGLDLNLPIGVTGSNPKKTPCLEBDFW 480
DB 421 PLAMGNINLPDYDTLVSGKALNLMVPBGLDLNLPIGVTGSNPKKTPCLEBDFW 480
QY 481 SSVVKFPDMSVIEEHANMSVREAGFSYSHAGLSNRLARNDLRENDKEOLRAICTRDP 540
DB 481 SSVVKFPDMSVIEEHANMSVREAGFSYSHAGLSNRLARNDLRENDKEOLRAICTRDP 540
QY 541 SEITEOKDFLMGHRHYCVTIPETILPULLSVKXNSRDEVAQWYCLVKDWPPIKPEGAM 600
DB 541 SEITEOKDFLMGHRHYCVTIPETILPULLSVKXNSRDEVAQWYCLVKDWPPIKPEGAM 600
QY 601 LLDONYPDPVWVGPAVCEKYLTDOKLSOYLQIOLVOVLKYEQYLDNLLRFLIKKALTN 660
DB 601 LLDONYPDPVWVGPAVCEKYLTDOKLSOYLQIOLVOVLKYEQYLDNLLRFLIKKALTN 660

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QY 661 QRIQHEFFMHLKSEMHNTVSOQFGLLESYCRACGWYLGHLNROYEAMEKLIINTDILK 720
DB 661 QRIQHEFFMHLKSEMHNTVSOQFGLLESYCRACGWYLGHLNROYEAMEKLIINTDILK 720
QY 721 QEKKDEYQKQMFVLEQMRPDMALQGLSPINPAHOLGULRLEECIIMSAPLW 780
DB 721 QEKKDEYQKQMFVLEQMRPDMALQGLSPINPAHOLGULRLEECIIMSAPLW 780
QY 781 LMNENPIMSELLFONNEIIFKNGDDLROMLTLQIIRIMENTIMONOGILRMLPYGCLS 840
DB 781 LMNENPIMSELLFONNEIIFKNGDDLROMLTLQIIRIMENTIMONOGILRMLPYGCLS 840
QY 841 IGDVGLIEVVRNSHTIMQIQCKGKLGALQFNSHTLHQWLKDNKGEIYDAAIDLEPTRS 900
DB 841 IGDVGLIEVVRNSHTIMQIQCKGKLGALQFNSHTLHQWLKDNKGEIYDAAIDLEPTRS 900
QY 901 CAGYCATPFLIGIDRHSNIMWKDQQLPHIDFGHFLDHKKKFGYKRVRVPVLTQDF 960
DB 901 CAGYCATPFLIGIDRHSNIMWKDQQLPHIDFGHFLDHKKKFGYKRVRVPVLTQDF 960
QY 961 LIYISGAOECTRTEPERFQEMCYAYALIRQANLFTLFSMMLGSGMPELOSPDIA 1020
DB 961 LIYISGAOECTRTEPERFQEMCYAYALIRQANLFTLFSMMLGSGMPELOSPDIA 1020
QY 1021 YIRKTLALDKTEQALEYFMKQNDAHGGWTTKMDIIFHTIKOHALN 1068
DB 1021 YIRKTLALDKTEQALEYFMKQNDAHGGWTTKMDIIFHTIKOHALN 1068

```

RESULT 5  
AAM58570  
ID AAM58570 standard; Protein; 1044 AA.

AC AAM58570;

DT 12-OCT-1998 (first entry)

XX Human phosphatidylinositol 3-kinase p110 catalytic delta subunit.

XX Phosphatidylinositol 3-kinase; p110 delta; human; immune system;

XX carcinogenesis; diagnosis.

XX Homo sapiens.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

CC The sequence was deduced from a composite cDNA clone (see AAV58570)  
 CC derived from peripheral blood mononuclear cell and macrophage  
 CC cDNA. The following are claimed: (1) a purified and isolated  
 CC polynucleotide (PN) encoding p110 delta; (2) a vector comprising a  
 CC DNA as in (1); (3) a host cell stably transformed or transfected  
 CC with a DNA as in (1); (4) PN encoding a lipid kinase, and  
 CC hybridising to PN having the 5220 bp sequence; (5) a purified and  
 CC isolated p110 delta polypeptide as in (4); (6) an antibody  
 CC specifically immunoreactive with p110 delta; (7) a hybridoma cell  
 CC line (especially 208F (HB 12200) producing a monoclonal antibody as  
 CC in (6); and (8) a humanised antibody as in (6). p110 delta has  
 CC kinase activity and may play a role in PI 3-kinase mediated  
 CC signalling in the immune system and in carcinogenesis. The  
 CC products can be used to develop agents that modulating p110 delta  
 CC kinase activity and to develop diagnostic reagents (claimed). They  
 CC may also be used for detection and diagnosis of p110 delta in a  
 CC biological sample.

SO Sequence 1044 AA;

Query Match 34.7%; Score 1978.5; DB 19; Length 1044;

Best Local Similarity 39.9%; Pred. No. 3e-179;

Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

QY 16 MPP-----RIIVECLPVGMIVTLECLREATLTITKHELFKARKYPLHQ 60  
 DB 1 MPFGVDCMEFWTKENQSVVVDPLPTGVYLNFPVSNANLSTIKQLMRAQEBPLFH 60  
 QY LLODESSYIFVSVTQAEAREEFDETRRLCDLRLFOPLKYTEPEVNGREKILNREIGFA 120  
 DB 61 MLSCGEAVVFTICINQTAQCELEDBQRLCDVQPLPLRLVARGDVKKLINSQIL 120  
 QY 121 IGMVCEFDVWKPEVDQFRNINLVCKEAVDLRLNSPHSRAMVYVNVESPE---- 176  
 DB 121 IKGHLHFDLDCPEVNDFFRAKMCQFCCEAARQQLGEMAMLOYSFPLQLEPSKOTWGP 180  
 QY 177 ----LPKRIYVKLKGQIIVIVIVVSPNNDKOKTKLINDVCEQVIAEIRKRTSM 232  
 DB 181 GTLRLPNR-----ALVNVKFGESSESTFVSTKDVPLAMACLRK---- 224  
 QY 233 LLSSEQLCLVLEYGKYLKVCDEYFLEKYPYQKYRTSCIMLRMNLIMAKES 292  
 DB 225 ---ATVFPQPLVEQBEDTTLQVNGRHELYLGNYPICQFOYICSCLSHGLTPTLMVHSS 281  
 QY 293 LYSQLPMDCTWPSYSRRISTATPYMNGESTKSLWINSALRIKILCATYVNVNIRID 352  
 DB 282 ILAMDDEQSNPAQVQKPRAKPPPIPAKKSSVSLSLEQPRIELIGSKVNADER--M 339  
 QY 353 KIYVATGTYHGEPLCDNVNTRQRP--CSPNRNEMLANDIYIPDLPRARCLASICSV-- 409  
 DB 340 KLVVQAGLPHGEMLCKTVSSSEVSVCSEPVWKQRLPEFINICDLPKMARLCLFALYAVIE 399  
 QY 410 -----KGRKAKEHCPLAMGNINLPDYDTLVGKALNIMP--VPHGLDLDLNPIGT 462  
 DB 400 KAKKARSTKSKSKADCPILAMANLMLFDYKQDLKGERCLYMWPEVPDEKGLNPTGIV 459  
 QY 463 GSNPNKETP-----CLELEFDWFSSVYKFPDMSVIEEHANMSVSREAGEYSYHAGLSNRL 517  
 DB 460 RSNPTDSAAALLICLP--EVAHPHYVYPALKEILE-----L 494  
 QY 518 ARDN-----LRENDKQALRICTRDPLSETTEQEKDPLMHRHYCVT-IPEILPKLLSYK 573  
 DB 495 GHSSECVAHTEBEOQLREILERRSGGELYEHKDLWMLRHEVQEHFEALARLLLVTK 554  
 QY 574 WNSRDEVAQWYCLVNDMPRIKPEQAMLEDCNVYPPDMVAGFAPRCLEKLTDDKLSQYLI 633  
 DB 555 WKKEHDVAMLYLCSWPELPVLSALELDPSFPDCHVSSFAIKSLRK-LTDEDFQYLL 613  
 QY 634 QLVQVLKYEQYLDNLLVRLFKKALTNORIGHFFWHLKSEMNKNTVSGRFGILLSESYCR 693  
 DB 614 QLVQVLKYESYLDCELTKFLDLBALANRIGHPLFHLRSEMHVPSVALRFGILLEYAYCR 673  
 QY 694 ACGMYLKLINROVEAMEKLINLTLLIKQEKDETQVQMKFLVBO-MRPRDMDALQGL 752

DB 674 GSTHHKVLKKQGEALSKLALNDFVKLSQ--KTPKQTKELMHLGMBQEAYLEALSHLQ 732  
 QY 753 SPINPAHQNLNLEECRIMSSAKRPLNWNEMPDIMSELLPONNELLIRKNGDGLRQDM 812  
 DB 733 SPIDPSLTAEVCEBCTFMDSKKPLMWSNEAGSG--GSVGIIKNGDGLRQDM 789  
 QY 813 TLQIRIMENIMONOGDLMLPYGCLSGDVCGLIEVANSHTIMQIC-KGGLKALQ 871  
 DB 790 TLOMIGMDVLMQOEGDLRMTYGCPLPQDRGLLEVLRSPTIANIQNSMMAATA 849  
 QY 872 FNSHTLHMKDKNKKGEIYDAIDLTPRSCAGYCAVTFILIGDRINSNIMVKDQGLFH 931  
 DB 850 FNVDALNMLKSKNPGBALDRAIEFTLSCAGYCAVATYVLGIDRHSNDIMRESQGLFH 909  
 QY 932 IDFGHFLDKKKKFGYKREVPVLTQDFLIVISKGAOECTKREFEPQEWCYKAYLAI 991  
 DB 910 IDFGHFLGNFKTKFNGINRERVPILTDFVHVIOQG--KTNSEKFERFGRYGERATTL 967  
 QY 992 ROHANLPLNFSMWLGSMPLOSFDIAYIRKTLALDKTEOBALLEYFMKONDAHNGW 1051  
 DB 968 RRHGLPLHLPALMRAAGLPFLSCSKDIQYLKDSLALGKTEEBALKHFRYKFDALRESW 1027  
 QY 1052 TTQKDWIIFHTIKQ 1064  
 DB 1028 KTKVNLAHNVSK 1040

RESULT 6  
 AAW97390  
 ID AAW97390 standard; Protein; 1044 AA.  
 AC AAW97390;  
 DT 14-MAY-1999 (first entry)  
 DE p110-delta amino acid sequence.  
 KM Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase;  
 KM PI3-Kinase mediated signalling; immune system; phosphatidylinositol;  
 KM PI; kinase activity.  
 OS Homo sapiens.  
 UN US882910-A.  
 PD 16-MAR-1999.  
 PF 25-NOV-1997; 97US-0977871.  
 PR 25-NOV-1997; 97US-0977871.  
 PR 25-NOV-1996; 96US-0777405.  
 PA (ICOS-) ICOS CORP.  
 PI Chantry DH, Hoekstra MF, Holtzman DA;  
 DR WPI; 1999-214067/18.  
 DR N-PSDB; AAX15932.  
 PT Novel catalytic subunits derived from phosphatidylinositol 3-kinase  
 PT enzymes - useful as antigens and for identifying agents which  
 PT modulate the enzymes kinase activity or binding to substrates and  
 PT co-factors  
 PS Claim 1; Columns 23-30; 22pp; English.  
 XX The present sequence represents a catalytic subunit (p110-delta),  
 XX derived from a phosphatidylinositol 3-kinase enzyme which is  
 XX involved in PI3-kinase mediated signalling in the immune system.  
 XX p110-delta phosphorylates phosphatidylinositol (PI), and  
 XX derivatives of it at the 3'-hydroxyl of the inositol ring).  
 CC p110-delta may be used as an antigen in the production of

CC antibodies (using standard techniques) which may be used, for  
 CC example, to modulate (ie blocking, inhibiting or stimulating) the  
 CC binding between p110-delta and its binding partner. p110-delta may  
 CC also be used in assays to identify modulators which inhibit or  
 CC activate its kinase activity.

XX Sequence 1044 AA;

Query Match 34.7%; Score 1978.5; DB 20; Length 1044;  
 Best Local Similarity 39.9%; Pred. No. 3e-179;  
 Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

QY 16 MRP-----RIVLECLPENGMIITTECLREATLTITIKELFEKARKYPLHQ 60  
 DB 1 MPGVDCPMFEMTKENOSVYVDPLPTGVINFPVSRNANLSTIKQLMHRAYEPLFH 60  
 QY 61 LLDDESYIPVSTQEAEREFEDETRRLDGLRFLQFLVIEVGVNREKILNREGFA 120  
 DB 61 MLSGPEAYVETTCINQRAEQLEDEQRRLCDVQFLVRLVARREGGRVKKLINSQISLT 120  
 QY 121 IGMVCEFDVVKDPEVDFFRNILNWCSEAVIDLRDILNSPSRMYVYPPVNESSPE--- 176  
 DB 121 IKGGLHFPDSCPEVNDPFAKACQCFEEAARQQLGWEAMLOYSFPLQLEFSAQTMCP 180  
 QY 177 ----LPHIYINKLDGQIIVIVIVIVISPNNDKQYTLKINHDCVPEQVIAEAIKXTRSM 232  
 DB 181 GTLRLEPNR-----ALVNVVFEGSESESFTEQVSTKQVPLALMACARKK---- 224  
 QY 223 LLSSEQLKLVLEEQGYLIKVGCCDEYFLEKYPLOYKKTIRGCIIMGRMNLMAKES 282  
 DB 225 --ATVFRQPLVQRPEDYTLQVNGRHEYLGNYPLOQFOYICGLSHGLPRLTMWSSS 281  
 QY 293 LVSQLEPMDCFTMSYSRRISTATPYMNGETSTKSLWYVINALIKXICATVYVNIIRDID 352  
 DB 282 ILAMREGQSPARQVQKPAKPPPIPAKKESSVSLMSLEQPRILEIQSKVADER--M 339  
 QY 353 KIYVRTGIYHGSEPLCDNVNTQRP--CSNPRMNMENYDIYIDLPRAARLCLISCV-- 409  
 DB 340 KLVVQAGLTFHGNMLCKTVSSSEVSCSEPVWKQRLIEDINICDLPRMARLCPALAVIE 399  
 QY 410 -----KGRKGAEEHICPLANGINLPDITDLYVSGKMLNLP--VPHGLEDLINIGYT 462  
 DB 400 KAKKARSTKSKSKKACPIAMAMLMFYKDOUKTERCJLYMWPSPVDEKGEILNPTGTV 459  
 QY 463 GSNPNKETP-----CLELEFDMFSSVVKFPDMSVIEBHANWWSRRAGTSYSAGLSNRL 517  
 DB 460 RSNPNTDSAAALLICLP--EVAHPVYYPALKEIIE-----L 494  
 QY 518 ARDNE--LRNDKQQLRAICTRDLPLSEITQEKDFLWSHRHYCVT--IPEILPKLLSVK 573  
 DB 495 GRHSECVHTBEEQGLREILERRSGGELYEHKKDLVMKLRHVCJHFEFALARLLVTK 554  
 QY 574 WNSRDVVAQMYCLVKQWPRPKFEQAMELLDCNYPDMVNGFAVRCLKXYLTDDKLSQYLI 633  
 DB 555 WNKHEVVAQMYLCLCWPMLPVLSALELLDFSPDCHVCSFAIKSIRK--LTDDELQYLL 613  
 QY 634 QLVQVLYKQYQYLDNLVRFLLKALTNORIGHFEFHLKSEMKNKVSQRFGLLESYGR 693  
 DB 614 QLVQVLYKYSYLDCELTKFTLDBALNRRKIGHLPFHLRSEMHVPVALRFGILLEYGR 673  
 QY 694 ACGMYLXKHLNROVEAMEKLINLTDLIKQEKDETQVQMKFLVEQ--MRSPDFDALQGLF 752  
 DB 674 GSTHMKVLMKQGEALSKLKALNDPVKLSQ--KTPRQPKELMHLCMRQEAIVIALSHQ 732  
 QY 753 SFLNPAHQGNTRLEECRIWSSAKRPLMWNENPDIMSELLFONNEIIFKNGDDLRQDWL 812  
 DB 733 SPIDESTLLAEVCVEGCTFMDSKMKPLMYSNBEAGSG--GSVGIIFKNGDDLRQDWL 789  
 QY 813 TLQIIRIMENIMONOGDLRLMYPYGLSTGDCVGLLEVRNNSHTIMQIC--KGGKLGALQ 871  
 DB 790 TLQMTQLMDVLMKQEBDLRMTYPYGLCPGRDRTGLLEVLRSSTIANIQLKNSNMAATYA 849  
 QY 872 FNSHTLHQLKDKNKGEIYDAAIDLFTRSCAGYCVATFLIGDRHNSINIMVDDQLPR 931

DB 850 FNDQALNMLKSKNPGEDALDRAIEFTLSCAGYCVATYVLGIGDRSDNIMRESGLFH 909  
 QY 932 IDFGFLDHKKKKFGYKREVPVVLQDPLIYVSKAQEECTKREERPEQMYKAYLAI 991  
 DB 910 IDFGFLGNFKTKFGINREVPVILTYDFVHVIQOG--KNNSEKFERFGYCERAYTIL 967  
 QY 992 ROHANLFINLFSWMLSGMPELOSFDIAYIRKTLALDKTEQEALEFPMKQNDHNGW 1051  
 DB 968 RRGGLLFLHLFALMRAAGPELSCSDIQLKQSLALGTEEBALXHFVKFEALRESW 1027  
 QY 1052 TYQMDWIFHTIKQ 1064  
 DB 1028 KTKVNMVLAHVSK 1040

RESULT 7  
 AAY50179  
 ID AAY50179 standard; Protein; 1044 AA.  
 XX  
 AC AAY50179;  
 XX  
 DT 09-FEB-2000 (first entry)  
 XX  
 DE Human PI 3-kinase-related catalytic subunit p110-delta.  
 XX  
 KW lipid kinase; catalytic; subunit; p110-delta; PI 3-kinase;  
 KW phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation;  
 KW phosphatidylinositol (3, 4, 5) triphosphate; PI(3); activation; G protein;  
 KW cellular response; growth; differentiation; apoptosis;  
 KW phosphorylated lipid; protein kinase C; PKC; leukocyte activation;  
 KW interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator;  
 KW antagonist; agonist; treatment; disorder; cell growth;  
 KW cell differentiation; immune activation.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 141..310  
 FT /note="Ras regulatory region"  
 FT Domain 723..1044  
 FT /note="Catalytic domain"  
 XX  
 PN US959589-A.  
 XX  
 XX 16-NOV-1999.  
 XX  
 PF 06-JAN-1999; 99US-0225951.  
 XX  
 PR 25-NOV-1997; 97US-0977871.  
 PR 25-NOV-1996; 96US-0777405.  
 XX  
 PA (ICOS-) ICOS CORP.  
 PI Holzman DA, Hoekstra MF, Chantry DH;  
 DR MPI, 2000-012785/01.  
 DR N-FSDB; AA32882.  
 XX  
 PT Identifying modulators of lipid kinase subunit p110delta activity -  
 PS Claim 1; Columns 232-28; 22pp; English.  
 XX  
 CC This sequence represents a novel lipid kinase catalytic subunit,  
 CC p110-delta, related to phosphatidylinositol 3-kinase (PI  
 CC 3-kinase). PI 3-kinase is a heterodimer consisting of a membrane-  
 CC localising p85 subunit and a catalytic p110 subunit. These subunits both  
 CC have isoforms; p85 has two isoforms (alpha and beta) which are  
 CC differentially expressed, and p110 has to date three isoforms  
 CC (alpha, beta and gamma) that vary in their ability to associate with p85.  
 CC PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at  
 CC the 3' hydroxyl of the inositol ring with the primary product of PI  
 CC 3-kinase-mediated phosphorylation being phosphatidylinositol (3, 4, 5)

CC triphosphate (PIP<sub>3</sub>). PI 3-kinase is activated by interaction with G  
 CC proteins and PI 3-kinase activation is believed to be involved in a  
 CC range of cellular responses including cell growth, differentiation and  
 CC apoptosis. The downstream targets of the phosphorylated lipids generated  
 CC following PI 3-kinase activation have not been well characterised,  
 CC although some isoforms of protein kinase C (PKC) are directly activated  
 CC by PIP<sub>3</sub> in vitro. PI 3-kinase also appears to be involved in certain  
 CC aspects of leukocyte activation, such as interleukin-2 (IL-2) production  
 CC in T cells, and leukocyte signalling through G-protein coupled receptors.  
 CC p110-delta, or nucleotides encoding it, may be used to identify  
 CC modulators of p110-delta and/or PI 3-kinase activity. These may be useful  
 CC in the treatment of disorders associated with cell growth, cell  
 CC differentiation, apoptosis or immune activation.

SO Sequence 1044 AA:

Query Match 34.7%; Score 1978.5; DB 21; Length 1044;  
 Best Local Similarity 39.9%; Pred. No. 3e-179;  
 Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;

16 MPP-----RIIVECLPFGMIITLECLREATLTITHELFKEKARKYTHQ 60  
 1 MPFGVDCPMFMTKEENQSVVDFLPTGYLNPFSRNANLSTIKQLMHRQYEPFLH 60  
 61 LLODESSYIFVSTQEAEREFEFDETRLCDLRFQFLKVIKBPVGNREKILNREIGFA 120  
 61 MLSGPEAVYVFCLINQTAEOQLDEORLCDVQFPLRLVAREGKVKKLINSQSL 120  
 121 IGMVVCSEPDVWKOEDVDFRNILNVCKEAVDLRLNLSPHSRAMYVVPVNSPE--- 176  
 121 IKGILHEFDSLCDPEVNDFRKMKCFCEAAARQOLGEMWMLQYSPFLQLEPSAQWTGP 180  
 177 ----LPKHIYINKDKQGIIVIVYVSEPNDKQYTKINHCYPEQVYIAAIKIKTRSM 232  
 181 GTLRLPNR-----ALVVVKFEGSEESFTQVSTKDPVPLAMAAALRKK--- 224  
 233 LLSSEQLKCVLEVOGKTIYLVKCGDEYFLKPYLSQYKYTRSCIMLRMNLMAKES 292  
 225 ---ATVFQPLVEQPEDYTLQVNGRHEYLGNYPICQFOYCSLHSGTLTHLMVHSS 281  
 293 LYSQLPNMCFTMPSSRSRISTATPYMNGESTFKSLMVINSALRIKILCATYVNVNIRID 352  
 282 TLAMEDESNPAPOVQKPRAPKPPPIPAKPPSSVSLMSLEQPRIFLIGSKVNADER--M 339  
 353 KIYVRTGIYHGEPLCDVNTQVRP--CSNPRNEMLVNDIYIPDLPRARCLSLCSV-- 409  
 340 KLVVQAGLPHGNMLCKTVSSSEVSCSEPVWKORLEPDINICDLPMAARLCFALYAYIE 399  
 410 -----KGRGAKEHEHCPLAMGNINLPYDTTLVSGKALNLMV--VPHGLEDLNPIGV 462  
 400 KAKKARSTKKSGKADCPYAMANLMLFDYKDLKTGERCLYMPSPVDEKGBLNPPTGV 459  
 463 GSNPKETP-----CLELEFDMFSSVVKFPMDSVIEEHANWSYRBAFSSYSHAGLSNLT 517  
 460 RSNPNFDSAAALLICLP---EVAHPYVYPALEKILE-----L 494  
 518 ARDNE---LRENDKEQLRAICTRDLPLSEITTEOKDFLMSHRHYCVT--IPILFKLLLSYK 573  
 495 GRHSECVNTHTEEQQLREILERRSGELVYEHKDLVWKLRHVOCHFPFALARLLLVTK 554  
 574 WNSRDEVAQMYCLVKWPPIKRPOAMELLDCNYPDPMPVNGFAVRCLEKYTLDDKLSQYL 633  
 555 WNGHEVDAQMLYLLGWPBELPVLSALELDFSPDCVSGFALKSLRK--LTDDELQOYLL 613  
 634 QLVQVLYKIEOYLDNLVRFLLKKAITNORIGHFFMHLKSEMHNKTVSQFGLLBSYCR 693  
 614 QLVQVLYKIESYSLCELFLDLRALNRKLGHPFLMILRSEMVPSVALAFGLILBAYCR 673  
 694 ACQGVYLGHLNROYVAMEKTLINTDLILKQEKDETQVKQMFVEQ--MRPDPNADLOGFL 752  
 674 GSTHMKVLMKQSGALSKLALNDFVLSSQ--KPKQOTELMMLCMRQEVYIEALSHLQ 732  
 753 SPINPAHQNLRLBECRIMSSAKRPILMNWENPDINSELLFONNEIIFKNGDDLRLQDML 812

DB 733 SPLDSTLLAECVCEQCTCFMDSKKKPLMIWNSNEAGSG---GSVGLIFKNGDDLRLQDML 789  
 QY 813 TLQIIRIMENIMONGDLRLMPEYCGSLTGDCVGLIEVRNSHTLMQIQ--KGLGKALQ 871  
 DB 790 TLQMIQLMDVLMKQEGGLDRMTPYGCLPTGDRGLIEVLVLSDDITANIQLNKSNNAAATPA 849  
 QY 872 FNSHTLHOMLKDKNKGEIYDAIDLFTRSCGVCATFLLIGDRHNSINIMWKDGOULFH 931  
 DB 850 FKMDALLMWLSKKNGBELDRAIEEFITSLCAGYCAITVVLGIDHNSINIMRESGOLFH 909  
 QY 932 IDPGHFLHKKKFGKKEKRVFVLTOPFLVYSKAGQECTKREPERQEMCYAYIAI 991  
 DB 910 IDGHLFGFKTKFGINRERVFIITYDFVHVIQGG--KTNSEKFERFRGVCERAYTIL 967  
 QY 992 ROHANLFINLPSMMLGSGMPELQSPDIAVIRKTLALDKTEQDALEYFMKKNDAHSGM 1051  
 DB 968 RHHGLFLHLFLMLRAAGPELSCWDIQYLDKDSLALGTEBEALKHFRKFNLEALRESM 1027  
 QY 1052 TTKMDMIFHTTIQ 1064  
 DB 1028 KTKVNMLANHVS 1040

RESULT 8  
 AAM46625  
 ID AAM46625 standard; protein; 1044 AA.  
 AC AAM46625;  
 XX  
 DT 22-JUN-1998 (first entry)  
 DT 22-JUN-1988 (revised entry)  
 XX  
 DE Mammalian novel class I PI3 kinase designated p110-delta.  
 XX  
 KW Autophosphorylate; PI3; phosphatidylinositol 3-hydroxy; kinase;  
 KW activity; p110-delta; melanoma; lipid kinase; metacase;  
 KW phosphoinositide specificity; regulation; diagnosis; motility;  
 KW cancer cell; control.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 292..311  
 FT /note="proline-rich region"  
 FT 400..439  
 FT Domain /note="basic region leucine zipper-like domain"  
 XX  
 FN WO9746688-A1.  
 XX  
 PD 11-DEC-1997.  
 PD  
 XX  
 PF 30-MAY-1997; 97NO-CB01471.  
 PF  
 XX  
 PR 01-JUN-1996; 96GB-0011460.  
 PR  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 PA  
 PI Vanhasbroeck B, Waterfield MD;  
 PI  
 XX  
 DR WPI; 1998-042196/04.  
 DR  
 XX  
 DR P-PSDB; AAV16533.  
 DR  
 XX  
 PT Auto-phosphorylating peptide with phosphatidylinositol  
 PT 3-kinase-like activity, designated p110delta - useful for  
 PT controlling cell motility, particularly of metastatic cancer cells  
 PT  
 XX  
 XX  
 XX  
 XX  
 CC Disclosure: Fig 1A; 72pp; English.  
 CC  
 CC The present sequence represents a novel autophosphorylating protein  
 CC that has p13 (phosphatidylinositol 3-hydroxy) kinase activity, and  
 CC is designated p110-delta. The protein is expressed selectively in  
 CC white blood cells and melanomas. The protein is a lipid kinase with





CC prone to a disease or condition associated with the expression of PI3K,  
CC e.g. rheumatoid arthritis or asthma. The treatment works through the  
CC modulation (preferably inhibition) of the expression of PI3K. The  
CC antisense oligonucleotides may also be used for research and diagnostics,  
CC in pharmaceutical compositions and formulations, in the preparation of  
CC kits for detecting the level of PI3K in a sample, and as prophylaxis,  
CC e.g. to prevent or delay infection, inflammation or tumour formation.  
CC Antisense oligonucleotides, which are able to inhibit gene expression  
CC specifically, are used to elucidate the function of particular genes, and  
CC to distinguish between functions of various members of a biological  
CC pathway.

**SQ Sequence 1044 AA;**

Query Match	34.68;	Score 1976.5;	DB 21;	Length 1044;
-------------	--------	---------------	--------	--------------

Model	Best Local Similarity	Pred. No.	Gain
Model 1	39.9%	4.6e-179	97
Model 2	39.9%	4.6e-179	97
Model 3	39.9%	4.6e-179	97
Model 4	39.9%	4.6e-179	97
Model 5	39.9%	4.6e-179	97
Model 6	39.9%	4.6e-179	97
Model 7	39.9%	4.6e-179	97
Model 8	39.9%	4.6e-179	97
Model 9	39.9%	4.6e-179	97
Model 10	39.9%	4.6e-179	97
Model 11	39.9%	4.6e-179	97
Model 12	39.9%	4.6e-179	97
Model 13	39.9%	4.6e-179	97
Model 14	39.9%	4.6e-179	97
Model 15	39.9%	4.6e-179	97
Model 16	39.9%	4.6e-179	97
Model 17	39.9%	4.6e-179	97
Model 18	39.9%	4.6e-179	97
Model 19	39.9%	4.6e-179	97
Model 20	39.9%	4.6e-179	97
Model 21	39.9%	4.6e-179	97
Model 22	39.9%	4.6e-179	97
Model 23	39.9%	4.6e-179	97
Model 24	39.9%	4.6e-179	97
Model 25	39.9%	4.6e-179	97
Model 26	39.9%	4.6e-179	97
Model 27	39.9%	4.6e-179	97
Model 28	39.9%	4.6e-179	97
Model 29	39.9%	4.6e-179	97
Model 30	39.9%	4.6e-179	97
Model 31	39.9%	4.6e-179	97
Model 32	39.9%	4.6e-179	97
Model 33	39.9%	4.6e-179	97
Model 34	39.9%	4.6e-179	97
Model 35	39.9%	4.6e-179	97
Model 36	39.9%	4.6e-179	97
Model 37	39.9%	4.6e-179	97
Model 38	39.9%	4.6e-179	97
Model 39	39.9%	4.6e-179	97
Model 40	39.9%	4.6e-179	97
Model 41	39.9%	4.6e-179	97
Model 42	39.9%	4.6e-179	97
Model 43	39.9%	4.6e-179	97
Model 44	39.9%	4.6e-179	97
Model 45	39.9%	4.6e-179	97
Model 46	39.9%	4.6e-179	97
Model 47	39.9%	4.6e-179	97
Model 48	39.9%	4.6e-179	97
Model 49	39.9%	4.6e-179	97
Model 50	39.9%	4.6e-179	97
Model 51	39.9%	4.6e-179	97
Model 52	39.9%	4.6e-179	97
Model 53	39.9%	4.6e-179	97
Model 54	39.9%	4.6e-179	97
Model 55	39.9%	4.6e-179	97
Model 56	39.9%	4.6e-179	97
Model 57	39.9%	4.6e-179	97
Model 58	39.9%	4.6e-179	97
Model 59	39.9%	4.6e-179	97
Model 60	39.9%	4.6e-179	97
Model 61	39.9%	4.6e-179	97
Model 62	39.9%	4.6e-179	97
Model 63	39.9%	4.6e-179	97
Model 64	39.9%	4.6e-179	97
Model 65	39.9%	4.6e-179	97
Model 66	39.9%	4.6e-179	97
Model 67	39.9%	4.6e-179	97
Model 68	39.9%	4.6e-179	97
Model 69	39.9%	4.6e-179	97
Model 70	39.9%	4.6e-179	97
Model 71	39.9%	4.6e-179	97
Model 72	39.9%	4.6e-179	97
Model 73	39.9%	4.6e-179	97
Model 74	39.9%	4.6e-179	97
Model 75	39.9%	4.6e-179	97
Model 76	39.9%	4.6e-179	97
Model 77	39.9%	4.6e-179	97
Model 78	39.9%	4.6e-179	97
Model 79	39.9%	4.6e-179	97
Model 80	39.9%	4.6e-179	97
Model 81	39.9%	4.6e-179	97
Model 82	39.9%	4.6e-179	97
Model 83	39.9%	4.6e-1	

Matches	436;	Conservative	183;	Mismatches	311;	Inners	211	Cups	22
---------	------	--------------	------	------------	------	--------	-----	------	----

QY	16	MP-----RIIVCELLPMGMITTELCSEATLITITKHIEFFKARKYPLHQ	60
Db	1	MPGVCDCMEFNTKENOSVVDPLPFPVILNFPVSRNALSTIKOLIMHQAQEPFLPH	60
QY	61	LLODESSYI FVSVTQEAEREEREFDETRRILCLRLFOPLKATIEPQGNREBKLINEIGA	120
Db	61	MUSGEAVYFTCTINGTAQOELEDEQRRLCDVOPFLVRLVARBDRPKKILINSIL	120
QY	121	IGMPVCEPDMVNDPEVODPRRNLINAVCKEAVDLRLDINSHPAMVYYPNVESSPE----	176
Db	121	IGKGHIEPFLSDPEVNDPRAKKOCCEBAARROQLGWEANLQISFPQLEPSAQWGP	180
QY	177	-----LPKHLYNKLDKQIIVIMVIVYSPNNDKQYTLKINHCVBEQVIAEARIKKTISM	232
Db	181	GLRLPLNR-----ALLVNVKFEGBSESPFFQVSTKDVPLALMACLRK----	224
QY	223	LISSEQLKLCLEYGQKYILKVCGCDEYFLKPYLSQYKINSCLMGMPMLMAKES	292
Db	225	---ATVFRQPLVEQPEDYTLQVNGRHEHYUGSPLOQFOYICSLSHSGTLPHLTWHSS	281
QY	293	LYSOLPMDCFMPSYRRISTATFPYNNGETSTSLVWINSALRIKILCATYVNVNIRID	352
Db	282	ILAMRDEQSNAPDOVQPPRAKPPPIPAKKSYSVLSLEPRFIELIQSKVADR--M	339
QY	353	KIYVRTGIYHGSEPLCDNVNTQVTP--CSNPRNEMWLNIDYIPDLPRAPLCISTGSV--	409
Db	340	KLVVQAGLPRFGNEMLCKTVSSSEVSCSEBVMKORLEFDINICDLPMAELCALVAIE	399
QY	410	-----KGRKAGEBHCPLANGINLFDYIDTLYSGMAINLMP--VHGLEDLNPIGVT	462
Db	400	KAKKAASTKKKSKKADCPIMANILMFDYDOLGTGRCIYMPSPVDEKELLNPQTV	459
QY	463	GSNPNKETP-----CLEFDFMFSYVKKPFDMYSIEEHANVSREAGFSYSHAGSNRL	517
Db	460	RSNPNDSAAALLICLP--EVAPRYYVYALEKILE-----L	494
QY	518	ARDNE--LRENDKEOLRAICTRDPSEITEQEKPLMSHRHYVT--IPELPPLILSYK	573
Db	495	GRHSECVAHVEEQLOREILERRGSGELYEHENKOLWVKLRHEVOEHPRPALRLLVTK	55
QY	574	WNSRDEVAOMCYLVKMDPRPKFEQAMBELDONCYDDPMVRGPAVCLKELYLRDDLSQYL	633
Db	555	WIKRDEVAOMLYLLCSMPLEPVLSALELELDSPDCHGSAITSLRK--LTDDELFOYLL	613
QY	634	QLVQVLYUEOYLDYLVFLLKLLTQRIQHAFPMHLKSEMHNKTVYSQRFGLLESYCR	693
Db	614	QLVQVLYKTESYLDCELTFLDRRLAARKIGHLEFMHRSMDHVPVALRFGLLIEAYCR	673
QY	694	ACGVYLKHLNBOVEAMEKILNLTDLKQEKDETOKVOMKVLVBO--MRRPRPMALQOFL	75
Db	674	GRTHNMKVLMOGEALSTKLKALNPFVKSQ--KTRPKQTEIMHLCTMQEAVLEALSHIQ	73
QY	753	SPPLPAHOLGMLRDECRINSSAKRPLMLNENPDINSELLFONNEILFKNGDDLROML	81
Db	733	SPPLPSTLLAEVCQCTFMOSKMPPLWIMTINSBEAGS--GSVGITIFKNGDDLROML	78

Qy	813	TLGIIRIMENIWNQGLDLMFLPYGCLSTGBDCVGLIEVVRNHSHTIMQIC-KGGLKALQ	871
Db	790	TLQMTICLMDVLMKXQGBLDMTEPBGCLPBDRTGGLLEVRJRSBTIANIQLNKSMMATAA	849
Qy	872	FNSHTHQWLKDKRNGKEIYDAIDLFPSCAGYCVATFIIGIDRHSNIMVXDQGLFH	931
Db	850	FNDALNLMLKSNKPGESALDRAIEEFTLSCAGYCVATYVLGIDGRHSDNIMIRSGOLF	909
Qy	932	IDGHEFLDHHKKKRGYGRERVPFLTODPFLIVLSKGAOECTKTRPEFPOEMCYKALAI	991
Db	910	IDFHEFGNEFTKRGINRERVPFLITDPFVHVIQCG--KNNSSKFRPFRGCRYATIL	967
Qy	992	ROHANLEINTFSMWLGSQMBELOSFDIAIYRKTALDKTBOELLEYFMKMDNHHQGM	1051
Db	968	RRHGFLFLHLPALMRAGLPBLSCKSDIOYLKDSIALGKTEEALKHFRVKNELRESW	1027
Qy	1052	TTKMDWIFHTIKQ 1064	
Db	1028	KTKNVNLNHNYSK 1040	

## RESULT 10

AAU09685 standard; protein; 1044 AA  
ID

AAU09685;

DT 12-MAR-2002 (first entry)

Human p10delta isoform of PI3-kinase

XX Human; phosphatidylinositol 3-kinase, PI3K; p110delta isoform;  
 KW LAS-1; cancer; inflammatory disease; ophtalmic disorder; SH3 domain;  
 KW autoimmune disease; inflammatory bowel disease; bacterial pneumonia;  
 KW Type 1 diabetes mellitus; cytosstatic; immunosuppressive.

OS Homo sapiens.

PN WO200185986-A2

PD 15-NOV-2001

PF 10-MAY-2001; 2001WO-US15065-  
XX

PR 10-MAY-2000; 200005-202210  
XX

XX  
XX

(L) CDD / 2000 0000

XX 7  
0  
9  
9  
4  
0

DR N-PSDB; AAS14363.

PT Identifying a mod

PT binding partners to interact in the presence and absence of a test compound - PT

PS Example 1; page 48-51; 85pp; English.

The present invention relates to identifying a modulator of the phosphatidylinositol 3-kinase (PI3K; p13delta) enzyme that binds to the catalytic subunit via a SH domain-containing polypeptide such as LAMP-1. Also described are methods of assaying the specific binding affinity of the PI3-kinase binding partner. Such modulators are useful for the treatment of diseases characterised by the undesirable or excessive activity of PI3Kdelta. For example the modulators can be used for inhibiting the growth or proliferation of cancer cells (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues, Hodgkin's lymphoma, leukemias), inflammatory diseases (e.g. rheumatoid arthritis), opthalmic disorders (e.g. allergic conjunctivitis), autoimmune diseases (e.g. systemic lupus erythematosus), inflammatory

CC bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory  
 CC dermatoses (e.g. contact dermatitis; genital or peripheral nervous  
 CC system inflammatory disorders (e.g. meningitis), bacterial pneumonia,  
 CC and Type 1 diabetes mellitus. The present sequence represents human  
 CC p10delta isoform of p13k.  
 XX  
 SQ Sequence 1044 AA;  
 Query Match 34.6%; Score 1976.5; DB 23; Length 1044;  
 Best Local Similarity 39.9%; Pred. No. 4,6e-179;  
 Matches 436; Conservative 183; Mismatches 377; Indels 97; Gaps 19;  
 QY 16 MPP-----RILVCLPNGMIVTLECLREATLTITIKHELFKEARKYPLHQ 60  
 DB 1 MPPGVDCPMFEMTKENOSVVVDLPTGYLNPFPVSNANLSTIKOLMIRAQYPLFH 60  
 QY 61 LLDGESSYIVSVQAEAREEFPEETRCLDLRFQFPAKIEVGVNREKYLINREIGFA 120  
 DB 61 MLSGPEAVYFTCINQTAEOQLEDEORRLCDVQFPLRLVAREGDKVKLLINSQISL 120  
 QY 121 IGMPCFEDWVKDEVDFFRNILNVCKEAVDLRLNSPBRAMVYVPNVESSEPE--- 176  
 DB 121 IKGKIHFDLSCDEVDVDFRAKMGCFCEMAARQOLGEMNLQYSPPLQLEBPAQWGP 180  
 QY 177 ----LPHIYKLDKQIIVIVIVSPNNDKQYTKINHDVPEQVIAEARKTRSM 232  
 DB 181 GTLRPLNR-----ALVNVKFESESEFTQVSTKVDPLMLCALAKK----- 224  
 QY 223 LLSSEQKLCVLEYQKTIKVCOCDEYFLEKYPLOSQYKIRSCIMGRPNMLMAKES 292  
 DB 225 ---ATVRQPLVEQPEDYTLQVNGRHELYGSLYPLCOFOYICSLHGLPPLTMVHSS 281  
 QY 293 LYSQLPMDCFMPSYSRISATATPYMNGETSKLSLWINSALRIKICATVNVNINRDI 352  
 DB 282 ILAMDQSNPAPQVQPRAKRPPIPAKKESSVLSLEQFRLELIGQSVNADER--M 339  
 QY 353 KIYVRIGIYHGEPLCDNVATQVRP--CSNPRNEMLYDIYIPDLPRARLCLISCV-- 409  
 DB 340 KLVVQAGLPHGNEMLCVTSSEVSCSEPVWQRQLRPFIDINICOLPRMARLCPALYVIE 399  
 QY 410 -----KGRKGAKEHNPFLAMGNINLPDYITDLVSGMALNMP--VPHGLEDLINP 462  
 DB 400 KAKKARSTKSKKADCPRIAMNMLPFDYKDLTGRCCLYMPSPVDEKELLNPTGTV 459  
 QY 463 GSNPNKETP-----CLELFDPMFSSVYKPPDMSVTEEHAMSVREARFYSNAGLSNRL 517  
 DB 460 RSNPNDSAAALLICLP--EVAPHYVYPALEKILP-----L 494  
 QY 518 ARDNE--LRENDKEQDLRAICTRDLPLSEITEOEKDFLMSHRHYCVT--IPFILPYLLSVK 573  
 DB 495 GRSECVHVEEBQDLQREILERRGSEGLVNEHEDLVWKLRIHQVQHPREALRLLVTK 554  
 QY 574 WNSRDEVAQWYCVKMPPIKPEQAMLLDCNYRDPVNRGVARCLEKYLTDKLSYLI 633  
 DB 555 WNKHEDAWQWLYLCSMPBELPVLSALBLDFSPFCHGVGFAIKSLRK--LTDDELFOYLL 613  
 QY 634 QLVQVLKYEQYLDNLVRFLLKALTNQRIQHFEFMMHLKSEMHKNTQSQRGILLSEYCR 693  
 DB 614 QLVQVLKYESYLDCELFKFLDLRLARKTIGHFLMRSEBMHPSPVALRFGILLLEVYR 673  
 QY 694 ACGMYLNLNROYEAMEKLINTDLIKQEKDETQKQMFLEVO--RRRDPMDALOGFL 752  
 DB 674 GRTHMKVLMKQEBALSSTKALNDFVLSGQ--KTPKQOTELMHLCKRQAVALEASHLQ 732  
 QY 753 SPLNPAHQNLRLSECRINSSAKRPLMLWENDIMSELLPQNNELIIFKNGDDLRODML 812  
 DB 733 SPLDPSLTIAVECVCEQCTFMDSKKPLMIMYSNEASG--GSVGIIIFKNGDDLRODML 789  
 QY 813 TLGIIRMENIMONOGDLMLPYGCLSIDGCVGLIENVNSHTIMQIC--KGSGLKALQ 871  
 DB 790 TLWQIQMLMDVLMKQEBGLRLKRTYGCPLTGRGGLIENVLRSDTIANIQLNKSNMAATYA 849  
 QY 872 FNSHTLHQLKDKXKGEIYDAIDLFTSCAGYCVATFIIGDRHNSNIMVXDQGLFH 931

DB 850 FNNKALLNWLKSKNPGALBRAIEFPLSCAGYCVATYVIGIDRHSNINIRSGQLFH 909  
 QY 932 IDEGHELDHKKKRGYREVPVPLTODPLIVISKQOECTKREFRFQEMCKALAI 991  
 DB 910 IDEGHELDHKKKRGYREVPVPLTODPLIVISKQOECTKREFRFQEMCKALAI 967  
 QY 992 ROHANLFINFMMWLSGMPLEQSFDDIAYIRKTLADKTEQALVEYFMKQMDAHNGW 1051  
 DB 968 RHGHLFLHFLPALMRAAGLEPLSGSKDIQYUKOSIALGKTEBEALKFRYKFNALRESW 1027  
 QY 1052 TTKQDWTFHTIKQ 1064  
 DB 1028 KTKVNMVLAHVSK 1040  
 RESULT 11  
 AAB11124  
 ID AAB11124 standard; Protein; 1070 AA.  
 XX  
 AC AAB11124;  
 XX  
 DT 16-FEB-2001 (first entry)  
 XX  
 DE Human P13 kinase p10delta protein.  
 XX  
 KM Human; p13 kinase p10 beta; antisense inhibition; primer; cytosolic;  
 KM antiinflammatory; antiinfective.  
 OS Homo sapiens.  
 XX  
 PN US6133032-A.  
 XX  
 PD 17-OCT-2000.  
 XX  
 PF 09-SEP-1999; 99US-0392350.  
 XX  
 PR 09-SEP-1999; 99US-0392350.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Monia BP, Cowseert LM;  
 XX  
 DR WPI: 2000-686014/67.  
 DR N-PSDB; AAC65690.  
 XX  
 PT Antisense compound 8-30 nucleobases in length targeted to a start codon  
 PT of the coding region of human p13 kinase p10beta, useful for  
 PT inhibiting the expression of the human polynucleotide -  
 PS  
 XX Example 1; Column 43-50; 34pp; English.  
 XX  
 CC This invention describes a novel antisense compound (I) 8-30 nucleobases  
 CC in length targeted to a start codon or nucleobases 4-3174 of the coding  
 CC region of human p13 kinase p10beta (II), in which (I) specifically  
 CC hybridizes with and inhibits the expression of (II). The products of the  
 CC invention have cytostatic, antiinflammatory and antiinfective activity.  
 CC (I) is useful for inhibiting the expression of (II) in human cells or  
 CC tissues. The antisense compound can be utilized for diagnostics,  
 CC therapeutics, prophylaxis and as research reagents and kits. The  
 CC antisense compounds may also be useful prophylactically, e.g. to prevent  
 CC or delay infection, inflammation or tumor formation. The antisense  
 CC compounds are useful for research and diagnostics, because these  
 CC compounds hybridize to nucleic acids encoding (II).  
 XX  
 SQ Sequence 1070 AA;  
 Query Match 34.4%; Score 1966; DB 21; Length 1070;  
 Best Local Similarity 40.1%; Pred. No. 4.9e-178;  
 Matches 446; Conservative 194; Mismatches 371; Indels 102; Gaps 25;  
 QY 1 MPPRPS--GELWGIH--LMPRLIVCLPNGMIVTLECLREATLTITIKHELFKEARKY 56

Db 7 MPAMADLIDIAWVDSQIASDGSIPVDLPTGIYIOLEVPREATTIYIKOMLMKVHNY 66  
QY 57 PLHQLODESSYIFVSVTQEAEREFPETRLCDLRLFOFFLKVIEPVGNREKILNRE 116  
Db 67 PMRLMLNDISYMACVQRAVYELDELTRRLCDVAPFLPVLLVTRSCDPGSK-LDSK 125  
QY 117 IGFAIGMPVCEFDWVKDPEVDFRRNLINCKEAV-DLRDLNSPHSRAMYYPPNVSSP 175  
Db 126 IGVLIIGKLHEFFDSLKDPEVNEFRKRRKFESEKILSLVGL-SWMDMLKQTPP--BHEP 182  
QY 176 ELPRHITNKLKQGIIVIVWIVYVSPNNDKQYTKIKINHDCPEQVIAEAIKKRSMLS 235  
Db 183 SIPENLDEKLYGKGLIYAVHF---ENCQDVFSQVSPNNMPKYNELAIQK----- 231  
QY 236 SEQKLCVLEYQK-----YILKVGCDVEYLEKPLSQYXYISCSIMAGMPNML 287  
Db 232 -----LTIHGEDEVSFYDYLVQSGREYVFGDHPLOFOYIRNCVNNRALPHIL 283  
QY 288 MAKESLYSQLPMDCFMPSYSRRISTATPYNNGETSTK--SLWVINSALRIKILCATYV 344  
Db 284 VECCIKIKMYEQEMIAIEAALNRSSNLPLPLPKTRIIISHVENNNPFOIVLVKGN-- 341  
QY 345 NVNIRIDIKIYVRGIIYHGERPLCDNVTORVPCSNRP-VNEMINVDIYIPDLPPAARLC 403  
Db 342 KLNTBEETVKVHVRGLFPGTBLCKTIVSSEVSGKNDHIMBEPLEFDINICDLPMAALC 401  
QY 404 LSICS---VKGRKAK-----EEHCPLAMGNINLFDYDTLVSGMALNL 445  
Db 402 PAVYAVLDKVKTKSTKTIINSKYOTIKAKGNVHPVAMVNMVDFGQLRGTGIIHS 461  
QY 446 W-PVPHGEDLLNPIGVTGSNNKETPCLLEFDFSSVVKFPDM-----SYIE 493  
Db 462 WSPFDELEEMLNPMGTIVQNPYENAT-----ALHVKEPENNKKOPYYYPPEPKIIE 513  
QY 494 EHAMSVSRBAGFSISHAGLSRLARDNELRNDKEQALICTRPLSEITEQEOPFMS 553  
Db 514 KAAEIASDSANVS-SRGG-----KKLPVLKEIILDRPLSLCENEDLIWT 560  
QY 554 HRHYCVTI-PEILPKLLSVKNSRDEVAKQYCLVMDWPIKPEOAMELLDNCYPDPNVR 612  
Db 561 LRQDCREIFPQSLPKLLSIRKKNKEDVAGLOALLQIMPKLPPRELBELDDNYDQYVR 620  
QY 613 GRAVACLEKYLTDKLSQYLIQVLYVLYKYEYLDMLVFLIKKALTNORIGHFFPWHK 672  
Db 621 EYAVGCL-RQMSDELSQYLIQVLYKYEPEFLDCALSRFLERALLGNRRIOQFLFHHLR 679  
QY 673 SEMHNKTVSQRGLLIESYCRACGMVTKLKNQVEMELINLTILIOEKXKDEYQKVM 732  
Db 680 SEVHLPASVQPGVILEAVCRGSGVMKVLKQVEALNKLKTLNLSLTKLNAVKLNRKAK 739  
QY 733 KFLVQMRPDPMDALOGFLSPNPAHQGNLRECRIMSSAKRPLMWNENPDIMSEL 792  
Db 740 EAMHTCLKQSAVREALSDQSPNPFVILSELVEKCKTMDSKMLVYNN-KVFGS- 797  
QY 793 LFQNNELIPKNGDRLRQDMLTQIRIMENIWQNOGLDIRMLPYGLSLGDCYGLIEVVR 852  
Db 798 --DSGVVIFKNGDRLRQDMLTQIRIMENIWQNOGLDIRMLPYGLSLGDCYGLIEVVR 855  
QY 853 NSHTIWOIC-KGGLKGLAQFNSHTLHQLKDKNGKEIYDAALDLTRSGAGCVATFLL 911  
Db 856 TSETIADIDNSSNVAFAAFAFNKDALINMLKEYNSSGDDLDRALEBTLSCAGYCVASYL 915  
QY 912 GIGDRNSINMYVDDQOLFIDFGHFLDHKKKKYKREVRPVLTODFLIVISKAQRC 971  
Db 916 GIGDRNSINMYVDDQOLFIDFGHFLDHKKKKYKREVRPVLTODFLIVISKAQRC 973  
QY 972 TKTRFEREROEMCYKAYLAIROHANLFINLSMMLSGNPELOSPDIAYIRKTLALDKT 1031  
Db 974 GNTEKGRFROCEADAYLIRHGNLFITFLALMTLAGBELTSVXDIOYIKDSLALGKS 1033  
QY 1032 EOEALIEYFMKQNDAAHGGCTTGMDFHTIKQ 1064  
Db 1034 EEBALKOFKOFDEALRESWTTRVNNMAHTVRK 1066

RESULT 12  
ABP65170  
ID ABP65170 standard; Protein; 1070 AA.  
XX  
AC ABP65170;  
XX  
DT 12-NOV-2002 (first entry)  
XX  
DE Hypoxia-regulated protein #44.  
XX  
KW Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;  
KW antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine;  
KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;  
KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;  
KW preclampsia; atherosclerosis; inflammatory condition; wound healing;  
KW inflammation; erythropoiesis; hair loss; human.  
XX  
OS Homo sapiens.  
XX  
PN MO200246465-A2.  
XX  
PD 13-JUN-2002.  
XX  
PF 10-DEC-2001; 2001WO-GB05458.  
XX  
PR 08-DEC-2000; 2000GB-0030076.  
PR 08-FEB-2001; 2001GB-0003156.  
PR 25-OCT-2001; 2001GB-0025666.  
XX  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
XX  
PI White J, Mundy CR, Ward NR, Krige D, Kingeman SM, Harris RA;  
PI Rayner WN;  
XX  
DR WPI, 2002-627238/67.  
XX  
PT Identifying a gene involved in disease for treating hypoxia-regulated  
PT conditions, comprises comparing the transcriptome/proteome of two cell  
PT types under different conditions and identifying a differentially  
PT regulated gene  
XX  
PS Claim 35; Page 363; 538pp; English.  
XX  
CC The present invention relates to methods for identifying genes and  
CC proteins that are implicated in a specific disease or physiological  
CC condition. The method comprises comparing the transcriptome/proteome of a  
CC specialised cell type implicated in a disease or condition with that of a  
CC second specialised cell type, under two experimental conditions, and  
CC identifying a gene that is differentially regulated in the two  
CC specialised cell types under experimental conditions. ABV77673-ABV78116  
CC and ABP65061-ABP65257 were identified using the methods of the invention.  
CC The coding sequences and proteins are useful for treating a disease in a  
CC patient, for manufacture of a medicament for treating hypoxia-regulated  
CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,  
CC biological response to hypoxia conditions, or hypoxic-associated  
CC pathology in a patient. The coding sequences and proteins are also useful  
CC for monitoring the therapeutic treatment of a disease or physiological  
CC condition, such as cancer, ischaemic conditions, reperfusion injury,  
CC retinopathy, neonatal stress, preclampsia, atherosclerosis, inflammatory  
CC conditions, wound healing, inflammation, erythropoiesis or hair loss.  
XX  
SQ Sequence 1070 AA;  
XX  
Query Match 34.4%; Score 1966; DB 23; Length 1070;  
Best Local Similarity 40.1%; Pred. No. 4,9e-178;  
Matches 446; Conservative 194; Mismatches 371; Indels 102; Gaps 25;  
QY 1 MPBRES-GEIWGIR--LMPRIIVCELLPMGMVTELECAEATLITIKELFKEARX 56  
Db 7 MPAMADLIDIAWVDSQIASDGSIPVDLPTGIYIOLEVPREATTIYIKOMLMKVHNY 66

```

QY 57 PLHQLLODESSYIFVSVTOAEAREEFDETRRLCDLRFQPLKYIEPVGNREKILNRE 116
Db 67 PMFNLLMDIDSYMFACVNOQTAAYEELEDETRRLCDVRPFLPVKLVTNRSCDPGEK-LDSK 125
QY 117 IGFAIGMPVCEFDWKDEVDQFRNRILNVCKEAV-DLRDLNSHSAAMVYPPNVSSP 175
Db 126 IGVILGKGLHFEBSLKDPEVNERFRKRRKFSSEKITLSVGL-SYMDMLKQOTYPP--SHEP 182
QY 176 ELFRHLYNKLDKQIIVVIVIVIVSVPNNDKQYTLKINHDCVPEQVIAEARIKTRKSMILS 235
Db 183 SIBENIEDKLKYGKLIIVAHVF---EKCDVFSQVSPNNMPIKVNLAIOKR----- 231
QY 236 SEOLKLCVLEYOK-----YILKCGCDEFLKPYLSQYKTRSCIMLGMPLML 287
Db 232 -----LTIHCKEDEVSPLYDVLQVSGREYVFGDHPILQFOYIRNCVNNBALPHFIL 283
QY 288 MAKESLYSQPMOCFTMPSYRRIISTATPYMNGETSFK---SLMVINSARIKILCTYV 344
Db 284 VECCKIKKWEQEMIAIEAINNSSLPLPPEPKTRIIISHWENNPPQIIVLVKGN-- 341
QY 345 NVNIRIDIKLYVRTGYHGEPLCDNVNTOVPCSNR--NMEMLNYDIYIPDPARRLC 403
Db 342 KNTTEFTVKVHVAAGLPHGTELLCKTIVSEVSGKNDHINNEPLEPPIINICDIPRARLC 401
QY 404 LSTICS---VKGRKAK-----EEHCPLAMGNINLPDYTTDLVSGKMAI 445
Db 402 FAYVAIADKVKTKKSTTINPSKYQITIRKAGKHYPVAVNWTVPDEKQGLRTGDIILHS 461
QY 446 W-FVPHGLDLPNPGVTSNPNKTEPCLLEFEDWSSVYKPDN-----SVTE 493
Db 462 WSSFPDELEBMLPMGVQNTNYTENAT-----ALHAKFENKKOPYYPFPKITE 513
QY 494 EHAMSVSBEAGFSYSHAGLSNRLARDNELRENDKQLRAICRPDLSEITEOEKFLMS 553
Db 514 KAABISSSANVS-SRGC-----KKFLPVLKIIDRDLPSQCEHEMDLIWT 560
QY 554 HHHYCVTI-PEILPKLLSVKMSRDEVAOMCYLVKDWPIKEQAMELLDCNYPDMVR 612
Db 561 LRQDCBEIFPOSJPKLLLSIKMKNLEDAVQALQALQIOWPLPREALELDFNYPOQYVA 620
QY 613 GFAVRLCEKYLTDKLSOYLIOUVOYLAKYQOYLIDNLLVRLKALKALTNORIGFFWHLK 672
Db 621 ETAVGCL-KOMSEBESQYLOLVQVAKTEPFLDCAISRLLERAAIGNRITIGFLWHLR 679
QY 673 SEMHNKTVSQRFLLESYCRACGYLKLINROVEAMEKILNLTDLIKOEKKDEQXQVM 732
Db 680 SEHHRPAVGVQFVILAEATCRSGVGMKVLKSKOYEALNKLKTINSILKLAVALNPAKKG 739
QY 733 KFLVEQMRBPFMDALQGLSPUNPAHOLGNLREBSCRIMSSAKRPLMWNENPDIJMSL 792
Db 740 EAMHTCLKQSAVREALDLOSPLNPCIILSELYVERCKYVDSKXPLMLVYNN-KVFGF- 797
QY 793 LRQNNELIRKNGDDLQODMLTLOITIMENINONOGDLMLPYGCLSGDCVGLIEVVR 852
Db 798 --DSVGVIFRKGDDLRQDMLTLOMLRLMLLWKEADJLRMLPYGCLAGDREGLLEVVS 855
QY 853 NSHTIWOIC-KGGLKGALOFNSHTLHOWLKQNKKEIYDAIIDLFTRSAGCVATPIL 911
Db 856 TSETIADIDLNSNVAAAAAFKNDALLNMLKEVNSGDDLRALERTTLSCAGCVASVYL 915
QY 912 GIGDRHNSINIMYKDDQDLFIHDFHFLDHKKKFGYKRERVPVFLTODFLVIVSKAQC 971
Db 916 GIGDRHSDIMWKYKQQLPHIDFGHILGNFKSFGIKRERVPVFLTYDILHVIQOG--KT 973
QY 972 TITREBERQEMCYKAYLAIRQHANFIVLFSMMLSGMPELOSFDIYIYIKTLADLT 1031
Db 974 GNTKFKGRROCCEDYLLIRRHGNLFTILFALMLTAGLPBELTYSVDIOYLDKSLALGKS 1033
QY 1032 BOEALLEYFMKQNDAAHHGMITKMDIPIHTIKO 1064
Db 1034 EEBALKQFKQKDEALRESMTTKVMMALTVRK 1066

```

```

RESULT 13
AAU09688
ID AAU09688 standard; Protein; 1070 AA.
XX
AC AAU09688;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human p110beta isoform of PI3-kinase.
XX
KW Human; phosphatidylinositol 3-kinase; PI3K; p110beta isoform;
KW LAMP-1; cancer; inflammatory disease; ophthalmic disorder; SH3 domain;
KW autoimmune disease; inflammatory bowel disease; bacterial pneumonia;
KW Type I diabetes mellitus; cytostatic; immunosuppressive.
XX
OS Homo sapiens.
XX
PN W0200185986-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001MO-US15065.
XX
PR 10-MAY-2000; 2000US-203346P.
XX
PA (ICOS-) ICOS CORP.
XX
PI Sadhu C;
XX
WPI; 2002-075252/10.
DR N-PSDB; AAS14366.
XX
PT Identifying a modulator of p110delta polypeptide binding to SH3
PT domain-containing polypeptides e.g. LAMP-1, comprising allowing the
PT binding partners to interact in the presence and absence of a test
PT compound.
XX
PS Example 1; Page 68-71; 85pp; English.
XX
CC The present invention relates to identifying a modulator of the
CC phosphatidylinositol 3-kinase (PI3K; p110delta) enzyme that binds to
CC the catalytic subunit via a SH3 domain-containing polypeptide such as
CC LAMP-1. Also described are methods of assaying the specific binding
CC affinity of the PI3-kinase binding partner. Such modulators are useful
CC for the treatment of diseases characterised by the undesirable or
CC excessive activity of PI3Kdelta. For example the modulators can be used
CC for inhibiting the growth or proliferation of cancer cells
CC (e.g. malignant neoplasms of lymphoid and reticuloendothelial tissues,
CC Hodgkin's lymphoma, leukaemias), inflammatory diseases (e.g. rheumatoid
CC arthritis), ophthalmic disorders (e.g. allergic conjunctivitis),
CC autoimmune diseases (e.g. systemic lupus erythematosus), inflammatory
CC bowel diseases (e.g. chronic inflammatory bowel disease), inflammatory
CC dermatoses (e.g. contact dermatitis; central or peripheral nervous
CC system inflammatory disorders (e.g. meningitis), bacterial pneumonia,
CC and Type I diabetes mellitus. The present sequence represents human
CC p110beta isoform of PI3K.
XX
SQ Sequence 1070 AA;
XX
Query Match 34.4%; Score 1966; DB 23; Length 1070;
Best Local Similarity 40.1%; Pred. No. 4,9e-178;
Matches 446; Conservative 194; Mismatches 371; Indels 102; Gaps 25;

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Db 126 IGVILGKGLHEPDSLKDPEVNEFRMRKSEKILSLVGL-SWMDLQTYPP--EHEP 182
Qy 176 ELPKHIVNKLKDKQIIIVIMVIVSPNNNDKQYTLKINHDCVPROVIAEAIKRRKSMLS 235
Db 183 SIPEINEDKLYGKGLIVAAVHF---ENCQDVSPFQVSPNNPKVNEIAQKR----- 231
Qy 236 SEQLKLCVLEYQSK-----YLVKVCDEYFLEKYPKSYKXIRSCIMLRMPNML 287
Db 232 -----LTIHKEDEVPSPDYVLQVSGRVEYVFGDHPILQFOYIRNCVMNRPALPHFIL 283
Qy 288 MAKESLYSQLPMDCTMPSYSRRISTATPYMNGETSK--SLMVINSARIKILCATYV 344
Db 284 VECCIKIKMYEOEMIAIEAIIINRSSNLPPLPPKTRIIISHWENNPPQIVLVGN-- 341
Qy 345 NVNIRIDDKIVYRTGIVHGEPLCDNVNTPCSPNPR--NMEMLNYDIYIPDLPRARLC 403
Db 342 KLVTEETVKVHAGLGHTELLCKTIVSSEVSGKNDHINNEPLEFINICDLPRMARLC 401
Qy 404 LSICS---VKGRKAK-----EEHCPLANGNILEFDYDTLVSGKMAI 445
Db 402 PAVYAVLDKTKTKSTKSTINPSKYOTIRKAGKHVYPAVMVTVWFDFKGLRTGDIILHS 461
Qy 446 W-PVPHGLEDLNPIGVTGSPNKEPCLLEEFMFSSVYKFPDM-----SVIE 493
Db 462 WSPFDELEEMINMGTVQTPYENAT-----ALHYKFPENKKQPYPPPKXIE 513
Qy 494 EHNWMSYRREGFSYHAGLSNRLARONELRENDKEOLRAICTROPTSEITEQKDFLWS 553
Db 514 KAAETASSDSANVS-SRGG-----KKRLPVLEKILDDPISQLCENEMDLMT 560
Qy 554 HRHRCVTI-PEILPKLLSVKMSRDEVAQWYCIWKMPRIKPEQAMELLDCNTPDMVR 612
Db 561 LRQCRRIEFPQSLKLLSIKMNLEDAQIQALLQIWPKLPRBALELDFNYPDQYVR 620
Qy 613 GFAVRCEKYVTDKLSOYLQIYQVLYKYEOYLDNLVRFILKALTNQRIGHFFPMK 672
Db 621 EYAVGCL-RQMSDELSQYLLQIYQVLYKYEPFLCALSRFLERLGRRIQGFELFHLR 679
Qy 673 SEMNKYVSRPGLLESYACAGVYLGHILROYEAMEKILNLTILNQEKKDETOKYQM 732
Db 680 SEVHIVAVSVQFVLEAVYCRGSGVMKVLKQVEALNKLTLINSLILANVKLRAGK 739
Qy 733 KFLVQMRPDPMDLQGLSPLNPAHQILNLEECRINGSAKRPLMNMENPDIMSEL 792
Db 740 EAMHTCLKOSAYREALSDQSPNLCVILSELVEKCYKMSKMLMLVYNN-KVGE- 797
Qy 793 LFQNNELIFKGGDLRQMLTIQIRIMENTWONGDLRLMRYCCLSIGCVGLIEYVR 852
Db 798 --DSVGVIFKGGDLRQMLTIQMLRLMDLWKEAGDLRLMRYCGLATGDSGLIEVVS 855
Qy 853 NSHTMQIQ-C-KGKAGKALQFNSHTLHQMLKDKNKEIYDAIDLFTRSCAGYVATEIL 911
Db 856 TSETIADIQLNSSNVAALAAFNKDALNMLNKEYNSGDDIDRAIEFTLSACAGYVATL 915
Qy 912 GIGDEHNSINWYKDGOLFHDGFHLDHKKKKFGYKREVRPVLTODELIVISKAQDC 971
Db 916 GIGDHSNINWYKDGOLFHDGFHLDHILGFKSGFGIKREVRPEILTYDRIHIQGC--KT 973
Qy 972 TKTRFEFQEMCYKAYLAIQHANLFINLFSMILSGMPEIOSPDIAIYIKTIALDPT 1031
Db 974 GNTKFRGFRQCCEDYVILIRRHGNLFIPLFALMLTAGLPELTSVDIQLKDSLALGKS 1033
Qy 1032 EOEALFYPMKONDAHNGWTMKMDIHTIKQ 1064
Db 1034 BEBALKQFKQKDEALRESWTTKVMMAHTVRK 1066

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RESULT 14  
 ABB60424 standard; Protein; 1088 AA.  
 ID ABB60424  
 AC ABB60424;  
 XX . . .

```

Dt 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 8064.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KM pharmacetical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001MO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PEKE ) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR MPI; 2001-656860/75.
XX DR N-PDB; ABL04527.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX PS Disclosure; SEQ ID NO 8064; 21pp + Sequence listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
XX CC sequences (AB101840-AB116175) and the encoded proteins
XX CC (AB157737-AB172072).
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 1088 AA;
XX
XX Query Match 29.4%; Score 1677.5; DB 22; Length 1088;
XX Best Local Similarity 35.1%; Pred. No. 2e-150;
XX Matches 384; Conservative 217; Mismatches 365; Indels 107; Gaps 28;

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Qy 24 CLTPNGMIVTLECLREATLTIKHELKREARKYPLHQLDDESSYIFVSVTQAEAREEFF 83
Db 49 CLTPNGFLLELRVNPANTIOYIKEMVNOAKOMPLGVYIKACEYQYIGIS-TNIEIYPT 107
Qy 84 DETRLCDLRLFOPLKVIPEVGNRE-----KILNREIGFALGMVCEFDNVK 132
Db 108 DETRLASV---QYFGLIS-LGERTDTSSSDYELTKVMNGMIG-----TFPDHNR 156
Qy 133 ---DEVDQFRNINLVNKEAVLDLNLSPHSRMYTYVPPVASSPELPHKIIYNKLDGQ 189
Db 157 THGSPEDIDFLMYTQTCNDIELERSAYTWOORLYEHRLANSTKQBELIREHNPRT 216
Qy 190 IIVVWVIVSPNDKQKTLKINHDCVEQYIAEIRKRTSMILSSQLKLCVLEYQSK 249
Db 217 FLIV---VKQENDSTFTLVNEDQTPFSLESTLQKMRNSQMKMNR-----ISD 264
Qy 260 YLVKVCDEYFLEKYPKSYKXIRSCIMLRMPNIMAKESLYSQLPMDCTMPSYSR 309
Db 265 YLVKVGSRDEYILGYPILQFIYIOEMLSDAVPRVVL---QSVYR---LESYINHNMQ 318
Qy 310 RISTATPYMNGET-----STSLWVINSALRIKILCATYVNVNINPIDIKIYRTGIIYHG 364
Db 319 AMVTRPLPKRTVTLHKSISSLMDMGVYFQTLTSHISNVNFDKTRALVGVHCLYHGD 378

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QY 365 EPLCDNNTQVPCSNRNEMW-----NDYITIPDLPRAPLCLISCV---KRRKG 414
DB 379 KKDCAORSTD---SPNCFITFLFNDLVMPDIQMRNLPRWTRICIVIEFTWKMSRSKKS 435
QY 415 AKEEHC-----PLAMGNILFDYTLTVSGKALNMPVPHGLE--DLNPIGVY 462
DB 436 SNNKDIALKVPYKPKNPLAMVNTTIFDKDLRTGRHTLTWTYADDIQSVVEHPHIGTI 495
QY 463 GSNPNKETPCLLEEFDFSS---VVKFPDMSVIEEHANMSVSRAGFSYSHAGLSNRLAR 519
DB 496 EPNPRKE-ECALVDLFTLSSGTGYVRPSEEVLYQA---ADRDQ-----VNLQR 542
QY 520 DNELRENDKQOLRAICTR---DPLSEITQEKDFLWSHRYCV-TIPEILPKLLSVKM 574
DB 543 QLAGPEKPIELKELMANVYTGDLKIYEMVDNRNAVIERRNDILRELPEELSTILHCYVM 602
QY 575 NSRDEVANQWYCVKWDMPPIKPEQAMELLDNCPYPRMWRGFAVRRLKELVLDKLSQVLIQ 634
DB 603 KERDDVADMMYLYKOWPLISIERLELDYAVPDPVARRAIRCLH-FLKDEDLLLYLQ 661
QY 635 LVQVLKYEQYLDNLVFLFKKALTNRIGHFFFMHLSEMHKNTVSQRFGLLESYGRA 694
DB 662 LVQAIKHESYLESPLVFLERLARNRIGHYFMHLRSEMOTPSMOTRIGLLLEVYLGK 721
QY 695 CGMYLKHNLNQVEAMEKILNLTDLKQEKDETOQVQMKFLVEQMRPRDFMDALQGFLLSP 754
DB 722 CKHNVAPLRKQHLVLEKLGKSLAKKSKKXKVTMLQDFLRDQNSAVF---QNTQNP 777
QY 755 LNPFAHQGNLRLEECRIMSASAKRPLYMNMENPRDIMSLLQONNEITRKNGDDLRODMTL 814
DB 778 LNPSPFCGSGTTPRCXKWDKMRPLWVWFENAVNA---SDVHILIFKQNDDLRODMTL 833
QY 815 QIIRIMENIWQNGDLRLMPLPGCLSIGDCVGLLEVVRNSHTIMQJCKGKGLGALQ-FN 873
DB 834 QMRVWDQMLKRGMDPRKAIYVICISMESKLGMEVVRHAETIANIOXKGMMSATSPFK 893
QY 874 SHTLHOMLKDKNK-GEIYDAIDLFTSCAGYCVATFIIIGDRHNSNINWVKDQQLFHI 932
DB 894 KGLSLTMLKEHNPRADKLNAINEFLSCAGYCVATVGLVADRHSNINWKNQQLFHI 953
QY 933 DEGHFDHKKKKKGYRERYRPFVLTQDFLVISKGAOECTKTEPERFQMCYKAYLAIR 992
DB 954 DREHILIGHFEKLGVRERERPVLTDFVYVINKGFND-RESKEFCHFOELCERAFVLR 1012
QY 993 QHANLFINFSMMLGSGMPELQSFDDIAYIRKTLALDKTEQALIZYPMQMDAHHGWT 1052
DB 1013 KNGCLLSLFSMMISTGLPELSEKDLDIREFVLDVYTEKAREHPRAKSEPLANSWK 1072
QY 1053 TKMDWIFHTIKOH 1065
DB 1073 TSLNMASSHNSKN 1085

RESULT 15
AAW90089
ID AAW90089 standard; Protein; 1101 AA.
AC AAW90089;
XX
XX
XX 09-MAR-1999 (first entry)
DE Human G-protein regulated PI3K p120 adapter subunit protein.
XX
XX Phosphoinositide 3-hydroxylase; PI3K; trimeric G protein; human;
XX adapter subunit; regulatory subunit; p101; p120; catalytic subunit;
XX detection; diagnosis; activation disorder; haematopoietic system;
XX treatment; immune disorder; inflammation; arthritis; septic shock;
XX adult respiratory distress syndrome; pneumonia; asthma; allergy;
XX reperfusion injury; atherosclerosis; Alzheimer's disease; cancer.
OS Homo sapiens.
XX
XX US5856132-A.

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XX 05-JAN-1999.
PD 15-AUG-1997; 97US-0916917.
XX
PE 15-AUG-1997; 97US-0916917.
XX
XX 15-AUG-1997; 97US-0916917.
PR 27-JUN-1996; 96US-0672211.
XX
PA (ONXX-) ONXX PHARM.
XX
XX Brasselmann S, Hawkins PT, Stephens LJ,
XX WPI; 1999-105107/09.
DR N-PSDB; AAW74104.
XX
PT Nucleic acid encoding regulatory (p101) and catalytic (p120)
PT subunits of a heterodimeric phosphatidylinositol-3' kinase - useful
PT in treatment and diagnosis of immune system disorders, e.g.
PT arthritis, cancer and Alzheimer's disease
XX
PS Claim 15; Fig 13; 75pp; English.
XX
XX This sequence represents a novel catalytic subunit, p120, from human
XX phosphoinositide 3-hydroxylase (PI3K) which is regulated by beta-gamma
XX subunits of trimeric G-protein. Nucleic acid coding for p101 or p120, or
XX their fragments, are used as probes and primers for identifying p101 or
XX p120 gene mutations, allelic variations or regulatory defects,
XX particularly for the diagnosis of activation disorders (or
XX susceptibility) in cells of the haematopoietic system. The related
XX proteins, antibodies, agonists and antagonists can be used similarly. The
XX p101 and p120 proteins, peptides or fusion proteins are used to treat or
XX screen for potential agents for treating immune disorders, particularly
XX inflammation, e.g. arthritis, septic shock, adult respiratory distress
XX syndrome, pneumonia, asthma, allergies, reperfusion injury.
XX atherosclerosis, Alzheimer's disease and cancer.
XX
SQ Sequence 1101 AA.
QY
QY Query Match 25.7%; Score 1467; DB 20; Length 1101;
QY Best Local Similarity 35.3%; Pred. No. 2,8e-130;
QY Matches 358; Conservative 179; Mismatches 352; Indels 126; Gaps 33;
QY
QY 107 NREKILNEIGFALIMPCEFDMPVQDPRRRLNLVWCKEAVLDRJNSHRAMY 166
DB 143 SEESQAFQQLTRALIGYDVTDSNVHDELEFRRLVPRRAEVSRD-----PKLYA 196
QY 167 YPENVSSEPLRGHYNKLDKQIIVIVWIVSPNNDKOKYTLKINHDCVPEQVIAEAR 226
DB 197 MHPWVTSKP-LPEYLMKTIANNCTFIVI-----HSTTSQITKVPSPDTPGAILQSF 249
QY 227 K-KTRSMILSSQQLCYLEIYQKYLIVCGDEYFLKRYPLSQYKYTRSCIMLGRMPN 284.
DB 250 KPAKKKSLMDIPES-----QSEODFVLVCGRDEYLVGETPIKNQWNRHCHLKEEETH 303
QY 285 LML-----MAKESLSQLP--DCFTMPSYRRTSTARPYNNG-----TSTSLWVINS 332
DB 304 VVLDPTRPALDBVKKEWPLVDDCTGVYGHQLT-----IHGKHESVFTVSLMDCOR 358
QY 333 ALRIKILCATYVNVNIRDID-----KIYRTGIYHGEPLCDNNTQVPCSNR 382
DB 359 KFRVRK-----IRGIDIPVLRPNDLTLYFVEANIGHGOOVLCQRTSPKPFEEVL 408
QY 383 NNEMLNLYDIYIDLPRAPLCLISGVK---GRKAKEHCEPLAMGNINLPDYDTLV- 437
DB 409 MWVWLEFSIKIDLPKGLNLQIYCGKAPALSSKASAPSSSESGKVRLLYVYVLLLI 468
QY 438 -----SGKMLNMPVPHGLE--LNPICVT-GSNPNKE-TPELEFPDFSSVVKF 486
DB 469 DHRPFLRGEYLVHMQISGKEGDEQSFADKULTATNPDKNSISITLIDNYCHPIL 528
QY 487 PDMSVIEEHANMSVSRAGFSYSHAGLSNRLARDELRENDKQOLRAICTRDPLEITEQ 546
DB 529 PKHQPTPDEGDRV-----RAEMPNQLR-----KQLEAIATPTPLNPLTAE 569

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QY 547 EKDFLMSHRHYCTIPEILLKLLSVKMSRDEVAQWCL-----VKDWPPIKPEQAMEI 601  
DB 570 DKELLHFRRESIKHFKAYFKLSSVWQGEIVAKTYQLARREYWDOSALDVLGTLMO 629  
QY 602 LDCNYPDPWVGFVRCLEKYLTDKLSOYLIOVLKYEQYLDNLVRFLLKALITNO 661  
DB 630 LDCNFDENRAIAYOKLES-LEDDDVLYLLOLVQAVKPEPYHDSALAFLLKRGIRNK 688  
QY 662 RIGHFFFWHLKSEM-HNKTVSQRFGLLSEYCRACGMYLKG-LNRQVEAMEKILNT-DI 718  
DB 689 RIGHFLFWFLRSEIAQSRHYQORFVILBAYLRGCGTAMLHDFTOOVQVLEMLQKVTLDI 748  
QY 719--LKOEKXDETOKY--OMKFLVEQMRPDMDALOGFLSPUNPAHQNLRLSECRIMSS 774  
DB 749 KSLSAEKYDVSSQVISOVKOLENLQNSOLPES---FRVYPDPGLKAGALAIKCKYMAS 805  
QY 775 AKRPLMLNWE--NPDIMSELLFONNE--IIFKNGDDLRODMLTLQIIRIMENTWONQL 829  
DB 806 KKKPLMEFPKCADPTALS-----NETIGIIFKHGDDLRODMLILQILRIMESIMETESL 859  
QY 830 DLRLMPYGLSIGDCVGLIEVVRNSHTIMQI-QCKGGLKALOPNSHTLHQMLKDN-KG 887  
DB 860 DLCLLPYGCISTGBKIMIEIVKDATTIAKIQOSTVANTGA--FKDEVILNHWLKEKSPTE 917  
QY 888 EIVYNAIDLFTRGAGYCVATFIILGIGRHSNIMVKDDGOLFHIIDFGHFLDHKKKKG 947  
DB 918 EKFOAAVERFYSCAGYCVATFVLGIGRHNNDIMITETGNLFHIDFGHILGNKXFLGI 977  
QY 948 KREVRPVLTDQFLIVISKAQECTKTRERFQEMCYKAYLAIRQANLFINLPSMMLG 1007  
DB 978 NKEVRPVLTPDFLFWMGTSKKTSP-HFOKFQDLCVKAYIALRHHHTNLILILFSWMLM 1035  
QY 1008 SCMPLOSFDIDIAIRKTLADKTEQEALEYFMKQMDAHNGCWTCKMDIETHI 1062  
DB 1036 TGMPLTSKEDIERYIDALTVGKNEEDAKKYFLDOI EVCRDKGWTQVOPNMFHLIV 1090

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Job time : 52 secs